```
                          GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on:         March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                          (without alignments)
                                          1134.946 Million cell
updates/sec

Title:          US-10-572-905-2
Perfect score:  4751
Sequence:       1 ggcacgagcgagttcctgtc.........taaaaaaaaaaaaaaaaaaa 783

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:     834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      7335755.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES

                    %
Result            Query
   No.    Score   Match Length DB  ID                          Description
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     1  2120.5   44.6   2120  1  US-10-478-914-64        Sequence 64,
Appl
     2    2106   44.3   3210  1  US-10-478-914-4         Sequence 4,
Appli
     3  2098.5   44.2   2437  1  US-10-478-914-61        Sequence 61,
Appl
  c  4    2041   43.0   3210  1  US-10-478-914-4         Sequence 4,
Appli
  c  5  2024.5   42.6   2120  1  US-10-478-914-64        Sequence 64,
Appl
     6    2015   42.4   2198  1  US-10-478-914-17        Sequence 17,
Appl
  c  7  2013.5   42.4   2437  1  US-10-478-914-61        Sequence 61,
Appl
     8  1995.5   42.0   3589  1  US-10-478-914-21        Sequence 21,
Appl
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  c   9   1983.5   41.7   2083   1   US-10-478-914-3      Sequence 3,
Appli
  c  10    1980    41.7   2198   1   US-10-478-914-17     Sequence 17,
Appl
     11    1979    41.7   1946   1   US-10-478-914-62     Sequence 62,
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  c  12    1943    40.9   2022   1   US-10-478-914-60     Sequence 60,
Appl
     13   1930.5   40.6   2495   1   US-10-478-914-20     Sequence 20,
Appl
  c  14   1925.5   40.5   2495   1   US-10-478-914-20     Sequence 20,
Appl
     15    1921    40.4   2336   1   US-10-478-914-57     Sequence 57,
Appl
  c  16   1893.5   39.9   2336   1   US-10-478-914-57     Sequence 57,
Appl
     17   1887.5   39.7   2083   1   US-10-478-914-3      Sequence 3,
Appli
  c  18   1870.5   39.4   3589   1   US-10-478-914-21     Sequence 21,
Appl
  c  19    1848    38.9   1813   1   US-10-478-914-63     Sequence 63,
Appl
     20    1845    38.8   1813   1   US-10-478-914-63     Sequence 63,
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  c  21   1826.5   38.4   1946   1   US-10-478-914-62     Sequence 62,
  c  22    1796    37.8    820   1   US-10-478-914-39     Sequence 39,
Appl
     23    1795    37.8    867   1   US-10-478-914-6      Sequence 6,
Appli
     24    1792    37.7    889   1   US-10-478-914-5      Sequence 5,
Appli
     25    1791    37.7    816   1   US-10-478-914-15     Sequence 15,
Appl
  c  26    1785    37.6    811   1   US-10-478-914-37     Sequence 37,
Appl
  c  27    1781    37.5    816   1   US-10-478-914-15     Sequence 15,
Appl
     28    1781    37.5   2022   1   US-10-478-914-60     Sequence 60,
Appl
  c  29    1770    37.3    867   1   US-10-478-914-6      Sequence 6,
Appli
     30   1759.5   37.0    794   1   US-10-478-914-13     Sequence 13,
Appl
  c  31   1755.5   37.0    938   1   US-10-478-914-69     Sequence 69,
Appl
     32   1745.5   36.7    839   1   US-10-478-914-16     Sequence 16,
Appl
     33    1740    36.6    717   1   US-10-478-914-42     Sequence 42,
Appl
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Appli
     35    1735    36.5    938   1   US-10-478-914-69     Sequence 69,
Appl
  c  36    1729    36.4    839   1   US-10-478-914-16     Sequence 16,
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  c  37    1724    36.3    778   1   US-10-478-914-35     Sequence 35,
Appl
     38   1715.5   36.1    909   1   US-10-478-914-66     Sequence 66,
Appl
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  c  39    1708   36.0    909  1  US-10-478-914-67        Sequence 67,
Appl
     40   1701.5  35.8   1020  1  US-10-478-914-68        Sequence 68,
Appl
  c  41    1696   35.7    889  1  US-10-478-914-9         Sequence 9,
Appli
  c  42   1695.5  35.7    794  1  US-10-478-914-13        Sequence 13,
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  c  43    1686   35.5    788  1  US-10-478-914-54        Sequence 54,
Appl
     44    1678   35.3    889  1  US-10-478-914-9         Sequence 9,
Appli
  c  45   1671.5  35.2    845  1  US-10-478-914-18        Sequence 18,
Appl
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ALIGNMENTS

RESULT 1
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match   44.6%; Score 2120.5; DB 1; Length 2120;
  Best Local Similarity   36.4%; Pred. No. 3.7e-115;
  Matches 514; Conservative   0; Mismatches 264; Indels 635;
Gaps   73;

Qy   1 GGCACGAGCG-----AGTTCCTGTCTC---TCTGCCAACGCC-----
GCCCGG------- 40
            ||| || || || |||| | | || ||| |||||
Db   83
GGCGCGGACGTGCCCGGTGCCTGGCGCGTGGTAGCAGGCGCCCGGTGCCCCGGCCGGCGA 142

Qy   41 -----ATGGCTTCCC-----AAAACC-------GCGACCCAGCCG-----
CCACTAGCGT 78
                 ||||| | | || ||| ||| ||||| | || |
|
Db   143 AGACCATGGCGTTCATGGTGAAGACCATGGTGGGCGG-
CCAGCTGAAGAACCTCACTGGG 201
```

```
Qy        79 CGCC------GCCGCCCG--TAAAGGAGCTG-------------AGCCGAG---
CGGGG- 113
                |||      || ||  | ||| |||| ||            |||||    |
|||
Db       202
AGCCTGGGAGGCGGCGAGGATAAGGGAGATGGGGACAAGTCGGCAGCCGAAGCTCAGGGC 261

Qy       114 --GCGCCGCCCGGGGTCCGGTGGGCAAAAG--GCTAC------------
AGCAGGAGC-T 156
               | ||||   || || ||  | | ||  || ||        || |||||
Db       262
ATGAGCCGGGAGGAGTACGAGGAGTATCAGAAGCAACTCGTGGAAGAGAAGATGGGAGCGG 321

Qy       157 GATGACC----CTCATGATGTCTGGCGATAAAGGGATTTCTGC-------
CTTCC----C 201
                ||||  |    | ||  | |||     || |     ||||      |||||
|
Db       322
GATGCACAGTTCACACAGAGGAAGGCAGAGCGGGCCACACTGCGGAGCCACTTCCGAGAC 381

Qy       202 TGAATCAGACAACCTTTTCAAATG---GGTAGGGACC--
ATCCA--------------- 240
               |  | | | |||     |    |   | |  | || |  |||||
Db       382
AAATACCGGCTACCCAAGAACGAGACAGATGAGAGCCAGATCCAGATGGCAGGTGGAGAC 441

Qy       241 -TGGAGC---------AGCTGGAACAGTATAT----GAAGAC-
CTGAGGTATAAG----- 280
               ||||||        |||||| || ||     || | |||| ||||   | |
Db       442
GTGGAGCTGCCCCGGGAGCTGGCCAAGATGATCGAGGAGGACACAGAGGAGGAGGAGGAG 501

Qy       281 -----CTC--TC------------GCTAGAGTTCC---------CCAGTGGCT-
ACCCTT 311
                   ||| ||             || || ||||           || | |||| || |
Db       502 AAGGCCTCAGTCCTTGGGCAGCTGGCCAGCCTTCCTGGCTTGAACCTG-
GGCTCACTCAA 560

Qy       312 --ACAATGCGC---CCACAGTGAAGTTCCTCACGCC--CTGC-------
TATCACCCCAA 357
                 |||| || |  ||||| || |  |||| ||  | ||       | ||||
||
Db       561
GGACAAGGCCCAGGCCACACTGGGGGATCTCAAGCAATCAGCTGAGGAAGTGTCACGTCAT 620

Qy       358 CGTGGACA----CCCAGGGTAACATAT--GCCTGGACATCC-TGAAGGAAAAGTG---
GT 407
                |||  ||     ||| |||| ||  |    | |||| |  || ||| ||  ||| |
||
Db       621 -
GTGACCACTTCCCCGGGGTTACCCACTGGGCTGGGCCCCCATGAGGGCTAAGAGTGTGT 679

Qy       408 C-------------------------------------------TGCCCTGT-
ATGATGTC 424
                |                                         ||||| | | |
|
Db       680
CAACTTCCAGGGACCCATACTCCATTTGGGGCTTTGTTTCCCTTGCCCCATCCTAGTTCC 739
```

```
Qy         425 AGGACCATTCTGCTCTCCAT--CCAGAGCCTT--------------------
CTAGGA 460
               | |||| |||   |   ||||| |||  ||||||                    ||
|||
Db         740 AAGACCTTTC--
CCATCCATGCCCCAAGCCTATCTTCTGGTTTCTTCCTCTCCGCTGGGA 797

Qy         461 GAA-----CCCAACATTGATAGTCCCTTGA-------ACACACATGCT--GCC----
GAG 502
               | |    |||| | |   |    ||||| |       | |||  ||| |||
|||
Db         798
GTAAAGTCCCCATCTTCACTCTACCCTTCAGGACCCTCCCCACCAGCTCAGCCTGTGGAG 857

Qy         503 --CTC----------TGGAAAAACCCCACAGCTTTTAAG----------
AAGTACCTGCA 540
                 |||          |||| | |||| || |   |           ||||
|||||| 
Db         858
GCCTCCCAAGATTGTAGGAATAGGCCCATCCCTCTCTGGCCATGGCCCCAAGTTCCTGCA 917

Qy         541 ---AGAAACCTACTCAAAG---------CAGGTCACC-------------------
AGCC 569
                  || |  |  | || ||         |||| |||                  ||
|
Db         918
CACAGGAGCACCCACAGAGAGACACACACAGGACACAAAACCCCTGGCACGTTCAGAGAC 977

Qy         570 AGGAGCC-CTGAC----CCAGGC----------------------------------
TGC 590
                  || |||| | |||    || |||
||
Db         978
AGAAGCCACAGACACATCCCGGCACAGACAGACACACACGAGGCCAGCTCCCTTGCGTGT 1037

Qy         591 CCAGCCTGTCCT-------------------------------------------- 602
               |||||| |||
Db        1038
CCAGCCCCTCCAGCACCACCACTCAGAAACTCTGAGAGAGAGCATGGGCAGACACCCTC 1097

Qy         603 ---------------TGTGT--------
CGTCTTTTTAATTTTT--------------- 623
                               || ||       |  |||| |  || ||
Db        1098
AGCAGACAGGAGGCCTGAGTTCCAGTCTCCACCTTTATTGTTCTTGAAAGCCCCTGCTCT 1157

Qy         624 -------CCTTAGAT-----------------GGTCTGTCCT------TTTTGTG---
AT 650
                      |||||  |                 ||  ||||||     || |  |
|
Db        1158
CTCTGAGCCTTATTTCATCATCTGTAAAATGGGAATGTCCTGAATGACTTCTAAGGCTCT 1217

Qy         651 TTCTGTATAGGACT-------------CTTTAT-----
CTTGAG--------------- 676
               ||||| | | |||             |  ||     |||| |
Db        1218
TTCTGGCTTGAACTGTCAGAGCCAAGCCCACATCCCTCCTTGGGCAGGGCAGCAGCTGCT 1277
```

```
Qy        677 -----------------------CTGTGGTATTT-------------
TTGTTTTGTTTTT 700
                             |||||| | |              || | |||
Db       1278
GCCACAGCCTCCAGCGGCTGCCACTGTGGGCTCTGGGAGCCGGAGCGATGCTGTGTGAGA 1337

Qy        701 GTCT----------------------TTTAAATTAA----------
GCCTCGGTTGAG 726
                | |                    |  | | ||| 
|
                                                           ||||| ||
Db       1338
GGCAGAGTGCCAAGGATGAAGCTGGCACTGAACAGTAAGCGGCTCCAGGCCTCCTCTGGG 1397

Qy        727 CCCTTG------------TATATTAAATAAATG------------------
CATTTTTG 755
                |||  |           | | ||   |   ||                 |||
||
Db       1398
CCCAGGGCCCAGCCAATTTCTGTTCTGTTCCTGTAGAACGCTCTCTGGATTCCATAGCTG 1457

Qy        756 -----TCCTTTTTAAAAAAAAAAAAAAAAAAA 783
                   |||| | ||| |   ||||| ||||
Db       1458 GAATCTCCTCTCTTAGCTCAGTGAAAAATAAAA 1490


RESULT 2
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match            44.3%;  Score 2106;  DB 1;  Length 3210;
  Best Local Similarity  36.8%;  Pred. No. 3.6e-113;
  Matches  478;  Conservative   0;  Mismatches  290;  Indels  530;
Gaps    63;

Qy          1 GGCACGAGCG--------AGTTCCTGTCTCTCTGCCAAC---------
GCCGCCCGGATG 43
                ||| |   ||         ||||| |   ||   || |       ||| || ||
||
Db        680
GGCCCATCCGCAACCTCACGTTCCAGGACCTTCACCTGCACCATGGAGGCCACCAGGCTG 739
```

```
Qy        44 GCTTCCCAAAACCGCGACCCAGC----CGCCACTAGC----GTC-
GCCGCCGCCCGTAAA 94
              |  |  |  |  | ||||| ||    |||||| ||    ||| ||| ||| ||
|
Db       740 CCAACAC-
CAGCCACGACCTGGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCAT 798

Qy        95 GG-----------------------AGCTGAGCC-------
GAGCGG------------- 111
             ||                        | |||| ||      |||||
Db       799
GGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCTCTACTGCTGC 858

Qy       112 ---------------GGGCGCCGCC----------CGGGGTCCGGTGGGCAAAAG-
GCTA 145
                            ||| || ||        | |||||| | ||| |
|||
Db       859
CTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGTCCATGGTGCCATGGAGCTG 918

Qy       146 CAG-------CAGGAGCTGATG-ACCCTC-------ATGATGT--------------
CTG 176
                |||     |||| |||| ||| ||      || |||              |
Db       919
CAGGTGCAGACAGGCAAAGATGCACCATCCAACTGTGTGGTGTACCCATCCTCCTCCCAG 978

Qy       177 GCGA-----------------------------
TAAAGGGGATTTCTG------------- 194
             | ||                              |   ||| | ||||
Db       979
GAGAGTGAAAGTAAGGGACCAACCTCTTGCCCCTTTTGGGTTCTCTGTTTTCTTCTGTCC 1038

Qy       195 ----CCT--------TCCCTG----------------------------
AATCAGA--- 210
                 |||        |||||                            |||||
Db      1039
TCATCCTGCACCCAGACCCTGTTTGGAACTCTGGCCTCATCACCCCAAGCCCTCAGAACC 1098

Qy       211 ----------CAACCTTTTCAAATG-GGTAGGGAC---------
CATCCATGGAGCAG-- 248
                      |  |||||||| || | |  |        | ||| ||| |||
Db      1099
CCCCGGTCCTCCTCCTTTTCTGCTGCTGCACATCCCTTCTGCTTCCTCCTTGGTGCAATC 1158

Qy       249 --CTGGAACAGTATATGAAGAC-------CTGAGGTATAAGCT--------
CTCGCTAGA 291
                | | | |    | |      |        ||| || | |||      ||| ||
Db      1159
CCCAGAAGCCCACTCTCCTTCCATCTGCTCTGGAGTCTCTGCTCTCTTGACTCTCTGGA 1218

Qy       292 ------GTTCC----------CCAGTGGCTA---C----CCT---------
TACAATGC 318
                    || ||          || |||| |   |    |||          |||
Db      1219
GTGGCTGTGCCTTGGCAGTGACCTTTGGCCAGGGCAAGTGCCTCATGACAGGTACTGGGT 1278
```

```
Qy        319 GCCC---
ACAGTGAAGTTCCTCACGCCCTGCTATCACCC--------------------- 354
              ||||    |||  |||| || |  ||  | | |||
Db       1279
GCCCCAGGCAGCTAAGTGCCGCCCTGCCCACCAGCCCCCTATGGCTTGGGAAGGCTGGGG 1338

Qy        355 --CAACGTGGACACCCAGG-GTAAC------------------------
ATATGCCTGGA 387
                | | ||| ||  | || | |||                       || |||
||
Db       1339
GTCCTCTTGGCCAACAGGGTGAAACCCCATCTCTACTAAAAACACAAAAATTAGCCAGG- 1397

Qy        388 CAT----------CCTGAAGG---------
AAAAGTGGTCTG----------------- 410
              |||          ||||| ||        ||| || |||
Db       1398 CATGGTGGTGCGCGCCTGTAGTCCCAGCTACTCAAGAGG-
CTGAGGCAAGAGAATCGCTT 1456

Qy        411 ---CCC---TGTATGATGT----------CAGGA-----
CCATTCTGCTCTCCATCC--- 446
                 |||    || || ||     ||  ||| |||| ||||| |
Db       1457 GAACCCGGGAGTCAGAGGTTGCAGTGAGCCGAGATCGCGCCA--
CTGCACTCCAGCCTGC 1514

Qy        447 ----AGAG-------CCTTCTAGGAGAACCCAACATTGATAGTCCCTTGAA------
CAC 489
                  ||||        || |||   | || ||||     |    | ||| |
||
Db       1515
TGATAGAGCAAGACTCCATCTCAAAAAAAACAACCCAAAATTTGCCTGGCATGGTGGCAG 1574

Qy        490 ACATGCTG----CCGAGCT----------CTGGAAAAACCCCACAGCTTTT-------
AA 528
                 ||| |||     || |||           ||| | |    | ||||
|
Db       1575 GCAT-
CTGTAATCCCAGCTACTCGGGAGGCTGAGACATGAGAGCTGCTTGAACCTGGGAG 1633

Qy        529 GAAGTACCTGCAAGAAACCTA---CTCAAAGCAGGTCACCAGCCAG-----------
GAG 574
                | || |  ||||  | || |  | ||   | |  ||||||| |
|||
Db       1634
GCAGAAGTTGCAGTGAGCCGAGATCACACCACTGCACTCCAGCCTGGGTGACAGAGCGAG 1693

Qy        575 CC-CTGACCCAG------------------------------------------
GCTGC 590
                | ||| ||||                                          |
|||
Db       1694
ACTCTGTCCCAAAAAAATCAAAAAAATCACTTTTGGTAGAGATGCACTCTCGCTATGTTGC 1753

Qy        591 CCAGCCTGTCCTTGTG-TC---GTCTTTTTAATTTTTCCTTAGATGGTCTGTCCT---
TT 643
                |||| |||  ||||   ||   | |||   |  | |||    || | |||
|
Db       1754 CCAGGCTGGTCTTGAACTCCTGGGCTCAATTGATCTTCCCACCTTGACC--
TCCAAAGTG 1811
```

```
Qy        644 TTGTGATTTCT-GTATAGGACTCTTTATCTTGAGCTGTGGTATTTTTGT--------
TTT 694
               || |||| |  || |  | | |  |  || |      || ||| || |          |
|
Db        1812
CTGGGATTACAGGTGTGAGCCACCATGCCTAGCCTCAGGGAATTCTTATAAGAACTCTAT 1871

Qy        695 GTTTTTGTCTT-------TTAAATTAAGCCTCGGT---
TGAGCCCTTGTATATTAAATAA 744
               |  | | | |        ||   |  | || ||    ||| ||| |      | ||
Db        1872 GAAGTAGGCATCACCATCTTCTCTGTATCCATGGAAAGAGAGGCCTAG------
AGATGT 1925

Qy        745 ATGCATTTTTGTCCTTTTTTAAAAAAAAAAAAAAAAAAA 782
               ||||    ||| ||    | | | |     |      |  |
Db        1926 ATGCTAACTTGCCCAAGCTCACATAGCCCAGGGTAGCA 1963


RESULT 3
US-10-478-914-61
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match            44.2%;  Score 2098.5;  DB 1;  Length 2437;
  Best Local Similarity  37.1%;  Pred. No. 2.1e-113;
  Matches  522;  Conservative   0;  Mismatches  253;  Indels  631;
Gaps   78;

Qy          1 GGCAC--GAGCGAGTT----CCTGTCTCTCT----------GCCAACGCCGCCC--
GGAT 42
               | ||| | | ||||| |   || | | |  |          ||||| || |||| ||
Db        321 GTCACCTGCGAGAGTTCGAGCCCGACGCAATTGGTGGTGGAGCCAA-
GCAGCCCAAGGCA 379

Qy         43 G------------GCTTCC----------CAAAACCGCG----
ACC-------------C 63
               |              ||| ||         |  |||| |      ||
|
Db        380
GTGTTTGTGCTGAGCTGCCTGCTGAAAGGCCGGACCGTGGAGATCCTACGGGACATCATC 439
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```
Qy        64 AGCCGC---CACTAGC--------------GTCGC------------
CGCCGCCCGTAAA 94
             |||||  ||||  |              ||| |           ||| | ||
Db       440
TGCCGCAGTCACTTCCAGTATTGTGTGGTGGTCACAACCGTGAGCCACGCTGTCCACCTC 499

Qy        95 GGAGCTGA-----GCCGAGCGGGGGCGCCGCCCGGGGT-------------
CCGGTGGGC 136
              ||||  |       || ||||| |||  || ||| |              ||||||
|
Db       500
ACAGCTAATCATGTCCCAGCGGCGGCAGCGGCCGAGATGGAGGGGCAGCAGCCGGTGTTC 559

Qy       137 AAAAGGCTACAGCAGGAGCT---------GATGACCCTCATGATGT---
CTGGCGA---- 180
              |  ||| || || |||       |||| | ||||| |  | | |||
Db       560
GAGCAGCTGGAGGAGAAGCTGTGTGAATGGATGGGCAACATGAACTACACGGCCGAGGTG 619

Qy       181 -------TAAAGGGATTTC-TGC--------CTTCCC---------
TGAATCAGAC---- 211
              |   |  ||| | |||      || |||       ||| ||   |
Db       620
TTCCATGTCCCGTTATTGCTTGCCCCTGTTGCTCCCCACTTTGCCTTGACTCCAGCTTTT 679

Qy       212 ---AACCTTTT-CAAATG--------GGTAGGGACCATCC---ATGGAG--
CAGCTGGAA 254
              |||||| | | ||        || | |  | ||| || | | |
Db       680
GCATCCCTTTTCCCACTGCTACCCCAGGATGTGCACCTCCTTAATAGCGCCCGACCGGAC 739

Qy       255 CAGTATATGAAG----ACCTGAGGTATAAG--CTCTCGCTA-
GAGTTCCCCAGTG----- 302
              ||  | | |   |||| |  || |  |  ||||| |
Db       740 AAGAGGAAGCTGGGAAGCCTGGGTGATGTGGACTC-
CACTACGCTAACCCCAGAGCTGCT 798

Qy       303 GCTACCCTTACAATGC----------GCC------
CACAGTG------------------ 328
              ||| |  | ||||     | | |||
Db       799
GCTGCAGATCAGATGCCTAGTGTCAGGCCTCAGTTCTCTGTGTGAACATTTAGGAGTACG 858

Qy       329 ------------------AAGTTCCTCACGCC---------CTGC-
TATC---------- 350
              | |||||| | |        |||| |||
Db       859
GGAGGAGTGTTTTGCTGTAGGTTCCTTAAGTCAGGTCATCGCTGCGGATCTGGCCAATTA 918

Qy       351 -ACCCCAAC---------------------------------------------
GTGGA 363
              ||||  |
|||||
Db       919
TGCCCCTGCAAAGAACAGGAAGAAGACTGCTGCAGGCAGGGCATCAGTGGTTTTTGTGGA 978

Qy       364 C---ACCCAGGGTAACATA--TGCC--TGGACATCCTGAAG-----------
GAAAAG-- 403
              |  |||| || | |  || |   ||  |||||||| || ||        || |||
```

```
Db        979
CAGAACCCTGGATCTCACAGGAGCAGTTGGACATCATGGAGACAACTTAGTAGAGAAGAT 1038

Qy        404 --------------------------------------------
TGGT----------- 407
                                                            ||||
Db        1039
CATTTCAGCACTTCCCCAGCTCCCAGGCCACACAAATGATGTGATGGTTAACATGATAGC 1098

Qy        408 -----CTGCCCT------------------GTATGATGT--------
CAGG--------- 427
                  |||| ||                   ||| ||||         ||||
Db        1099
GCTCACTGCACTCCATACTGAGGAGGAAAATTATAATGTGGTTGCACCAGGCTGTCTTTC 1158

Qy        428 ACCATTCTG---CTCTCCATCCAGAGCCTTCTAGGA---------
GAACCCAA------- 468
                  || |||| |    | |   || ||| |||| | | |||         |||| | |
Db        1159
ACAATTCAGTGACACCACAGCCAAAGCCCTATGGGAAGCTTTACTGAACACTAAGCACAA 1218

Qy        469 -----CATTGATAG-------------TCCCTTGAACAC-ACATG----------
CTGCC 499
                       || |||| |              ||    || |  |  || |
                |||||
Db        1219
AGAGGCAGTGATGGAAGTTCGGAGACATCTAGTGGAAGCGGCAAGCAGAGAAAACCTGCC 1278

Qy        500 GAGC--------TCTG----GAAAAACCCC---ACAGCT--TTTAAGAAGTAC----
CTG 538
                  | |        | ||    ||   || ||  ||||||| | | |   | | | |
                ||
Db        1279
AATCAAGATGAGTATGGGGAGAGTCACACCGGGACAGCTCATGTCCTATATTCAGCTCTT 1338

Qy        539 CAAGAAACCTACTCAAAGC---------------AGG---TCACCAGCCAGGA---
GCCC 577
                  |||| |||   |||||||||                   ||    | ||||| |||
                |||
Db        1339 CAAG-
AACAACCTCAAAGCTCTAATGAATCATTGTGGCCTCCTCCAGCTTGGACTGGCCA 1397

Qy        578 TGACCCAGGC--TG-------CCCAGCCTGTCCTTGT--
GTCGTCTTTTTAATTTTT--- 623
                  | || | | ||       | ||| ||| || | | | | |  |||| |   ||||
Db        1398 CAGCTCAAACGTTGAAACACCCACAGACTG-
CCAAGTGGGACAACTTTCTGGCTTTTGAA 1456

Qy        624 -----------------CCTTAGATGGTC-----
TGTCCTTTTTG--------------- 646
                                 | || |||    ||||| ||| |
Db        1457
AGGGCTCCTTCTTCAGAGCATTGGGGAGTCAGCAATGTCCGTTGTGTTAAATCAGCTGCTG 1516

Qy        647 ----TGATTT---CTGTAT---------------AGGACTCTTTATCT--TGAGCTG-
TG 681
                      |||||    |||||                |||||||     || |  || |||
                ||
Db        1517
CCCATGATTAAGCCTGTAACCCAGAGAACCAACGAGGACTACAGCCCTGAGGAACTGCTG 1576
```

```
Qy        682 GTATTTTTGTTTTGTTTTGTCTTTTAAAT--TAAGC-CTCGGTTG----
AGCCCT---- 730
                  |  || |  | | ||| |  | | |    ||| | |||| |   || |||
Db       1577
ATCCTTCTCATATATATTTATTCTGTCACTGGAGAGCTCACGGTAGACAAAGACCTGTGT 1636

Qy        731 --------TGTATATTAAATAAATGCATT-------------------------
TTTG 755
                      | | |    |  || |||||
                      |||
Db       1637
GAAGCAGAAGAAAAAGTCAAGAAAGCATTGGCTCAGGTCTTCTGTGAGGAATCTGGATTG 1696

Qy        756 T--CCTTTTTAAAAAAAAAAAAAAA 779
                  |  ||||| |  ||||||| |  |
Db       1697 TCACCTTTGCTGCAAAAAATTACGGA 1722


RESULT 4
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match            43.0%;  Score 2041;  DB 1;  Length 3210;
  Best Local Similarity  35.1%;  Pred. No. 4.5e-109;
  Matches  508;  Conservative   0;  Mismatches  249;  Indels  692;
Gaps   82;

Qy         2 GCACGAGCGAGTTCCTGTCTCTCTGCCAACGC---CGCCCGGAT---GGC--
TTCCCAAA 53
                 |||   ||| | ||  | ||| |||| | |  |  | ||||| |   || ||| |
Db       1502 GCAGTGGCGCGATCTCGGCTCACTGCAACCTCTGACTCCCGGGTTCAAGCGATTCTC-
TT 1444

Qy        54 ACCGCGACC-------CAGCCG---CCACTAGCGT-CGCCGCC--
GCC------------ 88
                 || |  ||        ||| |  | || |||  | || ||  |||
Db       1443
GCCTCAGCCTCTTGAGTAGCTGGGACTACAGGCGCGCACCACCATGCCTGGCTAATTTTT 1384
```

```
Qy         89 --------CGTAAAGGAG----------CTG--
AGCCGAGCGGGGGCGCCGCC------- 121
                    ||| || |          |||   ||| || ||   | | |||
Db       1383 GTGTTTTTAGTAGAGATGGGGTTTCACCCTGTTGGCCAAGAGGACCCCCAGCCTTCCCAA 1324

Qy        122 -----CGGGGTCCGGTGGGCAAAAGGCTAC----AGCAGGAGCTGATG-
ACCC------- 164
                   |||| | ||||||| | |||  |   ||| |   ||| | |||
Db       1323 GCCATAGGGGGCTGGTGGGC--AGGGCGGCACTTAGCTG--
CCTGGGGCACCCAGTACCT 1268

Qy        165 -TCATGATG-TCTGGC----GATAAAGGGATTTCTGCCTT--CCCTGAATC-------
AG 209
                  |||||| | || ||   |  ||||| | |||||   | | |   |
||
Db       1267 GTCATGAGGCACTTGCCCTGGCCAAAGG--
TCACTGCCAAGGCACAGCCACTCCAGAGAG 1210

Qy        210 ACAA--------------CCTTTTCAAATGGGTAG-----GGAC-------------
CATC 238
                   |||            || | || |||| |   || | 
   ||
|
Db       1209 TCAAGAGGAGCAGAGACTCCAGAGCAGATGGAAGGAGAGTGGGCTTCTGGGGATTGCA-C 1151

Qy        239 CATGG----AGCA----------GCTGGAACAGTAT---ATGAAGACCTGAGG--
TATAA 279
                   || ||   ||||        || | || ||  |  | || |||| | ||  | |
|
Db       1150 CAAGGAGGAAGCAGAAGGGATGTGCAGCAGCAGAAAAGGAGGAGGACCGGGGGGTTCTGA 1091

Qy        280 GCTCTC-----------
GCTAGAGTTC------------------------------- 295
                   | || |||       || ||||||||
Db       1090 GGGCTTGGGGTGATGAGGCCAGAGTTCCAAACAGGGTCTGGGTGCAGGATGAGGACAGAA 1031

Qy        296 ------------CCC---AGTGGCTA---------
CCCTTAC----------------- 313
                    |||   || ||| |      ||||||||
Db       1030 GAAAACAGAGAACCCAAAAGGGGCAAGAGGTTGGTCCCTTACTTTCACTCTCCTGGGAGG 971

Qy        314 ------AATGCGCC-CACAG---------------------------
TGAAGTTCCT 336
                   | | || |||||                        || ||
|||
Db        970 AGGATGGGTACACCACACAGTTGGATGGTGCATCTTTGCCTGTCTGCACCTGCAGCTCCA 911

Qy        337 ---CAC-----GCCCTG-------------------CT-ATCACCCCAAC---------
GT 360
                   |||     |||||             || ||| || || 
||
Db        910 TGGCACCATGGCACCCTGTGCTCCGAGTGGTGGTGCCTGATCTCCACCACCAGGCAGCAGT 851

Qy        361 GGACACC---------CAGGGTAA-------CAT-------------ATGCC----
```

```
                          TGGA 387
                                        ||  ||        ||||| |      |||             ||||
                          |||
                          Db      850
                          AGAGGCCGCTATCCAGCAGGGTCAGGTTGCGCATGGTGATGGAGAAGTTGCCATGGTGGT 791


                          Qy      388 C---------ATCC-----------------------------------
                          TGAAGGAAAAGT 404
                                      |          |||                             ||   |
                          ||
                          Db      790
                          CGGAGGCCGACTCCAGCCCGTGGCGCTGAGCCAGGTCGTGGCTGGTGTTGGCAGCCTGGT 731


                          Qy      405 GGTCTGC-----------------CCTGTAT------------GATG---------
                          TCAG 426
                                      ||  || |                ||||  |          ||||            ||
                          |
                          Db      730
                          GGCCTCCATGGTGCAGGTGAAGGTCCTGGAACGTGAGGTTGCGGATGGGCCGGCGCTCTG 671


                          Qy      427 GACCATTCTGCTCTCCATCC--AGAGC-------------
                          CTTCTAGGAGAACCCAACAT 471
                                      |  ||||| |  ||  ||||            ||| ||| ||  | || |
                          |
                          Db      670
                          AGCAGGTCTGCACCTCGCCCCTCGAGCTGCGGTACCACGTCTTGTAGAAGGTCACATCGT 611


                          Qy      472 TGATAGTCCCTTGAACACA-----CATG---CTGCCG----------
                          AGCTCTGGAAAAA 513
                                      | || |||  ||||      || |  |||| |            | ||||
                          Db      610 -----
                          GCCCTTTGTCCACAGGGCCCAAGAGCCTGCAGGTGAGGGTGACGTTCTG------ 562


                          Qy      514 CCCCACAG------CTTTTAAGAAGTAC-------------------CTG-
                          CAAGAAACC 547
                                      |||| | |       | |  | | ||||              ||| ||
                          |||
                          Db      561
                          CCCCTCGGGACAGACATACAGGGAATACGGCGTGGCGACCTTGAAGGCTGCCACCGGACC 502


                          Qy      548 TACTCAAAG----------CAGGTCACCAGCCAG-----GAGC----CCTG----
                          ACCCA 584
                                      | |||| ||          |  |||||| | | |      | ||    ||||
                          ||||
                          Db      501
                          TGCTCAGAGAGAGGAGAGCCCTGTCACCTGACTGATCCAGTGCTACTCCTGGCAACCCCA 442


                          Qy      585 G------------------------GCTGCCCAGC---------------------
                          CT 597
                                      |                        || ||||||
                          ||
                          Db      441
                          GAGCGGGGAAGAACCTTAGCCTCTGCTACTTCCCAGCCACAGGCCAGGGGCATGTCAGCT 382


                          Qy      598 GTCCT---TGTGTC-GTCTTTTTAATTT------------------
                          TTCCTTAGATG--- 632
                                      | |||   | | | | ||| |  ||||             |||| | ||
                          Db      381
                          GACCTCCCTAAGACTGCCTTCTGCATTTGTTCACAAACCCCACTCCATCCTAGGCTGTTG 322
```

```
Qy        633 --------GTC---------TGTCCTTTTTG---------
TGATTTCTGTATAGGAC--- 663
                       |||         |   ||    |  |         ||   |  ||| |  ||| |
Db        321
TAGGGGGAGTCACAGAAGCTTCCCCAACTAGGGGTGCTCCTGGATGCTGGACAGGGCAGG 262


Qy        664 -----
TCTTTATCTTGAGCTGTGGTATTTTTGTTTTGTTTTTGTCTTTTAAATTAAG--- 715
                       |||       |  ||  ||| |      |  |   ||| |   ||||   |  |  ||
Db        261 GAGAGACTTGG---AGGGCAGTGATGCAGTCG-
GGTGTGTCCCTCTTCCCAGTAGAGTAT 206


Qy        716 --------CCT-------------CGGTTG--------------------------
AG 726
                            |||                 |||||
||
Db        205
ATGCAAAACCTGTTGGGTGGGAGGCAGGTTGGGGAGCAGGAAGGCTGTTTCGAACAGCAG 146


Qy        727 C-CCTTGTATAT------TAAATAAATGCATT-------
TTTGTCCTTTTTTAAAAAAAA 772
                       |  ||||||    |        |    ||    ||   |        |  ||  ||  ||   ||
Db        145
CTCCTTGTCCTTGGCCGCTCTGTAGGGGCCATCAACACCTCTGCCCCTTCCTACTCCTAG 86


Qy        773 AAAAAAAAA 781
                       |    ||  |
Db         85 GACTGAACA 77



RESULT 5
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match             42.6%;  Score 2024.5;  DB 1;  Length 2120;
  Best Local Similarity   41.8%;  Pred. No. 4.2e-109;
  Matches  472;  Conservative   0;  Mismatches  297;  Indels  359;
Gaps   64;
```

```
Qy          1 GGCAC------------
GAGCGAGTTCCTGTCTCTCTGCCAAC----------------- 31
              ||| |              |||| || |||| ||  ||||| |
Db       1399 GGCCCAGAGGAGGCCTGGAGCCGCTTACTGT-
TCAGTGCCAGCTTCATCCTTGGCACTCT 1341


Qy         32 GCCGCCCGGATGGCTTC---CCAAAACCGCGA-CCCA-----
GCCGCCACTAGCGTC--- 79
              ||| | |   |  || ||   ||     ||  || ||||     || ||| || | | |
Db       1340 
GCCTCTCACACAGCATCGCTCCGGCTCCCAGAGCCCACAGTGGCAGCCGCTGGAGGCTGT 1281


Qy         80 ---------GCCGCC--GCCCGTAAAG------GAGCTGAGC----------
CGAGC-- 109
                        || ||| ||||   ||       | ||| ||          | |||
Db       1280 
GGCAGCAGCTGCTGCCCTGCCCAAGGAGGGATGTGGGCTTGGCTCTGACAGTTCAAGCCA 1221


Qy        110 GGGGGCGCC------GCC---CGGGG---TCC---------GGTG--
GGCAAAAGGCT-- 144
              |  | |||      | |  | ||    |||         | ||  | | ||||||
Db       1220 
GAAAGAGCCTTAGAAGTCATTCAGGACATTCCCATTTTACAGATGATGAAATAAGGCTCA 1161


Qy        145 ---ACAGCAGGAGC-------------------TGATGAC----
CCTCATGATGTCTGGCG 179
                 | ||||||| ||                 || |||    |||| |    |||
|
Db       1160 
GAGAGAGCAGGGGCTTTCAAGAACAATAAAGGTGGAGACTGGAACTCAGGCCTCCTGTCT 1101


Qy        180 ATAAAGGGATTTCTGCC--TTCCCTGAATCAGACAACCT---------
TTTCAAATGGGT 228
              |||| | |||||| | | ||  ||||| || | | |
|||
Db       1100 GCTGAGGG-
TGTCTGCCCATGCTCTCTCTCAGAGTTTCTGAGTGGTGGTGTCTGGAGGGG 1042


Qy        229 AGGGACCATCCATGGAGC----------------------
AGCTGGAA------------ 254
              ||||  | | |||||               || || |
Db       1041 
CTGGACACGCAAGGGAGCTGGCCTCGTGTGTGTGTCTGTCTGTGCCGGGATGTGTCTGTGGC 982


Qy        255 --CAGTATATGAA--GACCTGAGGTATAAGCTCTCGCTAGAGTTCCCCAGTGGCTAC-
CC 309
              | || | |||   || | |||| |   || |   | || | | |||| | |
||
Db        981 
TTCTGTCTCTGAACGTGCCAGGGGTTTTGTGTCCTGTGTGTGTCTCTCTGTGGGTGCTCC 922


Qy        310 T---TACA-----ATGCGCCCA----CAGTGAAG----------
TTCCT----------- 336
              |   |  | ||    || | ||| |   ||| || |        |||||
Db        921 
TGTGTGCAGGAACTTGGGGCCATGGCCAGAGAGGGATGGGCCTATTCCTACAATCTTGGG 862


Qy        337 -------CAC--------------------GCCCTG----------------------
CT 347
                     |||                    | ||||
```

```
        ||
Db         861
AGGCCTCCACAGGCTGAGCTGGTGGGGAGGGTCCTGAAGGGTAGAGTGAAGATGGGGACT 802

Qy         348 ATCACCCCAACGTGGA-----CACCCAGGGTAACATATGCCT-
GGACATCCTGAAGGAAA 401
                |   ||||| ||  ||      |  | ||||   || ||| || | || |||   || ||
        ||
Db         801 TTACTCCCAGCGGAGAGGAAGAAACCAG---AAGATAGGCTTGGGGCAT--
GGATGGGAA 747

Qy         402 AGTGGTCT---------------------------GCCCTGTATGATGTCAGG--
ACC 430
                 |  |||||                         ||||    |||  ||  ||
        ||
Db         746 A--
GGTCTTGGAACTAGGATGGGGCAAGGGAAACAAAGCCCCAAATGGAGTATGGGTCCC 689

Qy         431 ATTCTGCTCTC-CATCCAGAGCCTTCTAGGAGAACCCAAC---
ATTGATAGTCCCC----- 481
                | | | || | ||||  ||   || || ||||  |   | ||  |||
Db         688 TGGAAGTTGACACACTCTTAGCCCTCATGG-
GGGCCCAGCCCAGTGGGTAACCCCGGGGA 630

Qy         482 -TTGAACAC---ACATG---CTGCCGAGCT-----CTGGAAAAACCCCA---
CAGCTTTT 526
                 || |||  || || | ||  | |||||   || | ||| |||||    || |
Db         629 AGTGGTCACATGACGTGACACTTCTCAGCTGATTGCTTGAGATCCCCCAGTGTGGCCTGG 570

Qy         527 AAGAAGTACCTGCAAGAAACCT-ACTCAAAGCAGGTC-ACCAGCCAGGAGCCCT--
GACC 582
                 || | ||   ||  | |||||| |||| ||   | |||||  |||||| ||||
Db         569 GCCTTGTCCTTGAGTGAGCCCAGGTTCAAGCCAGGAAGGCTGGCCAGCTGCCCAAGGACT 510

Qy         583 CAGG-CTGCCCAGCCT-GTCCT-TGTGTCGTCTT--TTTAATTTTTCCTTAGAT----
GG 633
                 ||| || ||  | ||| |||| |||||| || | | ||  || || ||
        ||
Db         509 GAGGCCTTCTCCTCCTCCTCCTCTGTGTCCTCCTCGATCATCTTGGCC--
AGCTCCCGGG 452

Qy         634 TCTG-TC-----CTTTTTGTGATTTCTGTATAGGACTC---
TTTATCTTGAGCTGTGGTA 684
                 | | ||      || |     ||  |||| || | |||   | | ||| | ||
        ||||
Db         451 GCAGCTCCACGTCTCCACCTGCCATCTGGATCTGGCTCTCATCTGTCTCGTTCTTGGGTA 392

Qy         685 -----
TTTTTGTTTTGTTTTTGTCTTTTAAATTAAGCCTCGGTTGAGCCCTTGTATATTA 739
                 | |||||| | ||   || || |  |  | ||  |  | ||| | | | |
Db         391 GCCGGTATTTGTCTCGGAAGTGGCTCCGCAGTGTGGCC-C-
GCTCTGCCTTCCTCTGTGT 334

Qy         740 AATAAATGCATTTTTGTCCTT----TTTTAAAAAAAAAAAAAAAAAAAAA 783
                 |  ||||| |||   ||| | |   | |  | |            | |
Db         333 GAACTGTGCATCCCGCTCCATCTTCTCTTCCACGAGTTGCTTCTGATA 286
```

RESULT 6
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match   42.4%; Score 2015; DB 1; Length 2198;
  Best Local Similarity 37.3%; Pred. No. 2.1e-108;
  Matches 529; Conservative   0; Mismatches 236; Indels 652;
Gaps   83;

Qy   2 GCACGAGC---GAGTTCCTGTCTCTCTGCCAACGCC---GCCCG------
GATGGCTTCC 49
             | ||| || | || || ||||| ||| | || ||| | ||| |
|||
Db   765 GAACGTGCTAAGCGTACC---
CTCTCTTCCAGCACCCAGGCCAGTATTGAGATCGATTCT 821

Qy   50 C---------AAAACCGCGACCCAGCCGCCACTAGCGTCGCCGCCGCCCG--
TAAAGGAG 98
             | || | | || ||| || | ||| ||||| | |
||
Db   822 CTCTATGAAGGAATCGACTTCTATACCTCCATTA----C-CCG-
TGCCCGATTTGAAGAA 875

Qy   99 CTGA--GCCGAGCGGGGGCGC--CGCCCGGGGTCCGGTGGGCAAAAGGCTAC-
AGCAG-- 151
             |||| || || | | || | ||| || || || | ||| || | || |
Db   876
CTGAATGCTGACCTGTTCCGTGGCACCCTGGACCCAGTAGAGAAAGCCCTTCGAGATGCC 935

Qy   152 GAGCTG---ATGACCC----TCATGATGTCTGGCGATAAAGGGATTTCTGC----
CTTCC 200
             | || | | | | ||||||| | || | || | |||| | |
||
Db   936 AAACTAGACAAGTCACAGATTCATGATAT-
TGTCCTGGTTGGTGGTTCTACTCGTATCCC 994

Qy   201 C-TGAATCAGA-----CAAC----CTTTTCAAATGGGTAGGGAC-------------
CAT 237

```
                    |  ||  |||||      |   |     |||  |  |||||   |  ||
       ||
Db    995
CAAGATTCAGAAGCTTCTCCAAGACTTCTTCAATGGAAAAGAACTGAATAAGAGCATCAA 1054

Qy     238 CC------------------ATGGAGCAGCTG---GAACAG------
TATATGAAGAC-- 268
                    ||                ||||  |||||||    |||     |  |  ||  |||
Db    1055
CCCTGATGAAGCTGTTGCTTATGGTGCAGCTGTCCAGGCAGCCATCTTGTCTGGAGACAA 1114

Qy     269 --CTGAG---GTATAA--------GCTC-------
TCGCTAGAGTTCCCC---------- 298
                     |||||   ||  ||         ||||       ||  ||     ||  |||
Db    1115
GTCTGAGAATGTTCAAGATTTGCTGCTCTTGGATGTCACTCCTCTTTCCCTTGGTATTGA 1174

Qy     299 -------AGTGG--------CTACCCTTACAATGCG-------------
CCCACAGTGAA 330
                        ||||        ||  |||  |  | |||            ||  ||     |
Db    1175
AACTGCTGGTGGAGTCATGACTGTCCTCATCAAGCGTAATACCACCATTCCTACCAAGCA 1234

Qy     331 GT-----TCC-TCACGCCCTG--CTATCACCCCAAC--
GTGGAC---------------- 364
                        |    || ||||  |||    ||  ||  ||    |  |||  |
Db    1235
GACACAGACCTTCACTACCTATTCTGACAACCAGCCTGGTGTGCTTATTCAGGTTTATGA 1294

Qy     365 ----------------ACCCAGGGTAACAT-
ATGCCTGG---------------------- 386
                                  ||  |||  |||||    |||  |||  || ||
Db    1295
AGGCGAGCGTGCCATGACAAAGGATAACAACCTGCTTGGCAAGTTTGAACTCACAGGCAT 1354

Qy     387 ACATCCTGAAGGAAAAGTGGTCTGCC-CTGTATGATGTC-------------
AGGACCAT 432
                    ||  |||||  |   ||  |  | | |  ||  |  |||          |  |
       ||
Db    1355 ACCTCCTGCA--
CCCCGAGGTGTTCCTCAGATTGAAGTCACTTTTGACATTGATGCCAAT 1412

Qy     433 ---------------TCTGC-------------------------------------------
TC 439
                                   |||||
       ||
Db    1413
GGTATACTCAATGTCTCTGCTGTGGACAAGAGTACGGGGAAAAGAGAACAAGATTACTATC 1472

Qy     440 TCCA---TCCAGAGCCTT-----CTAGGA-------GAAC-------
CCA---------- 467
                     |  |    | || ||| |    | ||||       ||||       |||
Db    1473
ACTAATGACAAGGGCCGTTTGAGCAAGGAAGACATTGAACGTATGGTCCAGGAAGCTGAG 1532

Qy     468 ----ACATTGAT-------------------------AGTC--
CCTTGAACACACATG-- 494
                    |||  | |                          |||  ||  |||  ||| ||
Db    1533
```

```
AAGTACAAAGCTGAAGATGAGAAGCAGAGGGACAAGGTGTCATCCAAGAATTCACTTGAG 1592

Qy        495 ----CTGCC----------GAGC-TCTG-------GAAAAACCCCACAGC---
TTTTA- 527
                |||          |||  |||       || |||| || ||     ||
|
Db   1593
TCCTATGCCTTCAACATGAAAGCAACTGTTGAAGATGAGAAACTTCAAGGCAAGATTAAC 1652

Qy        528 -------------AGAAGTACCTG-----------------------------
CAAG 542
                             |||||  |||
|||
Db   1653
GATGAGGACAAACAGAAGATTCTGGACAAGTGTAATGAAATTATCAACTGGCTTGATAAG 1712

Qy        543 AAACCTACT-CAAAGCAGG-------------TCACCAGC-----
CAGGAG--------- 574
                || | ||| | || |||        ||| |||     | ||||
Db   1713
AATCAGACTGCTGAGAAGGAAGAATTTGAACATCAACAGAAAGAGCTGGAGAAAGTTTGC 1772

Qy        575 -------------CC---CTGACCCAGGCTGC----------CCA--------
GCCTG-- 598
                            ||   |||  |||| |||           |||        |||||
Db   1773
AACCCCATCATCACCAAGCTGTACCAGAGTGCAGGAGGCATGCCAGGAGGAATGCCTGGG 1832

Qy        599 -----TCCTTGTG-------TCGTCTTTT---
TAATTTTTCCTTAGATGGTCTGTCCTTT 643
                  |||| |||   || | |    | |  ||||| ||  || |
||
Db   1833 GGATTTCCTGGTGGTGGAGCTCCTCCCTCTGGTGGTGCTTCCTCAG--
GGCCCACCATTG 1890

Qy        644 TTGTGATTTCT------------GTATAGG--------------ACTCTTT---
ATC--T 672
                | | ||| |           || |||              || | || | |
|
Db   1891
AAGAGGTTGATTAAGCCAACCAAGTGTAGATGTAGCATTGTTCCACACATTTAAAACATT 1950

Qy        673 TGAG----------------------CTGTGGTATTTTT-----GTTT---
TGTTTTTGT 702
                |||                   |||||| | ||||     |||   || ||
||
Db   1951
TGAAGGACCTAAATTCGTAGCAAATTCTGTGGCAGTTTTAAAAAGTTAAGCTGCTATAGT 2010

Qy        703 ----------------------CTTTTAAATTAAGC-----
CTCGGTTGA---------- 725
                                      ||| | ||| | |     | | | ||
Db   2011
AAGTTACTGGGCATTCTCAATACTTGAATATGGAACATATGCACAGGGGAAGGAAATAAC 2070

Qy        726 ---GCCCT----------TGTATATTAAAT---AAATGCATTTTTGTC----------
CT 759
                   || ||          ||||| ||| |   ||||||||    ||||
||
Db   2071 ATTGCACTTTATAAACACTGTATTGTAAGTGGAAAATGCA---
```

```
ATGTCTTAAATAAAACT 2127

Qy        760 TTTT------------TAAAAAAAAAAAAAAAAAAA 783
              |||              |||||||||||||||||||
Db       2128 ATTTAAAATTGGCACCATAAAAAAAAAAAAAAAAAAA 2164


RESULT 7
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

   Query Match             42.4%;  Score 2013.5;  DB 1;  Length 2437;
   Best Local Similarity   38.1%;  Pred. No. 4.7e-108;
   Matches  509;  Conservative    0;  Mismatches  254;  Indels  573;
Gaps    80;

Qy         1 GGCACGAGCGAGTTCC----TGTCTCTCTGCCAACGCCGCCCGGATGGC-----
TTCCC- 50
             | || |||| ||| ||    || ||||| |  || |  |  | |||    |||
|
Db      1323 GACATGAGC-
TGTCCCGGTGTGACTCTCCCCATACTCATCTTGATTGGCAGGTTTTCTCT 1265

Qy        51 -AAAACCGCGACC-----CAGCCGCC--
ACTAGCGTCGCCGCCGC--------------- 87
               |||| || | |   | || ||| | || | ||| |
Db      1264
GCTTGCCGCTTCCACTAGATGTCTCCGAACTTCCATCACTGCCTCTTTGTGCTTAGTGTT 1205

Qy        88 CCGTAAAG---------GAGCT-------------------------
GAGCCGAGCGGG 112
             | |||||||        | |||                        || |    |
||
Db      1204
CAGTAAAGCTTCCCATAGGGCTTTGGCTGTGGTGTCACTGAATTGTGAAAGACAGCCTGG 1145

Qy       113 GGC-GCCGC--------------CC-------GGGGTCCGGTGGGC---
AAAAGGCT--- 144
               || || |              ||       || || | ||| ||   | | | |
Db      1144
```

```
TGCAACCACATTATAATTTTCCTCCTCAGTATGGAGTGCAGTGAGCGCTATCATGTTAAC 1085

Qy         145 ----ACAGCA-------------GGAGCTG-------------
ATGACC----------- 163
                   ||| ||            |||||||            |||| |
Db        1084
CATCACATCATTTGTGTGGCCTGGGAGCTGGGGAAGTGCTGAAATGATCTTCTCTACTAA 1025

Qy         164 -----CT-CATGATGTCTGGC-----------
GATAAAGGGATTT-------------- 191
                    || ||||||||| |          ||| |||| | |
Db        1024
GTTGTCTCCATGATGTCCAACTGCTCCTGTGAGATCCAGGGTTCTGTCCACAAAAACCAC 965

Qy         192 --CTGCCTTCCCTGAATCAG---ACAACCTTTTCAAATGGGTAGGGACCAT-----
CCAT 241
                     |||| | |||| | |||    |  ||| |||  | |||| |
|||
Db         964 TGATGCCCTGCCTGCAGCAGTCTTCTTCCTGTTC---
TTTGCAGGGGCATAATTGGCCA- 909

Qy         242 GGAGCAGCTG----GAACAGTATATGAAGACCTGAGGTATAA----GCTCTCG-----
CT 288
                     || | || |   || | |   |   |||| | | ||   ||| ||
||
Db         908 -
GATCCGCAGCGATGACCTGACTTAAGGAACCTACAGCAAAACACTCCTCCCGTACTCCT 850

Qy         289 AGA-GTTC-CCCAGTG-GCTAC--CCTTACAAT--
GCGCC-------------------- 321
                    |  ||||| ||| | ||   ||| ||| | |  || |
Db         849
AAATGTTCACACAGAGAACTGAGGCCTGACACTAGGCATCTGATCTGCAGCAGCAGCTCT 790

Qy         322 --------CACAGTGAAGTTC----CTCACG-----CCCTGCTATCAC----
CCCAAC-- 358
                            |  |||| ||| |   |    ||| ||| | |  || |
Db         789
GGGGTTAGCGTAGTGGAGTCCACATCACCCAGGCTTCCCAGCTTCCTCTTGTCCGGTCGG 730

Qy         359 --------------GTGGACA-CCCAGGGTAACA-----------TATGC-----
CTGGA 387
                             ||| ||| ||  ||||| ||              ||||
|||||
Db         729
GCGCTATTAAGGAGGTGCACATCCTGGGGTAGCAGTGGGAAAAGGGATGCAAAAGCTGGA 670

Qy         388 CATCCTGAAGGAAAAGTGG--------------------------------------
TC 408
                    ||   |||| |||||||
||
Db         669 -GTC---
AAGGCAAAGTGGGGAGCAACAGGGGCAAGCAATAACGGGACATGGAACACCTC 614

Qy         409 TGCCCTGT-----ATGATGTCAGGACCATT----CTGC-
TCTCCATCCAG---------- 448
                    ||| |||    ||| ||| || | | |  |||||| |||||
Db         613 GGCCGTGTAGTTCATGTTGCCC-ATCCATTCACACAGCTTCTCC-
TCCAGCTGCTCGAAC 556
```

```
Qy        449 --------------AGCCTTCTAGG----AGAACCC-----
AACATTGATAG-------- 477
                         || ||| ||      |   ||     |||| |||
Db        555
ACCGGCTGCTGCCCCTCCATCTCGGCCGCTGCCGCCGCTGGGACATGATTAGCTGTGAGG 496

Qy        478 -------------TCCC--TTG-----AACACACA--------------
TGCTGCCGA-- 501
                         || | |||      | ||||||          ||| || ||
Db        495
TGGACAGCGTGGCTCACGGTTGTGACCACCACACAATACTGGAAGTGACTGCGGCAGATG 436

Qy        502 --GCTCTGGAAAAACCCCA-----CAGCTTTTAAGAAG------------------
TAC- 535
                    |  | | | | | |||    | || ||| || ||                 |
|
Db        435
ATGTCCCGTAGGATCTCCACGGTCCGGCCTTTCAGCAGGCAGCTCAGCACAAACACTGCC 376

Qy        536 -----CTGCAAGAAACCTACTCAAA--------------------
GCAGGTCACCAGCC 569
                      |||| |   || | | ||              |||||| | |||
|
Db        375 TTGGGCTGCTTGGCTCCACCACCAATTGCGTCGGGCTCGAACTCTCGCAGGTGA-
CAGTC 317

Qy        570 AGGAGCCCTGAC-----CCAG---------------GCTGCC------
CAGCCTGTC--- 600
                      ||| ||| ||    ||||              || |||     ||| || ||
Db        316
AGGGCCCCCACCGCCTCCAGGAGACGGGTGGATCCGCAGCCCCAGTGCAGGCTCTCGGC 257

Qy        601 -CTTGTGTCGTCTTTTTAA-----------TTTTTCCTTAGATGG--TCTG------
TCC 640
                      |  | | |||| |||          ||| | || | |  |||
|||
Db        256
GCAGGCGGCGTCCAGGTAAACCACAGCCCGTTTCACTTTGGCCAGCACCTGCTCCCATCC 197

Qy        641 TTTTTGTG---ATTTCTGTAT-----AGG-ACTCTTTAT--------------
CTTGAG- 676
                      || || |    |   | |||     ||| ||| | |              ||||
|
Db        196
TTGCTGGGTAAAGGACAGTACGCCCGAGGCGCTCATGGTTGGGGATTCGCAGACTTGGGA 137

Qy        677 --CTGTGGT-----ATTTTTGTTTTGTTTTTGTCTTTT----
AAATTAAGCCTCGG---- 721
                         || |||   | | ||| | ||||| || |||
Db        136
AACTACGGTGCAGGAACTTCTTTCAGAACTCACCGCTTCCGGAAATTGGGCTCCGGGAGA 77

Qy        722 --TTGA-----GCCCTTGTATATTAAATA-------AATGC------
ATTTTTGTCCTTT 761
                         ||||      || ||| | ||     | |||    | || | |
|
Db         76 CTTTGACAGTCTCCACAGTACACCCAGTAGGCCAACAGTGCTCGAGGAATTCCG-
CAGCT 18

Qy        762 TTTAAAAAAAAAAAAAA 777
```

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                 |||| |  | ||  ||
Db          17 TTTAGAGCAGAAGTAA 2
```

```
  Query Match            42.0%;  Score 1995.5;  DB 1;  Length 3589;
  Best Local Similarity  41.4%;  Pred. No. 6.5e-106;
  Matches  501;  Conservative   0;  Mismatches  263;  Indels  445;
Gaps   74;

Qy          2 GCACG-AGCGA---GTTCC---TGT-CTCTCTGCC--AAC--
GCCGCCCGGATGGCTTCC 49
              ||||   ||||   | |||   ||| | | ||| |   |  |||| ||  ||
|||||
Db         25
GCACACTGCGAGGGGCTCCGTGTGTGCGCCCTGTCTTGTCTGGCCGTCCTCATCCCTTCC 84

Qy         50 CAAAACCGCGACCCAGCCGCCACTAGCGTCGCCGCCGCCCGTAAAGGAGCT------
GAG 103
              |    || |  ||| |||||||||| || | |||| |||  |||| |||
||
Db         85 C----CCAC-CCCCTGCCGCCACTC-CGAC-CCGCT-CCC--
AAAGTGGCTTCACAATAG 134

Qy        104 CCG------AGCGG---GGGCGCCGCCCGGGGTCCG---GTGGGCAA----
AAGG----- 142
              ||       ||||   ||| ||| |  |||||    | | || |   ||||
Db        135
TCGGTCCTCGGCGGTGTAGGCTGCGCACCAGGTCCACACTTAAGCGAAATCAAGGAGACC 194

Qy        143 -----CTACAGC------------------------
AGGAGCTGATGACCCTCATG---- 169
                   ||||  |                     | ||||| ||   ||||
Db        195
CCCTTCTACTTCTACCTTTGGGTTTGGTGCTCAATGCGAAGCTGCTGCAACTCAGACACG 254

Qy        170 ---ATGTC------TGGCGATAAAGG------GATTT---------CTGCCTTC---
```

```
CCT 202
                       |  |||        ||  || |||||       |  |||            |||  ||
||
Db        255
CCTAAGTCAACTCATGCAGAAAAAGGAGAAAAGTTTTGGTATACAAATGCTCTCAGTCCA 314

Qy        203 GAATCAGACAACCTTTTCAAATGGGT-----------------------
AGGGACC---A 236
                 |   ||||| |||   | || || |                       |  |||||
|
Db        315 GC--CAGAC-
ACCAAGCCGAAAGGTTGTGCTGGCTGCAACCGAAAGATCAAGGACCGGTA 371

Qy        237 TC--CATGGAGCAGCTGGAACAGTA----TATGAAGA---CCTGAGGTAT--------
AA 279
                 || |   ||| ||||| | |    |||||||   ||||| || |
Db        372 TCTTCTAAAGGCA-
CTGGACAAATACTGGCATGAAGACTGCCTGAAGTGTGCCTGCTGTG 430

Qy        280 GCTCTCGCTAGAG----------TTC-CCCAGT-------GGCTACCCTTA--
CAATG-C 318
                  || ||||| | |          | | ||| ||      ||||  |||| |  ||
|
Db        431
ACTGTCGCTTGGGGGAGGTGGGCTCCACCCTGTACACTAAAGCTAATCTTATCCTTTGTC 490

Qy        319 GCC--------------CACAGTGAAGTTCC---TCAC-GCCCTGCT---------
ATCA 351
                 ||                | | || ||  |    | || ||||
|||
Db        491
GCAGAGACTATCTGAGGCTCTTTGGTGTAACGGGAAACTGCGCTGCCTGTAGTAAGCTCA 550

Qy        352 CCCCAAC-------GTGGACA------CCCAGGGTAACATAT---GCCTGGAC-----
AT 390
                 ||| |        ||| |       || ||| ||  | |   |||||||
Db        551
TCCCTGCCTTTGAGATGGTGATGCGTGCCAAGGACAATGTTTACCACCTGGACTGCTTTG 610

Qy        391 CCTGAAGGAAAAGTGGTCTGC-CCTGTATGATGTCAGGACCA--
TTCTGCT--------- 438
                 | ||   |     ||  || |    | | || ||    ||| |   ||  | ||
Db        611 CATGTCAGCTTTGTAATCAGAGATTTTGTGTTG--
GAGACAAATTTTTCCTAAAGAATAA 668

Qy        439 ----CTCCAT--CCAGA--GCCTTCTAGGA----------------------
GAACCCAA 468
                   ||| |  |||||  | | || | ||||                       |  ||||
|
Db        669
CATGATCCTTTGCCAGACGGACTACGAGGAAGGTTTAATGAAAGAAGGTTATGCACCCCA 728

Qy        469 CATTGATAGTCCCTTGAACA----CACAT----
GCTGCCGAGCTCTGGA----------- 509
                   ||   |   | |||| |   ||   |   | ||||| || |
Db        729
GGTTCGCTGATCTATCAACATCACCCCATTAAGAATACAGAGCACTACATTCTTTTATCT 788

Qy        510 --AAAACCCCACA-GCTTTTAAGAAGTACCTGCAAGAAACCTACTCAA-
AGC-------- 557
```

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                      |  ||||| |     |||||| | |    || |||||||| || |||
Db        789 TTTTTGCTCCACATGTACATAAGAATTGAC--
ACAGGAACCTACTGAATAGCGTAGATAT 846


Qy        558 AGGTCACCAG-----------------
CCAGGAGCCCTGACCCAGGCTG---------- 589
                  |||    ||                  ||| | ||| | | ||
Db        847
AGGAAGGCAGGATGGTTATATGGAATAAAAGGCGGACTGCATCTGTATGTAGTGAAATTG 906


Qy        590 -CCCAG--------------------------------CCTGTCCTTGTGTC--
GTC 611
                   |||||                          ||| | || | |
Db        907
CCCCAGTTCAGAGTTGAATGTTTATTATTAAAGAAAAAAGTAATGTACATATGGCTGGAT 966


Qy        612 TTTTTAATTTTTCCTTAGATGGTCTGTCCTTT---
TTGTGATTTCTGTATAGGACTCTT- 667
                  |||||   ||    || | | | |||| ||    || ||| | | | |||||
||
Db        967
TTTTTTGCTTGCTATTCGTTTTTGTGTCACTTGGCATGAGATGTTTATTTTGGACTATTG 1026


Qy        668 --TATCTTGAGCTGTGGTAT----------------------
TTTTGTTTTGTT------ 697
                  ||| ||   ||| |||                        |||| || ||||
Db        1027
TATATAATGTATTGTAATATTTGAAGCACAAATGTAATACAGTTTTATTGTGTTACCATT 1086


Qy        698 ---------TTTG--TCTTTTAAATTAAGCC-
TCGGTTGAGCCCTTGTATAT-------- 737
                  |||| ||||| | |   || | || | |  ||| ||
Db        1087
TGTGTTCCATTTGCTTCTTTGTATTGTTGCATTTAGTACAATCAGTGTTTAAACTTACTG 1146


Qy        738 TAAATAAATGCATT-----TTTGTC--CTTTTTTAAA----------------
AAAAAAA 774
                  || || |||| ||     ||| |  || |||||||                  |
|||
Db        1147
TATATTTATGCTTTCTGTATTTACCAGCTATTTTAAATGAGCTGTAACTTTCTAGTAAAG 1206


Qy        775 AAAAAAAAA 783
                  || ||||
Db        1207 AATTGAAAA 1215


RESULT 9
US-10-478-914-3/c
; Sequence 3, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
```

```
  Query Match            41.7%;  Score 1983.5;  DB 1;  Length 2083;
  Best Local Similarity  36.0%;  Pred. No. 1.4e-106;
  Matches  517;  Conservative   0;  Mismatches  256;  Indels  663;
Gaps   80;

Qy         2 GCACGAGCGAGTTCCTGTCTCTGCCAAC---GCCGCCCGGAT--
GGCTTCCCAAAACC 56
             ||||  ||  | ||  | ||| |||| | |   ||| ||| |  | ||     |||
Db      1791
GCACTGGCATGATCTCGGCTCACTGCAACCTCTGCCTCACGAGTTAGGTCAAGCAATTCT 1732

Qy        57 GCGACC-CAGCCGCC------ACTAG-----C--GTC---GCCGCC--
GCCCG------- 90
              | || ||||| ||        ||||      |  |||   ||| ||  ||| |
Db      1731
TCTGCCTCAGCCTCCCGAGGAGCTAGGATTACAGGTCCCTGCCACCATGCCTGAGTAATT 1672

Qy        91 ----------TAAAGGAGCTG--------------AGCCGAGCGGGG-GCG-----
CCG 119
                       ||   ||| ||             |||| ||| ||  ||    |
Db      1671
TTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTAGCCAAGCTGGTCTCGAATTCCTG 1612

Qy       120 CCCGGGGTCCGGTGGGCAAAAGGCTACAGC------AGGAGCTG-----------
ATGAC 162
                ||    || |||| |     | |||||     | | ||||
|||
Db      1611 ACC----
TCAGGTGATCCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACGGGCGTGAG 1556

Qy       163 CCTCATGATGTCTGG---CGATAAAGGGATTT--CTGCCTT---
CCCTGAA--------- 205
                || |  | || |||| | ||        ||| | |||| |||||||
Db      1555 CCAC--
GGTGCCTGGCCTCTATTTTTTATTTTAAATACCTTTTGCCCTGAAATCTATGTC 1498

Qy       206 -TCAGA----CAAC----CT------TTTCAAATGGGTAGGGA-----------
CCATCC 239
              || ||   |||    ||      ||| |  | || | |              |
||||
Db      1497
CTCTCGATTATCAACACTGCTTACCAGTTTTATTTTTGTTGGTATTTATTTCATTCAATCC 1438

Qy       240 ATG--GAGCAGC------------------TGGAACAGTAT-------ATGAAG-----
AC 268
              |     || |                 |||| ||||       || ||
|
```

```
Db      1437
CAGCTCTACAACTTACCAGTATAAAAATTTGGATCAGTTACTTAATCTTGCAGTTTCTTC 1378

Qy       269 CT-------GAGG-----TATAAGCTCTCGCTAGAGTTCCCCAGT----------
GGCT 305
             ||             ||       ||| | || ||       |  | ||||||
||
Db      1377
CTTTTAAAAATGGAATAATATTATCTATCATATAAAATGCCCAGTTAACAAATATGAACT 1318

Qy       306 -ACCCTTACAATGCGCC---CAC--------------AGTG-----AAGTTCC---
TCA 338
               || | ||||||| |||   |||              | ||     ||||||
||
Db      1317
AACACCTACAATGTGCCAGGCACCATTCTAGGGAATAGAATGTAAATAAGTTCAAGTTCT 1258

Qy       339 CGCCCTG----------------------------------------
CTATCAC------- 352
               | ||||                                      | || ||
Db      1257
TGACCTGAATAAGTTTACATTTTAGTGAGAAGACAGACAATAAATCAATAACATGTCCAT 1198

Qy       353 -----------------------CCCAACG--------------------------
TGG-- 362
                                    | ||| |                       |||
Db      1197
TATGCCAGATAGTTTTAAATGTCACAAAGAAAAAGGGGGAGCAATCAGATAGTGATGGAA 1138

Qy       363 ---ACACCC-----AGGG--------------------------
TAACAT--------- 378
                |||| |    ||||                         | ||||
Db      1137
GTTACACTCTAGAGAGGGTGGACAGAAAAAGTTTCTCTTAGGAGATGACATCTGAACAGA 1078

Qy       379 -------ATGCCTGG----ACATCCTGAAGGAAAAGTGGT----------------
CTGC- 411
                   ||| |||     | | ||  | |||||||||| |                |
||
Db      1077
GATCTAAATGACTGAGTACAAACCCCAATGGAAAAGTGATTGGTGTGTTGTGAAACAGCA 1018

Qy       412 ------CCTGTAT-----GATGTCAGGACCATTCTG-CT---------CT----
CCATC- 445
                   || || |    |||| || || || ||        ||
||||
Db      1017
ACACAGCCAGTTTGACTAGATGAGTAGATCAGAATGACTGAGGTGGGACTGTGGTCATCA 958

Qy       446 -------CAGAGCCTT---CTAGGAGAACC-
CAACATTGATAGTCCCTTGAACACAC--- 491
                   |||||   |  || |||   || || ||   ||  |||| ||| | |
Db       957 AAGAGATCAGAGAGGTAGCCTGGGAAGGCCACATCACAGAATGTCCTTTGGGC-
CTCTGT 899

Qy       492 --------------ATGCTG--CCGAGC----------------
TCTGGAAAAACCC-- 516
                   | | | | ||||                   || || || |
Db       898
AAGAGCGTTTTGAAAAAACAGTTCTGAGCAAAGGTTAGTCATTTAACTTGACTTACTCTT 839
```

```
Qy        517 ---------CAC---AGCTTTTAAGAAG-TACCTGCAAGAAACCT------------
ACT 551
                          |||    ||| || ||  |  | |  |  || |  |
|||
Db        838
TAGAAGGATCACTTTGGCTATTGAGTGGCAAACAACTGGAGAAGTGGTTAGGGGAGCACT 779


Qy        552 CAAAGCAGG-------------
TCACCAGCCAGGAGCCCTGACCCAGGCTGC-------- 590
                     |||||                | ||| | ||||||    ||    || |
Db        778
GTGGGCAGGAATAGAAGGAGGAAAAGCAGACTGGAGCCTAATCCAGTACTTCAGATGAGA 719


Qy        591 -------------CCAG-----------CCTGTC------CTTGTGTC--------
GTCT 612
                              || |           ||| ||     ||| |  |        ||
|
Db        718
AATGACAGATTTGCCTGGTACATCATTTCCTATCCCTTTACTTATAACTTATTGGTGTAT 659


Qy        613 TTTTAATTT-------------------------TTCCTTAGA----TGGTCTGTCC-
TT 642
                     ||||| |||                         |  || ||    || | ||| |
Db        658
TTTTATTTTAAGTGTAAATTTTTATAAATGAAGCATAATTTGAAGATTGATATGTTCGGA 599


Qy        643 TTTGTGATTTCTGT----ATAG-GACTCT---------
TTATC----------------- 671
                     ||||| ||||| |    || | | ||||          || ||
Db        598
CTTGTGTTTTCTATTATCATGGTGTCTCTCCACATACCTTTTCCCTTTAGTTCTGCTTCT 539


Qy        672 --TTGAGCT------GTGGTATTTTTGTT------------------
TTGTTTTTGTCT- 704
                       ||| |||       ||  |||||||||||                    ||||||
||
Db        538 TATTGTGCTCCTCAAGT-
CTATTTTTGTTCTTTCCCTCTACTTCTACTGTTTTGAACTG 480


Qy        705 ---------TTTAAATTAAGCCTCG-
GTTGAGCCCTTGTATATTAAAT------------ 742
                          |||  |||  ||| | |||   |||||  || ||   |
Db        479
TATATGCTATTTCTATTTTGCCAGGAGTTACCCCCTTCAATTTTCGTTGTACTCTCTCAG 420


Qy        743 ----AAATGCAT------------TTTTGTCCTTTTTTAAAAAAAAAAAAAAAAAA
782
                       |||   |||                || ||||||| | | | |    | ||
Db        419 TCTCAAACACATACCCATGCTCTCTTCTGTCCTTCTCTTCATATCATCTTCTAGAA
364
```


RESULT 10
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA

```
  Query Match          41.7%;  Score 1980;  DB 1;  Length 2198;
  Best Local Similarity   35.8%;  Pred. No. 3.3e-106;
  Matches  498;  Conservative   0;  Mismatches  281;  Indels  614;
Gaps   69;

Qy       1 GGCACGAGCGAGTT------------CCTGTCTCTCTGC----------
CAAC------- 31
             | | | || || ||         | |||| ||||||         || |
Db    1594
GACTCAAGTGAATTCTTGGATGACACCTTGTCCCTCTGCTTCTCATCTTCAGCTTTGTAC 1535

Qy      32 ------GCCGCCCGG------------ATGGCTTCC-----
CAAA--------------- 53
               ||  || ||             ||| |||||    ||||
Db    1534
TTCTCAGCTTCCTGGACCATACGTTCAATGTCTTCCTTGCTCAAACGGCCCTTGTCATTA 1475

Qy      54 ------------------------ACCG------CGACC-
CAGCCG-------------- 68
                                  |||       | || |||| |
Db    1474
GTGATAGTAATCTTGTTCTCTTTTCCCGTACTCTTGTCCACAGCAGAGACATTGAGTATA 1415

Qy      69 CCACTAGCGTC------------GCC------------GCCGCC-C---
GTAAAGGAG-- 98
             ||| | || ||            | |         | | | || | ||||| |
Db    1414
CCATTGGCATCAATGTCAAAAGTGACTTCAATCTGAGGAACACCTCGGGGTGCAGGAGGT 1355

Qy      99 ----CTG------------AGCCGAGCGGG-----------------GGCGC---
CGCC- 121
                 |||           ||| ||| ||               ||| |
Db    1354
ATGCCTGTGAGTTCAAACTTGCCAAGCAGGTTGTTATCCTTTGTCATGGCACGCTCGCCT 1295

Qy     122 -CGGGGTCCGG--TGGGCAAA--AGGCT-----ACAGC--
AGGAGCTGATGACC-----C 164
               |||       || |  ||| |  |||||       ||| ||| ||| | |
                                                                        |
Db    1294
TCATAAACCTGAATAAGCACACCAGGCTGGTTGTCAGAATAGGTAGTGAAGGTCTGTGTC 1235
```

```
Qy         165 T-CATGAT--GTCTGGCGATAAAGGGATTTCT---
GCCTTCCCTGAATCAGACAACCTTT 218
               |  | || |  |  ||| | ||    | ||  |   | |   | ||| ||   || |
||
Db        1234
TGCTTGGTAGGAATGGTGGTATTACGCTTGATGAGGACAGTCATGACTCCACCAGCAGTT 1175

Qy         219 TCAA----ATGGGTAGGG-----ACCATCCATGGAGCAG-----
CTGGAACAGTATATGA 264
               ||||   | |||| |     |||||    ||||||     || ||||| | |
||
Db        1174 TCAATACCAAGGGAAAGAGGAGTGACATCCA-
AGAGCAGCAAATCTTGAACATTCTCAGA 1116

Qy         265 ---------AGACCTGAGGTAT-------AAGCT-CTC-----GCTAGAG-
TTCCCCAGT 301
                        |||| || | |        |||| | |   || | |||  ||
|||
Db        1115
CTTGTCTCCAGACAAGATGGCTGCCTGGACAGCTGCACCATAAGCAACAGCTTCATCAGG 1056

Qy         302 G--GCTACCCTTA--CAATGC---GCC-----------
CACAGTGAAGTTCCTCACGC-- 341
               | | | | |||| || | |    ||           |   | |||| | || |  |
Db        1055
GTTGATGCTCTTATTCAGTTCTTTTCCATTGAAGAAGTCTTGGAGAAGCTTCTGAATCTT 996

Qy         342 ------CCTGCTATCACC-
CCAACGTGGACAC---------------------------- 366
               |  || ||| ||||| |||||
Db         995
GGGGATACGAGTAGAACCACCAACCAGGACAATATCATGAATCTGTGACTTGTCTAGTTT 936

Qy         367 -----------------------------
CCAGGGTAACATATGCCTGGACATC------ 391
                                         |||||||| ||    | || || |
Db         935
GGCATCTCGAAGGGCTTTCTCTACTGGGTCCAGGGTGCCACGGAACAGGTCAGCATTCAG 876

Qy         392 -----------------------
CTGAAGGAAAAGTGGT---------------------- 407
                                       || ||| | ||  ||
Db         875
TTCTTCAAATCGGGCACGGGTAATGGAGGTATAGAAGTCGATTCCTTCATAGAGAGAATC 816

Qy         408 ----------CTGCCCTGTATGATGTCA-----GGACCATTCTGC----
TCTCCATC--- 445
                         ||| |||| || ||  |    || | | ||   || | |
Db         815
GATCTCAATACTGGCCTGGGTGCTGGAAGAGAGGGTACGCTTAGCACGTTCACAAGCAGT 756

Qy         446 -CAGAGCCTTCTAGGAGAACCC-----AACATTGATAGTCC--------------
CTTGA 485
               | |||| | |||   ||  | |      || |||| ||||                 |||
Db         755 ACGGAGGCGTCTTACAGCTCTCTTGTTCTCACTGAT-
GTCCTTCTTATGCTTGCGCTTAA 697

Qy         486 ACACA-----------------CATGC---
TGCCGAGCTCTGGAAAAACC---------- 515
```

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                 || ||                  ||| |   || | |  |||       | ||
Db       696
ACTCAGCAATAAAATGGTTGACCATTCGGTTGTCAAAATCTTCTCCACCCAAGTGGGTGT 637


Qy       516 CCACAGCTTTTAAGAAGTACCTGCAAGAAACC-TACTCA------
AAGCAGGTCACCAGC 568
              |  ||||| |  |    | |||| |||| || | ||||       | |   | |||
Db       636 CTCCAGCTGTAGACTTG-
ACCTCAAAGATTCCATCCTCAATAGTGAGGATTGACACATCA 578


Qy       569 CAGGAGCCCTGACCCAGG---------------------CTGC-CCAGCC----
TGTCC 601
               | | |||    ||||||                   |||| ||| ||
||||
Db       577
AAAGTGCCACCTCCCAGGTCAAAGATGAGCACGTTTCTTTCTGCTCCAACCTTTTTGTCT 518


Qy       602 TTG--------------------
TGTCGTCTTTTTAATTTTTC---------------- 624
               |                       || | ||  ||||| |||
Db       517
AAGCCGTAAGCAATAGCAGCAGCAGTTGGCTCATTAATAATTCTAAGTACATTGAGACCA 458


Qy       625 ----------------CTTAGATGGTCTGTC-CTTTTTGTGATTTCTGTATAG--
GACTC 665
                              ||| | | ||| | ||    || |||   ||| ||   | |
|
Db       457 GCAATAGTTCCAGCATCTTTGGTAGCCTGACGCTGAGAGTCATTAAAGTA-
AGCTGGCAC 399


Qy       666 TTTATCTTGAGCTGTGGTA------------------------
TTTTTGTTTTGTTTT 699
               | | |   ||| |||||                            ||| || |
||
Db       398
TGTGACCACAGCATTGGTAACAGTCTTCCCAAGGTAGGCTTCTGCAATTTCCTTCATCTT 339


Qy       700 TGTCT----TTTAAATTAAGCCTC------------------
GGTTGAGCCCTTGTATAT 737
               ||||        || | |  ||||                 |||  |||||||||
Db       338 TGTCAGAACCATAGAAGACACCTCCTCTGGATAGAAGCTTTTGGTCTCTCCCTTGTATTC 279


Qy       738 TAAATAAA-------------TGCATTTTTGTCC--------------
TTTTTTAAAAAA 770
               || | | |             |||| || ||              | ||| | |
Db       278
TACTTGGACCTTGGGCCTGCCAGCATCATTCACCACCATAAAGGGCCAATGTTTCATATC 219


Qy       771 AAAAAAAAAAAAA 783
               | |   | || |
Db       218 AGACTGGACAACA 206



RESULT 11
US-10-478-914-62
; Sequence 62, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
```

```
  Query Match            41.7%;  Score 1979;  DB 1;  Length 1946;
  Best Local Similarity  38.5%;  Pred. No. 1.9e-106;
  Matches   490;  Conservative   0;  Mismatches  270;  Indels  514;
Gaps   76;


Qy         3 CAC-------GAGCGAGTT--
CCTGTCTCTCTGCCAACGCCGCCCGGATGGCTTCCCAAA 53
             |||        |  ||  |||  ||||  | |||   |||  ||| ||  |   ||  |||||
|
Db       294 CACATCTCTTGGGCCTGTTTACCTG-CGCTC--CCAGAGCCTCC--
GCCAGCATCCCAGA 348


Qy        54 ACCGCGA--CCCAGC------------------------CG-----
CCACTAGCGTCGC 81
             |  |  |  ||||  |                               ||     ||| ||||
|
Db       349
ATCTCCATCCCCATCTCTCACTTATACACACATCAGTCATCGGTTATCCATTAGCTAAAC 408


Qy        82 CGCCGCCCGTAAAGG------------AGCT-------
GAGC------------------ 104
             ||||  || |||  |               |||       || |
Db       409
CGCCTTCCTTAATAGCTTTACACTGTTTGCTTTCTCTGGAACATTTTTAGTTAAAATTTC 468


Qy       105 --CGAGCGGGGGCGCC---------GCCCGG--GG--------
TCCG------------G 131
                 || |  || |            | | |  ||         ||||
|
Db       469
ATAATGCAGTTGCACACAAATGAAGACACAGATGGCTGCATCCTCCGTCTCTTCCCCTCG 528


Qy       132 TGGGCAAAAGGCTACAG--CAGGAGCTGATG--------ACCCTCATGAT---
GTCTG-G 177
             |   ||  | ||| | |  ||||    | ||         |||| |||| |   | | |
|
Db       529
TTTACAGGAAGCTGCGGATCAGGGAGGGGTGTTAGGGTTACCCACATGGTAAGGGCAGAG 588


Qy       178 CGATAAAGGGATTTCTGCCTTCC--------------------------
CTGA------- 204
             |  | ||||  | |  ||||                            ||||
```

```
Db        589
ACAAGAGGGGACCCCAGTTTTCCATGCTGCACATGGTCATTGCTGGGGACTGAGGTTTGC 648

Qy        205 --ATCAGACAACCTT-------TTCAAATGGGTAGGGACCATCC---ATGGAGC-
AGCTG 251
              |||| | || |      || |||| | || ||      |||||||
|||||
Db        649 ACATCACCCTGCCCTGTTCTCCCTCCGCTGGG--
GAGAAAGTCAGGGATGGAGCAAGCTG 706

Qy        252 GAACAGTATATGAA-----------GACCTGAGGTATAAG-
CTCTCGCTAGAGTTCC--- 296
              | || | |||| |        | |||| | | ||| | ||  ||| ||
Db        707 CAGCATCTTCTGAAAAAGAAAAGGTGGCCTTGTCTCCAGGTCTCCC-
CTCAAGTCCCACC 765

Qy        297 --CCAGTGG----CTACC-CTTACAATG--------CGC--CCAC----
AGTGAAGTTCC 335
              || | |   || |||| ||      | | ||||     |||
||||
Db        766
TTCCCATAGTTTTCTGCCACTTCTCTTGATTTTCCTCTCTGCCACTTCTCTTGATTTTCC 825

Qy        336 TCAC-GCC-CTGCTAT--------CACCC--CAAC---------GTGG----
ACACCCAG 370
              || | ||| || || |     | | | || |      ||||    | ||
Db        826
TCTCTGCCACTTCTCTTGATTTTCCTCTCTGCAGCTGCTTTGAGGTGGGTTTTCTCCAGA 885

Qy        371 GGTA-ACATATGCCTG------GAC---ATCCTGAAGGAAAAGTGGTCT---
GCCCTGTA 417
              | | || |   |||| | | || ||| |||     ||| || |
||
Db        886
TGCACACTTTCCCCTGCTTTGCGTCCTTATTCTGGTAGAAGCACAATCTAAAGCTCATTA 945

Qy        418 TGATGTCAGGACCATTCT--------------------GCTCTCCATCCAG--AGC-
CT 453
              |   |   | |||||     | || |||| ||| |||
||
Db        946
AGGGAACTAATCAATTCTGTGCATGGCGCTAGCTCAGCAGATCACCACACAGGCAGCACT 1005

Qy        454 TCTA-------GGAG---AACCCA--------ACATTGATAGT-------CCC---
TTGA 485
              ||      || | ||| ||     ||| || |     ||| |
||
Db        1006
ATTAGCAAGTCGGTGCTTAACACATGGCACTTCCATGAATCGATATGGAGCCCGTGTAGA 1065

Qy        486 ACAC-ACATG-----------CTGCC---------GAGCT-----
CTGGAAAAACCCCAC 519
              ||| ||||        || || | || |   || ||| |
|
Db        1066
ACAAGGCATGGGTTTTTTTCTCTTCCCATTAAGAAAAACTGATGCCAAAAATAACTTCTC 1125

Qy        520 AG----------------CTTTTAAGAAG--------------
TACCTGCAAGAAACCTA 549
              ||             |||||| ||||        |   ||||| || |
```

```
        |
Db      1126 AGATATTTTCAAGTATGACTTTTATGAAGGGAAAAAGCATTTTTGTTTGCAA-
AATCATG 1184

Qy       550 C-TCAAAGCAGGTCACCAG--------------------------CCAGGAGC----
CC 577
             | |||  ||||||   ||||                              || || ||
        |
Db      1185 CTTCAGTGCAGG---
CCAGTTGTGAATTGTGATGGCTTTTATTTCTCCTGGGGCTGTAAC 1241

Qy       578 T------------------
GACCCAGGCTGCCCAGCCTGTC------------------ 600
             |                  || |||  | ||| |||   ||
Db      1242 TTTAAGGGTTTAGAATTTGGAACCA--
CAGCCTAGCTAATCATGACACACACACACACAC 1299

Qy       601 -----CTTG--------------------TGTCGTC--------------------
TTTT 615
                  | ||                    | ||                        |
Db      1300
ACACACATGCACACACATACACATACACAAAGCATCACGAAGAACCATACAAATTGTACA 1359

Qy       616 TAATTTTTC-CTTAGATGGTCTGTCCTTTTTGTGATTTCTGTATAGGACT---
CTTTATC 671
             | |||||| | | || | || | || ||     |  ||| | | ||    |   || |
        |
Db      1360 TTATTTTACACATGGAGGCTCACTCTAAAAT-
AGATACCATTTTAAATATTAACTAAAAC 1418

Qy       672 TTGAGCT-GTGGTATTTT--------------
TGTTTTGTTTTTGTCTTTTAAATTAAGC 716
             ||| |||  | |||| ||              || |||||| ||  | |||   || |
Db      1419 TTGTGCTCATTGTATGTTCATTCTATATGTACTGATTTGTTATTCACATTT-
CTTTCAAA 1477

Qy       717 CTCGGTTG-------
AGCCCTTGTATATTAAATAAATGCATTTTTGTCCTTTTTTAAAAA 769
             ||| |      ||||| |  ||||||||    |   | || |||| |
        |||
Db      1478 ATCGTTCAAATTTCTAGCCCACATCAATTAAATA-----
TTAATAGTACTTTCTACAAAC 1532

Qy       770 AAAAAAAAAAAAAA 783
             |  |    | ||||
Db      1533 ATGAGCGCACAAAA 1546


RESULT 12
US-10-478-914-60/c
; Sequence 60, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
```

  Query Match   40.9%; Score 1943; DB 1; Length 2022;
  Best Local Similarity 39.8%; Pred. No. 4.3e-104;
  Matches 487; Conservative   0; Mismatches 271; Indels 466;
Gaps   68;

Qy   2 GCACGAGCGAGTTCCTGTCTCTCTGCCAACGCCGCC-
CGGATGGCTTCCCAAAACCGCGA 60
             ||| ||| | || | ||| |||| | ||||| | ||| ||| || |
Db   1948 GCAATGGCGCGATCTCGGCTCACTGCAACTTCCGCCTC--CTGGGTTC---
AAGCTATTC 1894

Qy   61 CCCAGCC---GCCACTAGCGTCGCCG-----------CCGCC-CGTAAAGGA--GC-
TGA 102
             || ||| | ||| | | | || | | | | | || | |||| ||
|||
Db   1893 TCCTGCCTCAGCCTCCTGAGTAGCTGAGGTGAGAGGACTGACGCG-
AGAGGATTGCTTGA 1835

Qy   103 GCCGAG-----CGGGGGCGCCGC---CCGGGGT----
CCGGTGGGCAAAAGGCT------ 144
             ||| || | || || | | | | || ||| | |||||
Db   1834
GCCTAGGAGGTTGAGGTTGCAGTGAGCTGTGTTCACGCCACTGGACTCCAGGCTGGGTGA 1775

Qy   145 -ACAGCAGGAGCTGATGACCC----------TCATGATGTCTGGCGAT-
AAAGGGATTTC 192
              | |||| || | |||| | | || | | | || ||
|
Db   1774 CAAAGCAAGACC--
CTGTCTCAAAAACAAAAACAAACAAACAAACAAACAAAAAAATAAC 1717

Qy   193 TGCC------TTCCCTGAAT-------------------C-----
AGACAAC--------- 214
               | |||||| | | |||| |
Db   1716
CAACAAAAAAAACCCTGAGTTTAAGTTTGATTTTAAGACCTGTAGGGACAGCAGATTAGT 1657

Qy   215 -CTTTTCAAATGGGTAGGGACCATC-------
CATGGAGCA------------------- 247
               || | | |||||||| | | |||| || || ||
Db   1656
TCTACTTTAATGGGTATGCATCATCTGGAAAGCAAGGGTCATAAAAAGAAGATACATCTT 1597

Qy   248 -GCTGGAACAGT---ATATG----AAGACCTGAGGTATA-----------
AGCTCTCGCT 288
               |||| || | || | || ||| || || | ||| |
|
Db   1596

```
CACTGGCACCATCACATCAGTCATCAGTCCTTAGATACAGAACCTTTACTGACTCCCTCA 1537

Qy         289 AGAGTTCC------CCAGTGGCTACCCTTACAATGCGCCCACAGT---------
GAAGTT 333
               |  |  ||||      |||   ||| ||  || |  |  | |||  |        |||
||
Db        1536 AAACTTCCATGCTTCCA--
AACTAACCAAGCAGTTCTTCTACATTGGGATCATCGAATTT 1479

Qy         334 CC--------TCACGCCCTGCTATCACCCCA------
ACGTGGACACCCAGGGTAACATA 379
               ||        ||   | || || |  | ||      || | |||| ||   |
|||
Db        1478 CCCTTCATGTTCCAACTCTCCTCTAGCTTCAATATACACATAGACAACCTTAG--
CCATC 1421

Qy         380 TG----CCT-------GGACA-TCCTGAAGG-------
AAAAGTGGTCTGCCCTGT---- 416
               ||   |||    | |  ||| ||  |      |||| |||||| |
Db        1420 
TGAAAACCTACTTTTAGAATATTCCCGAGTGGTTCCACGTAAGTCCTCTGCCAGATTCAC 1361

Qy         417 ------ATGATGTC--------
AGGACCATTCTGCTC----------------------- 439
               || |  ||        |  | |||| ||| ||
Db        1360 
ATACCCATAAATTCTACTTCATAAGCCCATACTGTTCTTAAAAAAGAAATAGAAAAAATA 1301

Qy         440 --TCCAT-----------------CCAGAGCCTTCTAGGAGA-------
ACCCAA----- 468
               || ||                    |  | |||||  | |          | | ||
Db        1300 
TATCAATATAACTTTAAAATAAGACACAAACCTTCATGAAAATATAGTCATCAAATTTAT 1241

Qy         469 ---CATTGATAGTCCCTT-------GAACAC--------------------
ACATGC---- 495
               |||||  |  |||       ||| |                      ||||||
Db        1240 
TTTCATTGGGATGCCATTTTTTGAAGAATTCCTAAGACTAATGTTTCTTGACATGCAAGA 1181

Qy         496 ---TGC----CGAGCTCTGG-----AAAAACCCCACAGCTTTTAAGAAGTAC--
CTG--- 538
               ||       ||||  |    | ||| |  |||| ||  ||||||  |||
Db        1180 
GTTAGCATTAATAGCTTACGTTACTATAAATACTGCTGCTTGGAAGCAGTACAACTGTTT 1121

Qy         539 ------------CAAGAAAC-----
CTACTCAAAGC----------------------- 557
               |  |  ||  ||||||||| |
Db        1120 
TAGAGTTTTAAGACTACAGACTTTCATTACTCAAATCTTATTCAGTAAATGTAAAAATCA 1061

Qy         558 --AGG-TC--ACCAGC--------CAGG-AGCCCTGACCCAGG--------
CTGCCCAGC 595
               ||| ||  | ||||        ||| ||||  ||  ||||        |||| |
Db        1060 
GAAGGTTCTGAACAGCTGGTTAGGAAGGTAGCCAAGATGCAGGAAAGATGTCTGCGCCTC 1001

Qy         596 CTGTCCTTG---TGTCGTCTTTTTAATTTTTCCTTAGATG-------GTC----
```

```
TGTCCT 641
                ||  |   |    |      |  |  |  || || ||        |   | ||| ||           ||     ||
|||
Db      1000 CTTTTCAAGGGCAGCCAACTCTTGAA-----
CAGTAGGTGCCAAAATATCCACATGGCCT 946


Qy       642 TTTTGTGATTTC---------------------------TGTATAGGACT--
CTT--- 667
                || |  | || |                                |||| | ||| |   |||
Db       945 TTAT-
AGCTTCCACCTGCGTCACACACAAATAACAAAGTAATGTAAATGACATGCTTGAA 887


Qy       668 -
TATCTTGAGCTGTGGTATTTTTGTTTTGTTTTTGTCTTTTAAATTAAGCCT-------- 718
                || |||| | |   ||  ||| | |   ||  | |      ||||| |  || |
Db       886 ATAACTTGT-
CAGCAATACTTTGGCTCAATTATATCACTTTAAACTTTGCTTGCAGCAAT 828


Qy       719 --------CGGTTGAGC---------CCT----
TGTATATTAAATAAATGCATTTTTGTC 757
                              |  || ||          ||      | |   || || ||||| ||
||
Db       827 AAAATGTACTACTGGGCAAATTATCTCCAGAACTTTGACTTTAAAAAATG---
TTAAATC 771


Qy       758 CTTTTTTAAAAAAAAAAAAAAAAAA 781
                      || ||  || | ||| ||| ||
Db       770 AATTATTTCAATATAAATAAATAA 747



RESULT 13
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20
   Query Match        40.6%;  Score 1930.5;  DB 1;  Length 2495;
   Best Local Similarity   40.0%;  Pred. No. 9.3e-103;
   Matches  512;  Conservative   0;  Mismatches  261;  Indels  507;
Gaps   75;


Qy        1 GGCAC---------GAGC----------------
```

```
GAGTTCCTGTCTCT------------ 23
              || ||       ||||          || |||  |  ||||
Db        357
GGAACTATACTACAGAGCAATACAGTTCTACTTAGAATTCAAGCCTCTGTTGTTAAATGA 416

Qy        24 ----CTGCCAACGC---CGCC-CGGATGGCTTCC-----------CAA----
AACCGCG- 59
                 |||        ||     || ||||          |||     | ||
Db        417
TTTGCTGATGGTGCTGTCTCCACGGTTGGATCACACTCGTGCAGTCAATTATTTCAGCAA 476

Qy        60 ----ACCCAGCCGCCACTAGCGTCGCCGCC---GC---
CCGTAAAGGAGC---------- 99
               |  ||||  ||||| | |   |||      ||   | || |||  || |
Db        477
GGTTAAACAGCTACCACTGGTGAAACCGTATTTGCGTTCAGTTCAGAACCATAACAACAA 536

Qy        100 ---------TGAGCC---GAGC---------------
GGGGGCGCCGCCCGGGGTC---- 128
                  |||  |   || |             |  | |    | || ||
Db        537
ATCTGTGAATGAATCATTGAACAATCTTTTATTACAGAAGAAGATTATCAGGCTCTGCG 596

Qy        129 -----CGGTGG--GCAAAAGGCTAC---AGCAGGAGCT-
GATGACCC------------- 164
                  | | | ||  | | | ||      ||  | | | | |  | |
Db        597
AACATCAATAGATGCTTATGACAACTTTGACAATATCTCGCTTGCTCAGCGTTTGGAAAA 656

Qy        165 TCATGATGTC-TGGCGATAAAGGGATTT-CTGC------CTTC--------------
CCT 202
                 |||||  || | | | | | | || || ||||     |||| |
Db        657
ACATGAACTCATTGAGTTCAGGAGAATTGCTGCTTATCTCTTCAAAGGCAACAATCGCTG 716

Qy        203 GAATC----------------------
AGACAACCTTTTCAAATGGGTAGGGACCATCCA 240
                  ||| |                  ||||| ||||| |||   ||  |   | ||
||
Db        717 GAAACAGAGTGTAGAGCTGTGCAAGAAAGACAGCCTTTACAA---GGATG---
CAATGCA 770

Qy        241 TGGAGCAGCTGGA---------ACAGTAT---ATGAAGACCT------
GAGGTATAAGCT 282
                  || ||| |       || | ||   |||||| ||      | ||| |
||
Db        771
GTATGCTTCTGAATCTAAAGATACTGAATTGGCTGAAGAACTCCTGCAGTGGTTTTTGCA 830

Qy        283 -------------------CT----CGCTAG----------AGTTCC-------------
CC 298
                  ||    ||| |       ||| |
||
Db        831
GGAAGAAAAAGAGAGTGCTTTGGAGCTTGTCTGTTTACCTGTTACGATCTTTTAAGGCC 890

Qy        299 AG-TGGCTACCCTTACAATGC------GCCCA----
CAGTGAAGTTCCTCACGCCCTGCT 347
                  || ||| | ||    | | |||      || ||   || || || | || |||||
|
```

```
Db        891 AGATGTCGTCCTAGAAACTGCATGGAGGCACAATATCATGGATTTTGC-CATGCCCT-
AT 948

Qy        348 ATCACCCC-------AACGTGGAC---ACCCAG--GGTAACAT---
ATGCCTGGACATC- 391
              ||| ||        | | | ||    || || || | ||   |||| |
              |||
Db        949
TTCATCCAGGTCATGAAGGAGTACTTGACAAAGGTGGATAAATTAGATGCTTCAGAATCA 1008

Qy        392 CT---------GAAGGAAAAG-----------------------
TGGTCTGCCCTGT 416
              ||         |||| | |||                    ||||| ||||
Db        1009
CTGAGAAAAGAAGAAGAACAAGCTACAGAGACACAACCCATTGTTTATGGTCAGCCCCAG 1068

Qy        417 ATGATGT------CAGGACC--ATTCTGCTCTCCATCCAGAG---
CCTTCTAGG------ 459
              |||||         ||||||| |  | ||  ||| ||| | ||   |||| | |
Db        1069
TTGATGCTGACAGCAGGACCCAGTGTTGCCGTCCCTCCCCAGGCACCTTTTGGTTATGGT 1128

Qy        460 -----AGAACC-CAACATTGATAGTCCC---------TTGAACACA-CAT----
GCTGCC 499
              | ||| |  || || | ||| |      |||  ||| |||   | ||
Db        1129
TATACCGCCACCACCGTATGGACAGCCACAGCCTGGCTTTGGGTACAGCATGTGAGATGAA 1188

Qy        500 GAGCT------------------------CTGGAAAA--------ACCC----
CACAGC 522
              | |||               ||| ||  |   |||| |
              |||
Db        1189
GCGCTGATCCTGTAGTCACCTATTTTCGTACTGAAACATCGTCTTTACCCACTTCTCAGT 1248

Qy        523 TTTTAA----GAAGTACCTGCAA---------GAAACC--
TACTCAAAGCAGGTCACCAG 567
              || |||    | |  || ||||       | |||| || | | ||| |  |
Db        1249
TTATAATGGGGGAAAACAGGCAACGTGTTCTTGTAACCTTTATTTCATGAAGGACTTCTT 1308

Qy        568 CCAG----GAGCCCTGACCCAGGCTGCCCAGCCTGT-----CCTTGTGT---------
CG 609
              |     | |  | | | || | ||    |||     |||| |
              |
Db        1309 TTTGTTTCTAACTATAAACTTGGATCACCT--
ATGTTAAAACCTTATTTCACATTCCACA 1366

Qy        610 TCTTTTTA-ATTTTTCCTTAGATGG--------------------TC---
TGTCCTTTT 644
              || ||||| | |||   || || ||                    ||   ||
              |||||
Db        1367
TCATTTTAGAATTTATTTTCGAAGGGGAATAGTTTCAATGTTTTATTCACTTGGGCTTTT 1426

Qy        645 TGT--------GATTTCTGTATAGGACT-CTTTATCTT-
GAGCTGTGGT----------A 684
              | |        |  |||| || ||| ||  || ||  | ||||| ||
              |
Db        1427
```

```
TTTCTTCCCCCTCTTTCTTTAAAGAACTGCTCAATATTCAATCTGTTGTGAAGAACCTGA 1486

Qy      685 TT-----TTTGTTTTGTTT----------------------TTG--
TCTTTTAAATTAA 714
            ||      | |||  |||||                     ||| ||| ||||||||
|
Db      1487
TTTGCACTCTGTAGTGTTTAAAGAAACAAAGAAACTCTAATATTGAATCTCTTAAATTTA 1546

Qy      715 GCCTCGGTTGAGCCCTTGTA------TATTAAATAAATGCATTTTTGTC--
CTTTTTTAA 766
            |  |  || |   ||| |     |||| |||||||||||| || ||| ||
|
Db      1547
GTGTATGTAAACAGCTTACAAATACGTATTGTCTAAATGCATTTAAATCTGTTTTATTCA 1606

Qy      767 AAAAAAA---AAAAAAAAAA 783
            || |||| ||| |||||
Db      1607 AAGAAAAGCTAAAGCAAAAA 1626


RESULT 14
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match             40.5%;  Score 1925.5;  DB 1;  Length 2495;
  Best Local Similarity   40.4%;  Pred. No. 1.9e-102;
  Matches  477;  Conservative    0;  Mismatches  294;  Indels  411;
Gaps    64;

Qy        1 GG---CACGCAGCGAGTT-CCTGTCTCTCTGCCA------------------------
ACG 32
            ||    || || |  ||| ||||| | ||  |||
|||
Db      1286 GGTTACAAGAACACGTTGCCTGT-
TTTCCCCCATTATAAACTGAGAAGTGGGTAAAGACG 1228

Qy       33 ------CCGCCCG------GATGGCTTCCCAAAACCGCGACCCAGCCGCCACTAGC-
GTC 79
            | |  ||     | || | |  | ||| || |   ||| ||
```

```
 ||
Db      1227 ATGTTTCAGTACGAAAATAGGTGAC-TACAGGATCAGCGCTTCATC--
TCACATGCTGTA 1171

Qy        80 GCCGCCGCCCGTAAAGGAGCTGAGCCGAGCGGGGGCGCCG-----------CC--
CGGGG 126
              ||   |||| |    |  |||| ||   ||| || || |              ||
 ||
Db      1170 CCCAAAGCCAG-GCTGTGGCTGT-
CCATACGGTGGTGCGGTATAACCATAACCAAAAGGT 1113

Qy       127 TCCGGTGGGCAAAAGGCTACAGCAGGAGCTGATGAC--CCTCA--
TGATGTCTGGCGATA 182
              || | ||     | |||| |||   ||  ||| || |  |  ||  ||  | ||| |
 |||
Db      1112 GCCTGGGGAGGGACGGCAACACTGGGTCCTGCTGTCAGCATCAACTGG-
GGCTGACCATA 1054

Qy       183 AA----GGGAT--------------------TTCTGCCTTCC---------
CTGAATCAGA 210
              ||   ||| |                    |||| ||| |       ||||| ||
Db      1053
AACAATGGGTTGTGTCTCTGTAGCTTGTTCTTCTTCTTTTCTCAGTGATTCTGAAGCATC 994

Qy       211 CAACCTTTTCAAATGGGT-AGGGAC-CATCCATGGAGCAGCTGGAACAGTATATG--
AAG 266
              ||  | ||| | || | | || |  | | |||     | || || ||  |||
 ||
Db       993
TAATTTATCCACCTTTGTCAAGTACTCCTTCATGACCTGGATGAAATAGGGCATGGCAAA 934

Qy       267 ACCTGAGGTATAAGCTCTCGCTAGAGTTCCCCAGTGG----CTACCCTTA------
CAAT 316
              | |   | |||     ||| | |||| |  |   |    || |||||        |
Db       933
ATCCATGATATTGTGCCTCCATGCAGTTCTAGGACGACATCTGGCCTTAAAAGATCGTA 874

Qy       317 GC--GCCCACAGTGAAGTTCCT---CACGCCCTGCTATCACCCCAACGTGGACACC-
CAG 370
              | |   |||| ||| ||| |||    ||| || | || ||          |||
 |||
Db       873
ACAGGTAAACAGACAAGCTCCAAAGCACTCTCTTTTTTCTTCCTGCAAAAACCACTGCAG 814

Qy       371 GGTAACATATGCCTGGAC---ATCCT--GAAGGAAAAGTGGTCTGCCCTGTAT-
GATGTC 424
              |   | | ||| |   ||| || | |  | ||| |||| || || ||
 |||
Db       813
GAGTTCTTCAGCCAATTCAGTATCTTTAGATTCAGAAGCATACTGCATTGCATCCTTGTA 754

Qy       425 AGGAC---CATTCT------GCTCTCCA-------TCCAG-------
AGCCTTCTAGGAG 461
              | | |   | ||||      ||||| ||      |||||       ||||| |
 |||
Db       753
AAGGCTGTCTTTCTTGCACAGCTCTACACTCTGTTTCCAGCGATTGTTGCCTTTGAAGAG 694

Qy       462 A-ACCCAACATTGATAGTCCCTTGAACACA-------CATG--
CTGCCGAGCTCTGGAAA 511
```

```
                    | |  || | |  |     || | ||||| ||        ||||    | || | | |||
|
Db       693 ATAAGCAGCAAT-----                                         639
TCTCCTGAACTCAATGAGTTCATGTTTTTCCAAACGCTGAGCA

Qy       512 AAC---------CCCA-----------CAGCTTTTAA-----                573
GAAGTACCTG------- 538
             | |           | |         || || ||   | || ||||
Db       638                                                           579
AGCGAGATATTGTCAAAGTTGTCATAAGCATCTATTGATGTTCGCAGAGCCTGATAATCT

Qy       539 ----------------------CAA-                                552
GAAACCTACTC--------------------- 552
                              ||| ||  | | ||
Db       578                                                           519
TCTTCTGTAATAAAAAGATTGTTCAATGATTCATTCACAGATTTGTTGTTATGGTTCTGA

Qy       553 ----AAAGCA-----GG--TCACCAG--------------                573
CCAGG-------------A 573
             || ||||     || ||||||||           || |
Db       518                                                           459
ACTGAACGCAAATACGGTTTCACCAGTGGTAGCTGTTTAACCTTGCTGAAATAATTGACT

Qy       574 GCCC-----TGACCC--------AGGCTGCC----CAGCCTGTCCTT--------
GTGTC 608
             || |     ||| ||       || | ||    |||| || ||        | |
|
Db       458                                                           399
GCACGAGTGTGATCCAACCGTGGAGACAGCACCATCAGCAAATCATTTAACAACAGAGGC

Qy       609 GT-CTTTTTAATTTTTCCTTAGATGGTCTGT--------------------
CCTT---- 642
             |  || ||| |  || |||   ||  | |||||                ||||
Db       398                                                           339
TTGAATTCTAAGTAGAACTGTATTGCTCTGTAGTATAGTTCCACATTGGCAACCTTGGTA

Qy       643 --------TTTGTGAT----TTCTGTATAGGACTC----------TTTATCTTG--
AGCT 678
                     |||| |  | |||| | ||| ||       || ||| || |
|
Db       338                                                           279
ATGATATCTTTGAATTGCCCTTCTTTCCAGGCATCAGTTGGATGATTCATCATGGTAATT

Qy       679 GTGGTATTTTTGTTTTGTT----TTTGTCTTTTAAA--------TTAAG-
CCTCGGTTGA 725
             ||| ||| |  | || ||    ||||| |  |||         || | ||  |
|||
Db       278                                                           219
ATGGCATTATCATATTCTTCATACTTGTCATACAAAAACACCAGTTCTGCCCAAAGATGA

Qy       726 GC-------------
CCTTGTATATTAAATAAATGCATTTTTGTCC-------------- 758
             ||                  || | | || || || | | | ||
Db       218                                                           159
GCTTGTTCTGCAGCTCTTAGCACCTTGGGAATATTCACTCTAGACCAGAACAGCTCCAGG

Qy       759 ----------TTTT-------TTAAAAAAAAAAAAAAAAAAAA 783
                      ||||      |||||   | |  | | ||| |
Db       158 TGCTCCCTCATTTTCTGAGGCTTAAATTTAGAGTATAGAATA 117
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RESULT 15
US-10-478-914-57
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match            40.4%;  Score 1921;  DB 1;  Length 2336;
  Best Local Similarity   33.1%;  Pred. No. 2.5e-102;
  Matches  512;  Conservative    0;  Mismatches  264;  Indels  772;
Gaps    80;

Qy         1 GGCACG----------------AGC--
GAGTTCCTGTCTCT------------------- 23
             ||| ||                 ||| | ||||| || |||
Db       100
GGCGCGGTTCAATACCTCGTCTAGCCTGGGTTCCAGTATCTAATTTTTTTTTTGTTTTAA 159

Qy        24 CTGCCAA--------CGCCGC-----CCGGA--------TGGC------
TTCC------- 49
             ||| |||        | |  |     | |||         ||||     ||||
Db       160
CTGACAAACTCATTTCTCTACTGGGACAGGATGCTGTGCTGGCTGGAAGTTCCATTTCTA 219

Qy        50 ---CA--AAACC------GCGACCCAGCCG----
CCACTAGCGTCGCCGCCGCCCG---- 90
             ||  || || ||       |  | || |||  |      || ||||| | | || || ||
Db       220 CAGCAAGAATCCTATCTGGAAACACAGAAGTTGTCCTCTAGC--
CACAGCAGCTCGAACT 277

Qy        91 --------TAAAGGAGCTG----AGCCGAGCGGGGGCGCC-----------
GCCCGGGGT 127
                        | |  | ||||     || | |      | ||          | |   |
|
Db       278 TTTTTGATTGTCGTTGCTGCTTTCTCCCATC----
ACCCCCATCCCCTTTTGACAAAGAT 333

Qy       128 CCGGTGGGCAAAAGGCT------ACAG--
CAGG--------------------------- 152
             ||    |  |||||| ||        |||| ||||
Db       334
CCAACTGTAAAAAGTCTTACGTAACAGTTCAGGACTACTTCGGTTCTTTTACTGGGTAAG 393
```

```
Qy        153 --------------------AGCTGATGACC---------------
CTCATGA------ 170
                                | ||| ||                  || |||
Db        394 CACTTTCAATTTTTTTTTTTTAACTAAAAGCCATTTTAAAATTGAATCTGTTGAGGGGCT 453


Qy        171 TGTCTGG---CGATAAAG-------------GGATTTCTGCC----------TTC--
CCT 202
                || ||       |     |         ||| | ||| |       ||| |
Db        454 TGACTAAAATCTTTAAGTAATTTGTGTAATGGAATACTGTCAGTGGATTTTTTCGTCTC 513


Qy        203 GAATCAG-AC---AACCTTT----TCAAATGGGTAG--------
GGACCATCCATGGAGC 246
                  || | ||     ||||| ||| |  | ||      || ||||
||
Db        514 ATTTCTGCACGTGCTCCTTTGTTCTCAGAACAGAAGCTTTTTATACACATCCCATAACGC 573


Qy        247 AGCTGGAACAGTATATGAAGACCTGAGGTATAAG---CTC-
TCGCTAGAGTTCC------ 296
                |||||||  ||||||| |  |||||| | |   | | |  ||||
Db        574 AGCTGGAGAGAGTTATGAAGTCAGTTATTATAAGGAACACAAAGGTTGCTTTCCATTCTT 633


Qy        297 --CCAGTGGCTAC---------------
CCTTACAATG---------------------- 317
                 || | | ||               |||| ||||
Db        634 TGCCTTTAGATAATTAATTTTTTTGTTTTCTTAAAATGGAGTATTTAAAGAAGGAAGAAA 693


Qy        318 --CGC-------CCACAG--------------------TGAAGTTCCTCACGCC-
CTGCT 347
                   | |       || |            |||||| | | || |
||
Db        694 TTCACAAGAAATAAACTGTTGGAGAATTTAGAAAAGTTTGAAGTTTTTACCACCTTTTCT 753


Qy        348 ATCAC-------------CCCAACG--TG-
GACACCCAGGG------------------- 372
                ||| |          || ||| || | | || |||
Db        754 ATCTCTAGTTTTGTGTGGCCAAACACTTGTGCCGCCTGGGGCGGTGGGGGTAGAGGCAAG 813


Qy        373 ---TAACA---------TATGCC-----TGGACA------------------------
TC 391
                   |||       || |||   ||||||
||
Db        814 CATAGACAGAGAGGAACTAAGCCAGACATGGACAAAGGCACGAGCCAAAACCAGACAGTC 873


Qy        392 CTG---------AAGG--AAAAGT----------
GGTCTGCC------------------ 412
                |||       ||| | |||       |||| |||
Db        874 CTGGCCGTTCGATAGGCCAGCAGTGGGTGAGACAGGTCAGCCAGCTGCAGGGGCGGGAGC 933


Qy        413 ----------------------CTGTATGA--------------------
TGTCAGGA-- 428
```

```
                                        ||| |||                      || |  ||
Db       934
GGGGGGGCGGGTAGGGACATGGATGTGTGAGGTGCTCATGCGTGCGATCGTGACTAGATT 993

Qy       429 -------------CCATT----CTGCTC--------------------------
TCCAT 444
|
                              |||||    | ||||                                ||
Db       994
CTGAAACTGCCAGCCATTTTCCCAGCTCCGCTTTGTGCAATCTAAAGGAATGCATCCCCT 1053

Qy       445 --------------CCAGAGCCT--TCTAGGAGA--------------ACC-
CAACAT-- 471
                           ||||||||| |  |||||            ||| ||||||
Db       1054
CTGAAGCAGTCTTGCCAGAGCCTAGTGAGGGAGAGAAGTATGGTAAATACCACAACATAT 1113

Qy       472 ------TGATAGTCCCTTGAAC--------ACA------
CATGCTGC------------ 498
                        || | | ||  ||||       ||        |||| |
Db       1114
GGAATCAGAAAATACCGGGAACTGGAGTGGGCAAGGGGGAATGCAGAGGGTGTGGAAATT 1173

Qy       499 ----CGAGCTCTGGAA-------------------------------
AAACCCCACAG-- 521
                      | | |||||||                           ||||||
Db       1174
TTTTAGTGATCTGGAATGTGTTGAGTGACAGGAAGTGCCCCAAGCTTCTCCCCCACCAAC 1233

Qy       522 -CTTTTAAGAAGTACCTG-------------
CAAGAAACCTACTCAAAGCAGGTCAC--- 564
                         ||| || |  ||||         |  | || |||| ||   | | | ||
Db       1234
TCTTCTCAGTCGCGCCTGCTTTTGTCTAACTCTTGTAATCTACACACTACTGCTTACAAA 1293

Qy       565 -CAGCCAG---------------GAGCCCT----GAC-CCAGGCTGC------
CC----- 592
                       | | | |               ||  |||   | | ||  || |        ||
Db       1294
GCTGTCTGAGTTTAAGACAAAAGAAACCTAAAAGTCTCCTTACTTCATAGTACCTGTGA 1353

Qy       593 ----------------AGCCTGTCC--TTGTGTC----
GTCTTTTT------------- 616
                                   ||| || ||  || | |    | | ||||
Db       1354
TATGGAAGGAATGTAAAAGCATGACCCTTTAAGCCTATGGACATTTTTTCAGGTATACAG 1413

Qy       617 -------------AATTTTTCCTTAGA-----------------------
TGGTCTG--T 638
                                 | |||||| |||                      | ||| |
Db       1414
GAGAAAGATAAAATAATTTTCCACAGAAAAATGAGAATTATGAATTATATAGTTCAGGTT 1473

Qy       639 CC----------TTTTTGTGATTTCTGTATAGG--
ACTCTTTATCTTGAGCTGTGGT--A 684
                         ||            ||| || ||||| | || |||||  |     ||| |||
Db       1474 CCAAATCTAATTTTTAAAAGAATTCTGATTCTGCTACACTTTA-
CAAATGCTTAGGTTGG 1532
```

```
Qy        685 TTTTTGTTTTGTTTTTGTCT-------
TTTAAATTAAGCCTCGGTTGAGCCCTTGTATAT 737
              || |  |||| | | ||      ||| | | || | | | | ||||| |
|
Db      1533
TTCCTAATTTGAAGGAGACTTGTTTTATTTGGTTAATGCATTGCATTTGAACTTGTTTCT 1592

Qy        738 TAAATAAATGCAT--TTTTGTCCTTTTTTAAAAAAAAAAAAAAAAAAA 783
              |  ||||| |||| |||| | ||||| ||| || |
Db      1593 ATTTTCTTTGCATAAATTTGGACTTTGGGAGAAAAATGCAAAGTAATA 1640


Search completed: March  9, 2010, 15:51:40
Job time : 5.10998 secs

                        GenCore version 6.3
                Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:        March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                          (without alignments)
                                          1134.946 Million cell
updates/sec

Title:         US-10-572-905-3
Perfect score: 6921
Sequence:      1 gccgctgccaccgcaccccg..........tcacaaaaaaaaaaaaaaa
1124

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:      417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:     834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      7335755.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result          Query
  No.   Score  Match Length DB  ID                      Description
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    1  3132.5   45.3   3210  1  US-10-478-914-4            Sequence 4,
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Appli						
2	3018	43.6	2437	1	US-10-478-914-61	Sequence 61,
Appl						
3	2987.5	43.2	2120	1	US-10-478-914-64	Sequence 64,
Appl						
c 4	2960.5	42.8	3210	1	US-10-478-914-4	Sequence 4,
Appli						
c 5	2907	42.0	2120	1	US-10-478-914-64	Sequence 64,
Appl						
6	2840	41.0	2198	1	US-10-478-914-17	Sequence 17,
Appl						
c 7	2833.5	40.9	2437	1	US-10-478-914-61	Sequence 61,
Appl						
c 8	2800	40.5	2198	1	US-10-478-914-17	Sequence 17,
Appl						
9	2795	40.4	3589	1	US-10-478-914-21	Sequence 21,
Appl						
10	2747	39.7	1946	1	US-10-478-914-62	Sequence 62,
Appl						
11	2704	39.1	2336	1	US-10-478-914-57	Sequence 57,
Appl						
12	2697.5	39.0	2495	1	US-10-478-914-20	Sequence 20,
Appl						
c 13	2653.5	38.3	2495	1	US-10-478-914-20	Sequence 20,
Appl						
c 14	2653	38.3	2083	1	US-10-478-914-3	Sequence 3,
Appli						
c 15	2628.5	38.0	2022	1	US-10-478-914-60	Sequence 60,
Appl						
c 16	2588	37.4	2336	1	US-10-478-914-57	Sequence 57,
Appl						
17	2574	37.2	2083	1	US-10-478-914-3	Sequence 3,
Appli						
18	2565	37.1	1813	1	US-10-478-914-63	Sequence 63,
Appl						
c 19	2548.5	36.8	1946	1	US-10-478-914-62	Sequence 62,
Appl						
c 20	2512.5	36.3	1813	1	US-10-478-914-63	Sequence 63,
Appl						
c 21	2506.5	36.2	3589	1	US-10-478-914-21	Sequence 21,
Appl						
22	2464.5	35.6	2022	1	US-10-478-914-60	Sequence 60,
Appl						
23	2179	31.5	717	1	US-10-478-914-42	Sequence 42,
Appl						
24	2145.5	31.0	867	1	US-10-478-914-6	Sequence 6,
Appli						
25	2119	30.6	889	1	US-10-478-914-5	Sequence 5,
Appli						
c 26	2098.5	30.3	867	1	US-10-478-914-6	Sequence 6,
Appli						
c 27	2086.5	30.1	816	1	US-10-478-914-15	Sequence 15,
Appl						
c 28	2055.5	29.7	839	1	US-10-478-914-16	Sequence 16,
Appl						
29	2042	29.5	816	1	US-10-478-914-15	Sequence 15,
Appl						
c 30	1992	28.8	717	1	US-10-478-914-42	Sequence 42,
Appl						
c 31	1987	28.7	820	1	US-10-478-914-39	Sequence 39,

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Appl
      32   1982.5    28.6    794  1  US-10-478-914-13          Sequence 13,
Appl
  c   33   1975.5    28.5    889  1  US-10-478-914-5           Sequence 5,
Appli
  c   34     1970    28.5    938  1  US-10-478-914-69          Sequence 69,
Appl
  c   35     1967    28.4    794  1  US-10-478-914-13          Sequence 13,
Appl
      36     1967    28.4   1020  1  US-10-478-914-68          Sequence 68,
Appl
      37   1964.5    28.4    938  1  US-10-478-914-69          Sequence 69,
Appl
      38     1963    28.4    839  1  US-10-478-914-16          Sequence 16,
Appl
  c   39   1952.5    28.2    889  1  US-10-478-914-9           Sequence 9,
Appli
  c   40     1943    28.1    811  1  US-10-478-914-37          Sequence 37,
Appl
  c   41   1938.5    28.0    816  1  US-10-478-914-38          Sequence 38,
Appl
      42     1916    27.7    889  1  US-10-478-914-9           Sequence 9,
Appli
  c   43   1901.5    27.5   1020  1  US-10-478-914-68          Sequence 68,
Appl
  c   44     1879    27.1    814  1  US-10-478-914-36          Sequence 36,
Appl
      45   1873.5    27.1    816  1  US-10-478-914-38          Sequence 38,
Appl
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                                    ALIGNMENTS

RESULT 1
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match   45.3%; Score 3132.5; DB 1; Length 3210;
  Best Local Similarity 38.5%; Pred. No. 1.5e-186;

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  Matches  747; Conservative   0; Mismatches  360; Indels  831;
Gaps  111;

Qy        1 GCCGCTGC-CAC----CGCACCCCGCCATGGAGCGG----------
CCGTC--------- 36
            || | ||| | |    || ||| | || ||| ||        | |||
Db       35
GCAGGTGCTCTCTTAGTGCTCCCTGGCAAGGATGGGAAGGCATGTTCAGTCCTAGGAGTA 94

Qy       37 -------GCTGC----------GCGCCCTGCTCCTCGGC----
GCCGCTGGGCTGCTGCT 75
                   || |       || |||| |   |||| | | | ||||||||
                                                          |
Db       95 GGAAGGGGCAGAGGTGTTGATGGC-
CCCTACAGAGCGGCCAAGGACAAGGAGCTGCTGTT 153

Qy       76 C----CTGC--TCCTGC-CCCTCTCCT--CTTCCTC-------------------
CTCTT 107
            |     | || |||||| |||   ||| |||| || |
            ||||
Db      154
CGAAACAGCCTTCCTGCTCCCCAACCTGCCTCCCACCCAACAGGTTTTGCATATACTCTA 213

Qy      108 C---------GGACAC------CTGCGGC----
CCCTGCGAGCCGGCCTCCTGCCCGCCC 148
            |         ||||||     |||| |   |||| | || | | |||||||
            |
Db      214 CTGGGAAGAGGGACACACCCGACTGCATCACTGCCCTCCAAGTC-
TCTCCCTGCCCTGTC 272

Qy      149 CTGCCCCCGCTGGGCTGCC--TGCTGGGCGAGAC--
CCGCGACGCGTGCGGCTGCTGCCC 204
            | || || | ||| ||   | |||| || | | ||| | | | |
            |||
Db      273 CAGCATCC-AGGAGCACCCCTAGTTGGG-
GAAGCTTCTGTGACTCCCCCTACAACAGCCT 330

Qy      205 --------------
TATGTGCGCCCGCGGCGAGGGCGAGCCGTGCGGGGGTGGCGGC--- 247
                          | |||| |   |  | || ||| || | | || ||| | ||
Db      331 AGGATGGAGTGGGGTTTGTGAACAAATGCAGAAGGC-AGTCTTAGGGAGGT--
CAGCTGA 387

Qy      248 ----------GCC---GGCAGGG----------------GGTACTG---
CGCGCCGG--- 272
                      ||| ||| |||              ||| ||   ||| | ||
Db      388
CATGCCCCTGGCCTGTGGCTGGGAAGTAGCAGAGGCTAAGGTTCTTCCCCGCTCTGGGGT 447

Qy      273 -GCATGGAGT-GC--------------GTGA-----------------AGAGCCG--
CAA 297
             || ||||| ||              ||||                ||| | | |
Db      448
TGCCAGGAGTAGCACTGGATCAGTCAGGTGACAGGGCTCTCCTCTCTCTGAGCAGGTCCG 507

Qy      298 GAGGCGG-----AAGG--GTAAAGCC------------------------
GGGGCAG--- 323
            | ||| |     |||| | | |||                         |||||||
Db      508
GTGGCAGCCTTCAAGGTCGCCACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAAC 567
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Qy        324 -----------CAGCCGGC-----GGTCCGGGTG---TAAG----
CGGCGTGTGCGTGTGC 361
                      | || |||   || || |||    |||   || ||| | ||
|
Db        568
GTCACCCTCACCTGCAGGCTCTTGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTAC 627


Qy        362 AAGA------GCCGCTACCCGGTGTGCG------------GC----
AGCGACGGCAC--- 396
                  ||||       |||| | || | |||          ||   |||| |||| |
Db        628
AAGACGTGGTACCGCAGCTCGAGGGGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATC 687


Qy        397 ------------------------CACCT--ACCCGAGCGGCTGCCA-
GCTGCGCGCCGC 429
                                       ||||| |||  | ||| ||| ||||| |  |
|
Db        688 CGCAACCTCACGTTCCAGGACCTTCACCTGCACCATGGAGGCCACCAGGCTGC-
CAACAC 746


Qy        430 CAGCCA-GA--GGGCCGAGAGCCGCGG---GGAGAAGGCC----
ATCACCCAGG------ 473
                  |||||| ||   ||| || ||| |||    |||| ||||    | |||| ||
Db        747
CAGCCACGACCTGGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCATGGCAACTT 806


Qy        474 -----TCAGCAAGGGCA-------CCTGCGAGCAAG-GTCCT-------
TCCATAGT--- 510
                       ||| || ||| ||||| |  || ||| |||||         | | ||
Db        807
CTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCTCTACTGCTGCCTGGTGGT 866


Qy        511 --------GACGCC-CCCCAAGGACATCTGGAATGTCACTGGTGCCCAGGTG-
TACTTGA 560
                      | | || || | ||| | || |||  ||||||| || | |
|
Db        867 GGAGATCAGGCACCACCACTCGGAGCACAGG---
GTCCATGGTGCCATGGAGCTGCAGGT 923


Qy        561 GCTGTGAGGTCATCG--GAATC--CCGAC----------ACCTGTCCTCAT--
CTGGAAC 604
                  || | ||| || | | | |||| ||         ||| ||||| |  | |||
Db        924 GCAGACAGG-
CAAAGATGCACCATCCAACTGTGTGGTGTACCCATCCTCCTCCCAGGAGA 982


Qy        605 AAGGTAAAAAGGG-----------
GTCACTATGGAGTTCAAAG----------------- 636
                  |  | |||||    || | || | |||    |
Db        983
GTGAAAGTAAGGGACCAACCTCTTGCCCCTTTTGGGTTCTCTGTTTCTTCTGTCCTCAT 1042


Qy        637 ----------GAC-------AGAACTCCTGCCTGGTGAC----------
CGGGACAACCT 669
                   |||     |||||| |||| | ||           | | ||
||
Db       1043
CCTGCACCCAGACCCTGTTTGGAACTCTGGCCTCATCACCCCAAGCCCTCAGAACCCCCC 1102


Qy        670 GG--------------------------CCATTCAG----ACCCGGGGTG----
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```
GCCCA 694
                  ||                      || ||| |       ||  ||||
||||
Db     1103
GGTCCTCCTCCTTTTCTGCTGCTGCACATCCCTTCTGCTTCCTCCTTGGTGCAATCCCCA 1162

Qy        695 GAAAAGCA------------------TGAAGTAACTG-------------
GCTGG----- 718
                  |||   ||                    || ||| |||          ||||
Db     1163
GAAGCCCACTCTCCTTCCATCTGCTCTGGAGTCTCTGCTCCTCTTGACTCTCTGGAGTGG 1222

Qy        719 --GTGC--TGGTA-TCTCCTCT---------AAGT-----
AAGGAAGATGCTGG------ 753
                  ||||  ||| | |   ||| |        ||||     | |  || | ||||
Db     1223
CTGTGCCTTGGCAGTGACCTTTGGCCAGGGCAAGTGCCTCATGACAGGTACTGGGTGCCC 1282

Qy        754 --AGAATATGAGT---GCCATG-CATCCAATTCCCAAGGAC------
AGGCT-------- 793
                  | |  | ||  ||| ||  |  ||| ||| | |     |||||
Db     1283
CAGGCAGCTAAGTGCCGCCCTGCCCACCAGCCCCCTATGGCTTGGGAAGGCTGGGGGTCC 1342

Qy        794 ---------TCAG----------CATC-----------AGCAAAAATTA--CAG---
TGG 818
                      |||         ||||          ||||||||| |||
|||
Db     1343
TCTTGGCCAACAGGGTGAAACCCCATCTCTACTAAAAACACAAAAATTAGCCAGGCATGG 1402

Qy        819 TTGATGC-CTTACATGAAATACCAG-------------------------------
TGAA 846
                   || ||| |   | || | ||||
||||
Db     1403 -TGGTGCGC--
GCCTGTAGTCCCAGCTACTCAAGAGGCTGAGGCAAGAGAATCGCTTGAA 1459

Qy        847 ----------AAAAGGTGAAG-GTGCCGAGCTATAAAC------
CTCCAGAATATTATTA 889
                      | | | || || | ||||||  |        |      ||||||  |  |
||
Db     1460
CCCGGGAGTCAGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGCTGATA 1519

Qy        890 G------------TCT----------------------------
GCATGGTTAAAAGT--- 907
                   |            |||                        |||||||   | |
Db     1520
GAGCAAGACTCCATCTCAAAAAAAACAACCCAAAATTTGCCTGGCATGGTGGCAGGCATC 1579

Qy        908 --------------------------AGTCATGGATAACTACAT-
TACCTG--------- 931
                                          || ||| || | || | |  |||||
Db     1580 TGTAATCCCAGCTACTCGGGAGGCTGAGACAT-
GAGAGCTGCTTGAACCTGGGAGGCAGA 1638

Qy        932 --------------------------------TTCTTGCCT---------------
AATAA 945
                                          ||  ||||               | |
```

```
Db        1639
AGTTGCAGTGGAGCCGAGATCACACCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCT 1698

Qy         946 GTTTCTTTTAATCCAATC---CACT-----------AACACTTTAGTTATATT---
CA-- 986
               ||  |    |||| ||    ||||          |||| |  | ||| ||   ||
Db        1699
GTCCCAAAAAATCAAAAAAATCACTTTTGGTAGAGATGCACTCTCGCTATGTTGCCCAGG 1758

Qy         987 CTGGT------------------------TTTACACAGAGAAATACAAAAT--
AAAGAT 1019
               |||||                        ||  |||   ||  | |||| |
|||
Db        1759
CTGGTCTTGAACTCCTGGGCTCAATTGATCTTCCCACCTTGACCTCCAAAGTGCTGGGAT 1818

Qy        1020 CACA---------CATCAAGACTATCTACAAAAATTTATTATA-----
TATTTACAGAAG 1065
               |||         || || | ||| | || | |  || |||||    | | | ||
||
Db        1819
TACAGGTGTGAGCCACCATGCCTAGCCTCAGGGAATTCTTATAAGAACTCTATGAAGTAG 1878

Qy        1066 --AAAAGCATGCATATCATTAAACAAATAAA-----------------
ATACTTTTTATC 1106
               |  | ||| | || || || || || |||                    || ||   |
|
Db        1879 GCATCACCAT-
CTTCTCTGTATCCATGGAAAGAGAGGCCTAGAGATGTATGCTAACTTGC 1937

Qy        1107 ACAAAAAAAAAAAAAAAA 1124
               |||    | | |     |
Db        1938 CCAAGCTCACATAGCCCA 1955


RESULT 2
US-10-478-914-61
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match          43.6%;  Score 3018;  DB 1;  Length 2437;
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```
   Best Local Similarity   36.6%;  Pred. No. 1.2e-179;
   Matches  758;  Conservative   0;  Mismatches  357;  Indels  956;
Gaps  120;

Qy         1 GCCGCTG----CCAC-CGCAC------CCCGC-------
CATGGAGCGGCCGTCG----C 38
             || || |   || | ||||      || |        || | | | |||
|
Db        19
GCTGCGGAATTCCTCGAGCACTGTTGGCCTACTGGGTGTACTGTGGAGACTGTCAAAGTC 78

Qy        39 TGC--GCGCCCTGCTCCTCGGCGCCGCTGGG--CT----GCTGCTCCTGCTCC-----
TG 85
             | | | |||| | ||| || || || |    | | |||||| ||
|
Db        79 TCCCGGAGCCCAATTTC-
CGGAAGCGGTGAGTTCTGAAAGAAGTTCCTGCACCGTAGTTT 137

Qy        86 CCCC--TCTCCTCTTCCTCCTCTTCGGACACCTGCGGC-------------
CCCTGC--- 127
             |||   ||| |   ||| |   |  | ||| |||          ||| ||
Db       138
CCCAAGTCTGCGAATCCCCAACCATGAGCGCCTCGGGCGTACTGTCCTTTACCCAGCAAG 197

Qy       128 -----------GAGCCGGCC----------------------TCCTGCCCGCC-
CCTGCC 153
                         | || ||||                    |||| ||||
|||||
Db       198
GATGGGAGCAGGTGCTGGCCAAAGTGAAACGGGCTGTGGTTTACCTGGACGCCGCCTGCG 257

Qy       154 CC---------CGCT-GGGCTGC------------CTGCTG--GGC-----
GAGACCCG- 183
             ||         | || |||||||             || ||| |||    | | |||
Db       258
CCGAGAGCCTGCACTGGGGCTGCGGATCCACCCGTCTCCTGGAGGCGGTGGGGGGCCCTG 317

Qy       184 -------------------------CGACGC--------GTGCGGC--
TGCTGCCC---- 204
                                      ||||||       ||| ||   || ||||
Db       318
ACTGTCACCTGCGAGAGTTCGAGCCCGACGCAATTGGTGGTGGAGCCAAGCAGCCCAAGG 377

Qy       205 -----TATGTGC------GCCCGCGGCGAGGGCGAGCCGTG---------
CGGGGGTGGC 244
                  | |||||     ||| ||| | ||| || |||||       |||   |
|
Db       378 CAGTGTTTGTGCTGAGCTGCCTGCTGCTGAAAGGCCGGACCGTGGAGATCCTACGG----
GAC 433

Qy       245 GGCGCCGGCAGGGGGTACTGCGCGCCGGGCATGGAGTGCGTGA---
AGAGCCG------- 294
                | | || | ||| |   | ||| | | ||| | |    |||||
Db       434
ATCATCTGCCGCAGTCACTTCCAGTATTGTGTGGTGGTCACAACCGTGAGCCACGCTGTC 493

Qy       295 ---------------------CAAGAGGCGGAAGGGTAAAGCC--------
GGGGCAGCA 325
                                  | || ||||| || |    |||
|||||||||
```

```
Db       494 CACCTCACAGCTAATCATGTCCCAGCGGCGGCAGCG----
GCCGAGATGGAGGGGCAGCA 549

Qy       326 GCCGGCGGTC------CGGGTG------------------------------
TAAGC 346
                 ||||| | ||      | ||| |                            ||
|
Db       550
GCCGGTGTTCGAGCAGCTGGAGGAGAAGCTGTGTGAATGGATGGGCAACATGAACTACAC 609

Qy       347 GGC----GTGTG-CGTG---------TGCAAGAGCC----
GCTACCCGGTGTGC------ 382
                 |||    |||| | ||      ||| | ||   ||| ||| | |||
Db       610
GGCCGAGGTGTTCCATGTCCCGTTATTGCTTGCCCCTGTTGCTCCCCACTTTGCCTTGAC 669

Qy       383 ---------GGCA--------------GCGAC---------GGCACCACCT-------
AC 403
                         |||              || ||      ||||| |||
|
Db       670
TCCAGCTTTTGCATCCCTTTTCCCACTGCTACCCCAGGATGTGCACCTCCTTAATAGCGC 729

Qy       404 CCGAGCG-----------GCT-----GCCAG----------------
CTGCGC------- 424
                 |||| ||          ||| |   ||| |           || |||
Db       730
CCGACCGGACAAGAGGAAGCTGGGAAGCCTGGGTGATGTGGACTCCACTACGCTAACCCC 789

Qy       425 ---GCCGC--CAGC----CAGA-----------GGGCC------------
GAGAGC---- 448
                   || || | ||    ||||           ||||          | || |
Db       790
AGAGCTGCTGCTGCAGATCAGATGCCTAGTGTCAGGCCTCAGTTCTCTGTGTGAACATTT 849

Qy       449 -------CGCGGGGA----------GAAGG--
CCATCACCCAGGTCAGCAAGG------- 482
                 || | |||          | ||| || | | ||||||| |   |
Db       850
AGGAGTACGGGAGGAGTGTTTTGCTGTAGGTTCCTTAAGTCAGGTCATCGCTGCGGATCT 909

Qy       483 ----------GCACCTGC---GAGCAAG-----GTC--------------
CTTCCATAGT 510
                          || ||||| || || |    | |            | || |
||
Db       910
GGCCAATTATGCCCCTGCAAAGAACAGGAAGAAGACTGCTGCAGGCAGGGCATCAGTGGT 969

Qy       511 -------GAC---GCCC-------CCCA--------AGGACATC-
TGGA----------- 533
                 ||| ||| ||| | ||| |         |||||| ||||
Db       970
TTTTGTGGACAGAACCCTGGATCTCACAGGAGCAGTTGGACATCATGGAGACAACTTAGT 1029

Qy       534 ------------------ATGTCACTGGTGCCCAGG------------
TGT-------A 555
                   | || | | |||||||                 |||
|
Db      1030
AGAGAAGATCATTTCAGCACTTCCCCAGCTCCCAGGCCACACAAATGATGTGATGGTTAA 1089
```

```
Qy        556 CTTGA----GCT-------------------------------GTGAGGT--
CATCGG- 576
              | |||     |||                             || ||| || |
              |
Db       1090
CATGATAGCGCTCACTGCACTCCATACTGAGGAGGAAAATTATAATGTGGTTGCACCAGG 1149

Qy        577 -----AATCCC--------GACACC--------TGTCCT--------CAT--CTGGA-
AC 604
                   || |        ||||||        | |||        | |  ||| |
              ||
Db       1150
CTGTCTTTCACAATTCAGTGACACCACAGCCAAAGCCCTATGGGAAGCTTTACTGAACAC 1209

Qy        605 AAGGTAAAAAGGGGTCACTATGG-AGTTCAAAG--------------GAC------
AGA 642
              | |  | |||| ||    |||| ||||| ||               | |
              |||
Db       1210
TAAGCACAAAGAGGCAGTGATGGAAGTTCGGAGACATCTAGTGGAAGCGGCAAGCAGAGA 1269

Qy        643 ACTCCTGCC--------------TGGTG--------ACCGGGACA--ACCTGGCC---
AT 675
                 |  ||||||             ||| |        ||||||||| | || ||
              ||
Db       1270
AAACCTGCCAATCAAGATGAGTATGGGGAGAGTCACACCGGGACAGCTCATGTCCTATAT 1329

Qy        676 TCAG-------------ACC-----------------CGGGGTGGC-----
CCAG----- 695
              ||||             |||                 | |||||    ||||
Db       1330
TCAGCTCTTCAAGAACAACCTCAAAGCTCTAATGAATCATTGTGGCCTCCTCCAGCTTGG 1389

Qy        696 ------AAAAGC-------ATGAAGTA-------ACTGGC---TGGG------
TGCTGGT 726
              | |||       |||| |       |||| |  |||| |
              ||||
Db       1390
ACTGGCCACAGCTCAAACGTTGAAACACCCACAGACTGCCAAGTGGGACAACTTTCTGGC 1449

Qy        727 AT--------CTCC----TCTAAGTAAGGAAGATGCTGGAGAATATG-
AGTG-------- 765
              |          ||||    || || |   | |    | | ||  |  | |||
Db       1450
TTTTGAAAGGCTCCTTCTTCAGAGCATTGGGGAGTCAGCAATGTCCGTTGTGTTAAATCA 1509

Qy        766 -------CCATGCAT---CCAAT-TCCCA-AGGAC------
AGGCTTCAGC-------A 799
                      |||||  |   || |  |||| || ||        | || ||||
              |
Db       1510
GCTGCTGCCCATGATTAAGCCTGTAACCCAGAGAACCAACGAGGACTACAGCCCTGAGGA 1569

Qy        800 TCAGC---------------------------------
AAAAATTACAGTGGTTGATGC 825
              | ||                             | |  | || || |   |
              |
Db       1570
```

```
ACTGCTGATCCTTCTCATATATATTTATTCTGTCACTGGAGAGCTCACGGTAGACAAAGA 1629


Qy        826 CTTACAT------GAAATACCAGTGAAAAAAG------------------
GTGAAGGTGC 861
              |  |   |       |||  |  ||| || ||||                |||| |
|
Db       1630
CCTGTGTGAAGCAGAAGAAAAAGTCAAGAAAGCATTGGCTCAGGTCTTCTGTGAGGAATC 1689


Qy        862 CGAGCTATAAAC----CTCCAGAATATT------------------ATTAGTCTG-
CAT- 897
               |  | | | |    || || || |||               |||| ||||
|||
Db       1690
TGGATTGTCACCTTTGCTGCAAAAAATTACGGACTGGGACTCTTCAATTAATCTGACATT 1749


Qy        898 -----GGTTAAAAGTAGTCATGGA--------
TAACTACATTACCTGTTCTTGC------ 938
                  |  ||| | ||| ||||         | ||| || |  |   | | ||||
Db       1750
TCACAAATCCAAAATTGCCGTGGATGAACTCTTTACTTCACTTCGGGATATTGCTGGAGC 1809


Qy        939 -------------------------CT-AATAAGTTTCTTTTAATCCAATCCACTA-
AC 970
                                        ||  ||| ||| ||  |||| | |||| |
|
Db       1810
TCGGAGTCTCCTGAAACAGTTTAAGTCTGTATATGTTCCTGGAAATCATACCCACCAGGC 1869


Qy        971 ACTTTA------GTTATATTCACTGGTT------------TTACA--
CAGAGA------A 1004
              |  |||       || |     |  |||           || ||  | ||||
|
Db       1870
ATCTTATAAGCCATTGTTGAAGCAAGTTGTGGAGGAAATATTTCATCCCGAGAGGCCAGA 1929


Qy       1005 ATAC-AAAATAAAGATCACA---CATCAAGACT-----ATCTAC--
AAAAATTTATTATA 1053
              | |    |||  || |||| | ||| ||    |||| | |||| |  |||
Db       1930
TTCCGTTGATATTGAACACATGTCTTCAGGCCTCACTGATCTCCTTAAAACTGGATTTAG 1989


Qy       1054 TATTTACA-GAAGAAAAGCATGCAT-ATCAT------
TAAACAAATAAAATACTTTTT-- 1103
              || | || |||| |||  ||| || | || |      || |     || || |||
Db       1990
CATGTTCATGAAGGTGAGCCGGCCTCATCCTAGTGACTACCCCCTCCTGATCCTCTTTGT 2049


Qy       1104 ----------ATCACAAAAAAAAAAAAAAAA 1124
                        |||||        ||  |||
Db       2050 GGTAGGTGGGGTCACAGTCTCTGAAGTGAAA 2080
```

RESULT 3
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA

```
  Query Match         43.2%;  Score 2987.5;  DB 1;  Length 2120;
  Best Local Similarity   41.5%;  Pred. No. 6e-178;
  Matches  669;  Conservative   0;  Mismatches  410;  Indels  533;
Gaps   93;

Qy          1 GCCGCTG---------CC--------ACC---GCAC--------------CCC--
GCCA- 23
              || ||||         ||        ||| || |             |||
||||
Db        519
GCAGCTGGCCAGCCTTCCTGGCTTGAACCTGGGCTCACTCAAGGACAAGGCCCAGGCCAC 578

Qy         24 --TGGAG------CGGCCGTC-GCTG--------CGCGCCCTG-------
CTCCTCGGCG 59
                ||| |         || || ||||       | || | ||       ||| |||
Db        579
ACTGGGGGATCTCAAGCAATCAGCTGAGAAGTGTCACGTCATGTGACCACTTCCCCGGGG 638

Qy         60 ----CCGCTGGGCTG-----------------------------------------
CTG 73
                  || ||||||||||
Db        639
TTACCCACTGGGCTGGGCCCCCATGAGGGCTAAGAGTGTGTCAACTTCCAGGGACCCATA 698

Qy         74 CTCC--------------------TGCTCC-----------------------------
TG 85
              ||||                    ||| ||
Db        699
CTCCATTTGGGGCTTTGTTTCCCTTGCCCCATCCTAGTTCCAAGACCTTTCCCATCCATG 758

Qy         86 CC----------------------CCTCTCCTCT-----------
TCCTCCTCTTCGGAC 112
              ||                    ||||||||| ||         ||| | |||||
Db        759
CCCCAAGCCTATCTTCTGGTTTCTTCCTCTCCGCTGGGAGTAAAGTCCCCATCTTCACTC 818

Qy        113 --ACCTGCGG------CCCCTGCG----AGCC------
GGCCTCCT-------------- 140
                ||| | |       |||| |     ||||      |||||||
```

```
Db        819
TACCCTTCAGGACCCTCCCCACCAGCTCAGCCTGTGGAGGCCTCCCAAGATTGTAGGAAT 878

Qy        141 --GCCCGCCCCT-----------GCCCC-----------
CGCTGGGCTGCCTGCTGGG-- 174
               |||| ||||          |||||        | | ||    || | ||
Db        879
AGGCCCATCCCTCTCTGGCCATGGCCCCAAGTTCCTGCACACAGGAGCACCCACAGAGAG 938

Qy        175 -------------CGAGACCCGCGACGCGTGC---
GGCTGCTGCCCTATGTGCGCCCGC 217
                      | | |||| | | |||| | | | ||| |   | | ||
                                                                  |
Db        939
ACACACACAGGACACAAAACCCCTGGCACGTTCAGAGACAGAAGCCACAGACACATCC-C 997

Qy        218 GGCGAGGGCGAGC-CGTGCGGGGGTGGCGGCGCCGGCAGG-GGGTACTG-
CGCGCCGGGC 274
               ||| | | |  | | |||| | | |||| | | | || | | | || | |
                                                                  |
Db        998 GGCACAGACAGACACACACGAG---GCCAGCTCC--
CTTGCGTGTCCAGCCCCTCCAGAC 1052

Qy        275 A-----------------TG---
GAGTGCGTGAAGAGCCGCAAGAGGCGGAAGGGTAAAG 314
               |               || |||  || ||   || | |   || || || |
                                                                  |
Db        1053 ACCACCACTCAGAAACTCTGAGAGAGAGCATGGGCAGACACCCTCAGCAGACAGG--
AGG 1110

Qy        315 CCGGGG----------------------------CAGC--------
AGCC---- 328
               || | |                              | ||        ||||
Db        1111 CCTGAGTTCCAGTCTCCACCTTTATTGTTCTTGAAAGCCCCTGCTCTCTCTGAGCCTTAT 1170

Qy        329 -------------------GGCGGTCC-GGGTG------TAAGC-------
GGCGTGTGC 355
                      | |||| | || | || ||| ||
Db        1171 TTCATCATCTGTAAAATGGGAATGTCCTGAATGACTTCTAAGGCTCTTTCTGGCTTGAAC 1230

Qy        356 -GT--GTGCAAGAGCCGCTACCCG--GTGTGC--GGCAGCGACGGC-
ACCACCTACCCGA 407
               || | ||| | || | ||| || || |||||| | || |||| | |
                                                                  |
Db        1231 TGTCAGAGCCAAGCCCACATCCCTCCTTGGGCAGGGCAGCAGCTGCTGCCACAGCCTCCA 1290

Qy        408 GCGGCTGCCAGCTGC--GCGCCGCCAGCCAGAG---------------
GGCCGAGAGCCG 450
               |||||||||| |||   || | | |||| |          ||| |||
                                                                  |||
Db        1291 GCGGCTGCCA-
CTGTGGGCTCTGGGAGCCGGAGCGATGCTGTGTGAGAGGCAGAGTGCCA 1349

Qy        451 CGG--GGAGAAGGCCATCACCCAGGTCAG-----CAAGGGCACCTGCGAG--
CAAGGTCC 501
               || | |  ||| ||| | | || ||  |  ||| | ||| |  || | || ||
Db
```

```
         ||
Db       1350 AGGATGAAGCTGGCACTGAAC--
AGTAAGCGGCTCCAGGCCTCCTCTGGGCCCAGGGCCC 1407

Qy        502 TTCCAT----AGTGACGCCCCCCAAGGAC---ATCTGGAAT--GTCACTGG--
TGCCCAG 550
                  |||         ||   |  ||   || ||    |||||| |   |  |||| |  ||
Db       1408 AGCCAATTTCTGTTCTGTTCCTGTAGAACGCTCTCTGGATTCCATAGCTGGAATCTCC-- 1465

Qy        551 GTGTACTTGAGCTGTGAGGTCATCGGAATCCC---------GAC-
ACCTGTCCTCATCTG 600
                  | |  | | | |||| ||   ||||||          | | |||| || |
                  |||
Db       1466 -TCTCTTAGCTCAGTGA-
AAAATAAAAATCCCAAATGGTGTGCCTACCTTCCCACTTCT- 1522

Qy        601 GAACAAGGTAAAAAGGGGTCACTATGGAGTTCAAAGGACAGAACTCCTGCCT------
GG 654
                  || ||   ||| |||   ||||||||| ||  |       |||||||
                  ||
Db       1523 -TAC-TGGCTTCCAGGAGTC---
TTGGAGTTCATAGCCCCCGAGCCTGCCTTAAAGGGG 1577

Qy        655 TGACCGGGACAACCTGGCCATTCAG--ACCC----GGGGT---GGC--
CCAGAAAAGCAT 703
                  || ||    || ||     | | ||| | |    ||||    ||| ||||      ||
Db       1578 TGTCC--TCCACCCCCCACCTACAGCTTCACAGGAGGGGAGAGGGCATCCAG---
TGCTA 1632

Qy        704 GAAGT--AACTGGCT-GGGTGCTGGTATCTC----CTCTAAGT-
AAGGAAGATGCTGGAG 755
                  | |||  || || ||  |   ||| ||||    | || || |||| |   ||||
                  |
Db       1633 GGAGTAGAAGTGTCTCCAGCTCTGTTCTCTTGGGGCCCTGGGTGAAGGTGGGGTCTGGGG 1692

Qy        756 AATATGA---------GTGCCAT------------GCATCC-
AATTCCCAAGGACA---- 789
                  |||||         | || |               ||| ||  |||      || |
Db       1693 CTTATGAAATAGGTCTGGGCTTTGAGGAGGATGGGAGCAGCCTCATTATGTGGGGAAGATG 1752

Qy        790 -GGCTTC---
AGCATCAGCAAAAATTACAGTGGTTGATGCCTTACATGAAATACCAGTGA 845
                  ||| ||   || ||| |  ||   | || ||   | || |||      || |    |
                  ||
Db       1753 GGGCCTCTGGGGCGTCA-CTGAGACCACA---
GGTGGGGCCGGGGCTGGACCGCAGCTG- 1807

Qy        846 AAAAAGGTGAAGGTGCCGAGCTATAAACCT---
CCAGAATATTATTAGTCTGCATGGTTA 902
                  |||| ||||| || ||   ||| ||  | |          | ||||
Db       1808 TCTTGGGTGCCTGTGCC-TGCACCCCTCCTCACCCTAGAGACGGAAGATGTGCA-
AAAAG 1865

Qy        903
AAAGTAGTCATGGATAACTACATTACCTGTTCTTGCCTAATAAGTTTCTTTTAATCCAAT 962
                  |||| ||  | ||  |||| |||| |||| || |   |   | | | |   ||| | ||
                  |
```

```
Db      1866 AAAGAAGG-AAGGGCAACTGCATT-CCAGCCC---
CACACTGTGATGACTTTGAGCCTGT 1920

Qy       963 CCACTAACACTTTAGTTATATTCACTGGTTT-
TACACAGAGAAATACAAAATAAAGATCA 1021
              ||  |  |  | ||     |  |   || | | | |   |||| | | |
 ||
Db      1921 CCTTTCCCTCCTTGAGCCTGT---
CTTGCTTGTCCCCTGTAAAATGAACAGTCCCCCTCT 1977

Qy      1022 CAC---------ATCAAGACTATCTACAAAAATTTATTATATATTTA-
CAGAAGAAAAGC 1071
              | |        |  || ||    |  ||||   | |  ||  |||  |  || ||  || ||
 |
Db      1978
CCCCCAAATAGTAATAATACATGTTTCAAAGGGTGACCATTTATAAAGCATATGACAAAC 2037

Qy      1072 ATGCATATCATTAAACAAATAAAATACTTTTTATCACAAAAAAAAAAAAAAAA 1123
              |||||||| ||||    |    ||  ||||| |  | ||||||||||    |
Db      2038 ---CATATCAATAAATGTAACTCATTCTTTTAAAAAAAAAAAAAAAAAAAGGCCA 2086


RESULT 4
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match             42.8%;  Score 2960.5;  DB 1;  Length 3210;
  Best Local Similarity   35.9%;  Pred. No. 2e-175;
  Matches  746; Conservative   0; Mismatches  357;  Indels  973;
Gaps  126;

Qy         1 GCCGCTG----------------CCACC---GCA-----------CCCCGC--
CATG--- 25
              ||| |||                 |||||  |||            |||| |  | ||
Db      2134
GCCTCTGAAAGTCAGGATACTGACCACCTCGGCATCTCTCCCCTTCCCCACTGCTTGCGA 2075

Qy        26 ------GAGC-GGCC--GTCGCTGCGCGC-CCTGCT----CCTCGGCGCCGC---
TGGGC 68
              | || ||||    || |   ||| || |||    || | | || ||    ||
```

```
             ||
Db      2074
ATGCCAGTGCTGGCCTGTTCCTTAAACGCACCAGCTCATCCCCCAGAGCAGCCTGTGTGC 2015

Qy        69 T---------GCTGCTCCTGCTCCTGCC--CCTCTCCTCTTCCTCCT-------
CTTC-- 108
                 |       |||||  ||  |||||  ||   ||||   |||  | |||        || |
Db      2014 TCTGCCAGCGACTGCTACTTCTCCT-
CCGGCCTCAGCTCAACATCCCAGCTATGCTACCC 1956

Qy       109 ----------------GGACA------CCTGC-------
GGCCCCT-------------- 125
                               || ||       | | |       |||| ||
Db      1955
TGGGCTATGTGAGCTTGGGCAAGTTAGCATACATCTCTAGGCCTCTCTTTCCATGGATAC 1896

Qy       126 -GCGA----------
GCCGGCCTCCT--------------------------------- 140
                   | ||        ||| | || |
Db      1895
AGAGAAGATGGTGATGCCTACTTCATAGAGTTCTTATAAGAATTCCCTGAGGCTAGGCAT 1836

Qy       141 ----GCCCGCCCCTG---CCCCCGC----------------
TGGGCTG-----------C 166
                      || | | ||||    ||| ||                |||| |
|
Db      1835
GGTGGCTCACACCTGTAATCCCAGCACTTTGGAGGTCAAGGTGGGAAGATCAATTGAGCC 1776

Qy       167 CTGCTGGGCGAGACCCGC---GAC----------
GCGTGCGGCTGCTGCCCTATGTG--- 210
                   | | |  | ||||| ||   | |       | |||| || || ||  | |||
Db      1775 CAGGAGTTCAAGACCAGCCTGGGCAACATAGCGAGAGTGCATCT-
CTACCAAAAGTGATT 1717

Qy       211 -------------------------CGC-------
CCGCGGCGAGGGCGAGCCGGTG---- 234
                               ||| |       || ||| || | ||| |||
Db      1716 TTTTTGATTTTTTGGGACAGAGTCTCGCTCTGTCACCCAGGC--
TGGAGTGCAGTGGTGT 1659

Qy       235 -----CGG----------------------GGGT---GGCGGC------------
GCC-- 250
                               |||                   ||| |  || ||              |||
Db      1658
GATCTCGGCTCACTGCAACTTCTGCCTCCCAGGTTCAAGCAGCTCTCATGTCTCAGCCTC 1599

Qy       251 ------GGCAGGGGGTAC---TGC--GC------
GCCGGGC------------------- 274
                           || ||| |||    ||| ||        ||| |||
Db      1598
CCGAGTAGCTGGGATTACAGATGCCTGCCACCATGCCAGGCAAATTTTGGGTTGTTTTTT 1539

Qy       275 -----ATGGAG---TGCGTGAAGAGCC-GCAAGAG-
GCGGAAGGGTAAAGCCGGGGCA-- 322
                           ||||||    |||    |   ||| ||  ||| |  | |  |   ||| ||
Db      1538
TTGAGATGGAGTCTTGCTCTATCAGCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACT 1479

Qy       323 GCAGCC---
```

```
GGCGGTCCGGGTGTAAGC-------------------------------- 346
                  ||| ||   | |   |||||| ||||
Db      1478 GCAACCTCTGAC-
TCCCGGGTTCAAGCGATTCTCTTGCCTCAGCCTCTTGAGTAGCTGGG 1420


Qy      347 ------GGCGTG--------TGC-------------
GTGTG------------------- 360
                |||| |   ||| 　    ||||
Db      1419
ACTACAGGCGCGCACCACCATGCCTGGCTAATTTTTGTGTTTTTAGTAGAGATGGGGTTT 1360


Qy   GG 384 -----------CAAGAG-----CCG--CTACCC---------------GGTGTGC--
                  ||||||    ||   || |||             |||| ||
                ||
Db      1359
CACCCTGTTGGCCAAGAGGACCCCCAGCCTTCCCAAGCCATAGGGGGCTGGTGGGCAGGG 1300


Qy      385 CAGC--------GAC---GGCACCACCTACC---CGAGCGGC---
TGCC----------- 416
                | ||        | |   ||||||  ||||   |  | |||   ||||
Db      1299
CGGCACTTAGCTGCCTGGGGCACCCAGTACCTGTCATGAGGCACTTGCCCTGGCCAAAGG 1240


Qy      417 -AGCTGC----GCGCCGCCA-GCCAGAGGGCCGAGAG-----------CC---
GC----- 451
                 ||||    || | |||| ||||||| | | ||||        ||   ||
Db      1239
TCACTGCCAAGGCACAGCCACTCCAGAGAGTCAAGAGGAGCAGAGACTCCAGAGCAGATG 1180


Qy      452 ---GGGGAGAAGGC--C-----AT--CACCCAGGT--------------------
CAGC 478
                   || ||| ||| |    ||  |||| |||
                ||||
Db      1179
GAAGGAGAGTGGGCTTCTGGGGATTGCACCAAGGAGGAAGCAGAAGGGATGTGCAGCAGC 1120


Qy      479 A-------------------------AGGGC-------------ACCTG-----
CGAG 493
                |                    |||||                || |     |
                |
Db      1119
AGAAAAGGAGGAGGACCGGGGGGGTTCTGAGGGCTTGGGGTGATGAGGCCAGAGTTCCAAA 1060


Qy      494 CAAGGTC--------------------------------------------
C------- 501
                || ||||                                              |
Db      1059
CAGGGTCTGGGTGCAGGATGAGGACAGAAGAAAACAGAGAACCCAAAAGGGGCAAGAGGT 1000


Qy      502 ---
TTCCATAGTGACGCCCCCCAAGGA--------------------------------C 526
                  | || || |  | | || | ||   |||
                |
Db      999
TGGTCCCTTACTTTCACTCTCCTGGGAGGAGGATGGGTACACCACACAGTTGGATGGTGC 940


Qy      527 ATC-TGGAATGTC----ACTGGTGC---------CCAGGTGTACTTGAGCT--
GTGAGGT 570
                ||| | |  ||||      ||| ||         ||| | | | || ||| | |
```

```
     |||
Db         939 ATCTTTGCCTGTCTGCACCTGCAGCTCCATGGCACCATG-
GACCCTGTGCTCCGAGTGGT 881

Qy         571 CAT--CGGAATCCCGACACCTG-------------------TCC-------
TCATCTGGA 602
                    |  | ||    || |||| |                    |||        ||| |
     |
Db         880
GGTGCCTGATCTCCACCACCAGGCAGCAGTAGAGGCCGCTATCCAGCAGGGTCAGGTTGC 821

Qy         603 ACAAGGT-
AAAAAGGGGTCACTATGGAGTTCAAAGGACAGAACTCCTGCCTG-------- 653
                || ||| |   || || | |||| | ||  ||| |    ||||| ||| |
Db         820 GCATGGTGATGGAGAAGTTGCCATGGTGGTCGGAGGCC--
GACTCCAGCCCGTGGCGCTG 763

Qy         654 ---------GTGACCGG----GACAACCTGG------CCATTCAGACCCGG-
GGTGGCCC 693
                    ||| | ||    | || |||||      ||||   | | ||| |  ||
     ||
Db         762 AGCCAGGTCGTGGCTGGTGTTGGCAGCCTGGTGGCCTCCAT--
GGTGCAGGTGAAGGTCC 705

Qy         694 AGAAAAGCATGAAGTAAC----TGGCTGG------GTGCTGGTAT-
CTCCTCTAAGTAAG 742
                 | || |||| || | ||    ||| ||    | || | || | ||||
     |
Db         704 TGGAA--
CGTGAGGTTGCGGATGGGCCGGCGCTCTGAGCAGGTCTGCACCTCGCCCCTCG 647

Qy         743 GAAGATGC------------TGGAGAATATGA----GTGCCATGCATCCAAT--
TCCCAA 784
                 || ||| |           || |||| | |   ||||| |   ||||
     |||||
Db         646 --
AGCTGCGGTACCACGTCTTGTAGAAGGTCACATCGTGCCCTTTGTCCACAGGGCCCAA 589

Qy         785 GGACAGGC--------------TTCAGCATC---AGCAAAAATTACAGTG--------
GT 819
                 |  |  ||             ||| || |    | | |||||| |
     ||
Db         588
GAGCCTGCAGGTGAGGGTGACGTTCTGCCCCTCGGGACAGACATACAGGGAATACGGCGT 529

Qy         820 TGATGCCTT----------ACATGAAATAC-CAGTGAAAAAAGG-----------
TGAAG 857
                 |  ||||      || || | ||| || | || |            |||
Db         528
GGCGACCTTGAAGGCTGCCACCGGACCTGCTCAGAGAGAGGAGAGCCCTGTCACCTGACT 469

Qy         858 GTGCC-GAGCTAT------AAACCTCCA-------GAATATTATTAG--
TCTGCATGGTT 901
                 |  || | ||||      |||| |||    ||| |  |||| ||||| |
     ||
Db         468 GATCCAGTGCTACTCCTGGCAACC-CCAGAGCGGGGAAGAACCTTAGCCTCTGC-
TACTT 411

Qy         902 AAAAG----TAGTCATG-----GATAACTACATTACCTGTTCTTGCCTAATAAGT---
TT 949
```

```
                    ||        |  | |  |       |  |  | |     |  | ||      ||| | |    | |
Db       410
CCCAGCCACAGGCCAGGGGCATGTCAGCTGACCTCCCTAAGACTGCCTTCTGCATTTGTT 351

Qy        950 CTTTTAATCCAATCCA--CTA-------------------ACA----CTT-------
TAG 977
                    |    |  ||| |||| |||                    ||| |   |||
                    |||
Db       350
CACAAACCCCACTCCATCCTAGGCTGTTGTAGGGGGAGTCACAGAAGCTTCCCCAACTAG 291

Qy        978 TTATATTCACTGGTTTT---ACA---CAGAGAAATAC----------
AAAATAAAG---- 1017
                    |  || |||| |      |||   ||| || | ||          || ||
Db       290 GGGTGCTC-
CTGGATGCTGGACAGGGCAGGGAGAGACTTGGAGGGCAGTGATGCAGTCGG 232

Qy       1018 ----ATCACACATC----AAGACTATCTACAAAAATTTAT--------
TATATATT---- 1057
                    || | | ||      ||| ||| | ||||| | |        |  ||
Db       231
GTGTGTCCCTCTTCCCAGTAGAGTATATGCAAAACCTGTTGGGTGGGAGGCAGGTTGGGG 172

Qy       1058 TACAGAA----------GAAAAGCA--TGCATATCAT--------------------
TAA 1085
                    |||  |           |||  | |  |  |  |                    |
                    |
Db       171
AGCAGGAAGGCTGTTTCGAACAGCAGCTCCTTGTCCTTGGCCGCTCTGTAGGGGCCATCA 112

Qy       1086 ACAAATAAAATACTTTTTATCACAAAAAAAAAAAA 1121
                    |||  |       ||| || | |  |   || |
Db       111 ACACCTCTGCCCCTTCCTA-CTCCTAGGACTGAACA 77


RESULT 5
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64
```

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  Query Match            42.0%;  Score 2907;  DB 1;  Length 2120;
  Best Local Similarity  38.2%;  Pred. No. 9.7e-173;
  Matches  678;  Conservative   0;  Mismatches  402;  Indels  696;
Gaps   98;

Qy         1 GCCGCTGCC--ACC------------GCAC-----CC--
CGCCATGGAGCGGCCGTCGCT 39
             || | |||| |    ||         ||||     || | | | || || | |
  |
Db      1885 GCAGTTGCCCTTCCTTCTTTCTTTTTGCACATCTTCCGTCTCTAGGGTGAGGAGG--
GGT 1828

Qy        40 GCGCGCCCTGCTCCTCGGCGCCGCTGGGCTGCTGC--
TCCTGCTCCTGCCCCTCT----- 92
             || || | |        ||| || |  | | ||||| ||| || || ||||| |
Db      1827 GCAGGCAC-------AGGCACC-
CAAGACAGCTGCGGTCCAGCCCCGGCCCCACCTGTGG 1776

Qy        93 CCTC--TTCCTCCTCTTCGGACACCTGCGGCCCCT---------GC-
GAGCCGGCCTCCT 140
               ||| | | || | || | || | |||         || | ||
||||||
Db      1775 TCTCAGTGACGCCCCAGAGG-
CCCCATCTTCCCCACATAATGAGGCTGCTCCATCCTCCT 1717

Qy       141 ----GCCC---------------GCCCCTGCCCCCG--------
CTGGGCTGCCTG---- 169
                 ||||               ||||| | ||||       | |||| | |
Db      1716
CAAAGCCCAGACCTATTTCATAAGCCCCAGACCCCACCTTCACCCAGGGCCCCAAGAGAA 1657

Qy       170 CTGGGC--GAGACCC-GCGACGCGT-
GCGGCTGCTGCCCTATGTGCGCCCGCGGCGAGGG 225
             | | || ||||| | | || | ||    | |||||| |  | || | |
Db      1656
CAGAGCTGGAGACACTTCTACTCCTAGCACTGGATGCCCTCTCCCCTCCTGTGAAGCTGT 1597

Qy       226 CGAGCCGTGCGGGGGTGGCGG-CGCC-------GGCA------
GGGGGTACTGCGCGCCG 271
             |    ||| |||||||| || | ||      |||| | ||||| || |
  ||
Db      1596 AG----GTG-
GGGGGTGGAGGACACCCCTTTAAGGCAGGCTCGGGGGGCTATGAACTCCA 1542

Qy       272 GG---CATGGAGTGCGTGAAGAGCC-GCAAGAGGCGGAAGGGTA---
AAGCC-------- 316
             |   | |||| |        |||| | |||| | || | ||||   |  ||
Db      1541 AGACTCCTGGA----------
AGCCAGTAAGAAGTGGGAAGGTAGGCACACCATTTGGGA 1492

Qy       317 -------------------------GGGG----CAGC------AGCC----
GGCGGTC- 335
                                      || |   |||| | ||   |||
  ||
Db      1491
TTTTTATTTTTCACTGAGCTAAGAGAGGAGATTCCAGCTATGGAATCCAGAGAGCGTTCT 1432

Qy       336 ------------CGGGTGTAAGCGG---CGTGTGC------
GTGTGCAAGAGCCGCTACC 374
```

```
                            |  |    |  || |    |  || ||        |  |    |  |||||||
                            |
Db      1431
ACAGGAACAGAACAGAAATTGGCTGGGCCCTGGGCCCAGAGGAGGCCTGGAGCCGCTTAC 1372

Qy       375 CGGTGTGCGGCAGCGAC------GGCAC-----------CAC-------------
CTACC 404
                |  |   |  | |||| |      |||||        |||           ||
                ||
Db      1371
TGTTCAGTGCCAGCTTCATCCTTGGCACTCTGCCTCTCACACAGCATCGCTCCGGCTCCC 1312

Qy       405 CGAGC-------GGCTGCC------------AGCTGC-GC-GCCG-CCAGCC---
AGAGG 439
                ||||      |||  |||           || || || || || |
                ||||
Db      1311
AGAGCCCACAGTGGCAGCCGCTGGAGGCTGTGGCAGCAGCTGCTGCCCTGCCCAAGGAGG 1252

Qy       440 GCCGAGAGC----CGCCGGGGAG--AAGGCCA----------------
TCACCCAGGTCA- 476
                |  |  | ||    | | |  ||    | ||||          |||  ||||
                ||
Db      1251
GATGTGGGCTTGGCTCTGACAGTTCAAGCCAGAAAGAGCCTTAGAAGTCATTCAGGACAT 1192

Qy       477 ---------GCA-----------AGGGCACC-
TGCGAGCAAGGTCCTTCCA--------- 506
                         ||          |  ||| |  | ||||| || | ||| |
Db      1191
TCCCATTTTACAGATGATGAAATAAGGCTCAGAGAGAGCAGGGGCTTTCAAGAACAATAA 1132

Qy       507 ---TAGTGAC----------GCCCCCCAAGGACATCTG-
GAATGTCACTGGTGCCCA--- 549
                   | | ||||          ||| ||    | | |||| |    ||||||
Db      1131 AGGTGGAGACTGGAACTCAGGCCTCCT---GTCTGCTGAGGGTGTC-----
TGCCCATGC 1080

Qy       550 --------GGTGTACTTGAGCTGTGAGGTCATCGGAATCCCGACAC---------
CTGTC 592
                        | ||  |||| ||| |||     |   |  |||||       |||
                |
Db      1079
TCTCTCTCAGAGTTTCTGAGTGGTGGTGTCTGGAGGGGCTGGACACGCAAGGGAGCTGGC 1020

Qy       593 CTCATCTGGAACAAGGTAAAAAGGG--GTCACTATGGAGT---
TCAAAGGACAGAAC--- 644
                ||| | ||    |     |      ||| || || ||| |   ||    | ||    |
Db      1019
CTCGTGTGTGTCTGTCTGTCGTGCCGGGATGTGTCTGTGGCTTCTGTCTCTGAACGTGCCAGG 960

Qy       645 ---------TCCTG---------------------CCTG-GTGACCGGGAC-----
AAC 667
                         |||||                     |||| ||| | || ||
                |
Db       959 GGTTTTGTGTCCTGTGTGTGTCTCTCTGTGGGTGCTCCTGTGTG-
CAGGAACTTGGGGCC 901

Qy       668 CTGGCC----------------ATTCAGAC---
CCGGGGTGGCCCAGAAAAGCATGAAGT 708
```

```
                 |||||              ||||  ||   |  |||  ||||   |  | ||  |||
|
Db        900 ATGGCCAGAGAGGGATGGGCCTATTCCTACAATCTTGGGAGGCCTCCACAGGC-
TGAGCT 842

Qy        709 AACTGGCTGGGTGCTGG-----------------------
TATCTCCTCTAAGTAAGGAA 745
                    ||  ||||  |||                      |   |||||        |
|||||
Db        841
GGTGGGGAGGGTCCTGAAGGGTAGAGTGAAGATGGGGACTTTACTCCCAGCGGAGAGGAA 782

Qy        746 GATGCTGGAGAATATGAGTG------------------------------------
----- 765
                    ||  |   ||   |||  |   ||
Db        781
GAAACCAGAAGATAGGCTTGGGGCATGGATGGGAAAGGTCTTGGAACTAGGATGGGGCAA 722

Qy        766 ------CCATGCATCCAAT----------TCCCAAG-----GACAGGCT-----
TCAGCA 799
                        |  |  ||  |  |||        ||||   |    ||||  ||       |
||
Db        721
GGGAAACAAAGCCCCAAATGGAGTATGGGTCCCTGGAAGTTGACACACTCTTAGCCCTCA 662

Qy        800 T-------CAGCAAA---AATTAC--------AGTGGT----TGA--
TGCC--------- 826
                        |      ||||  |     | ||      ||||||   |||  || |
Db        661
TGGGGGCCCAGCCCAGTGGGTAACCCCGGGGAAGTGGTCACATGACGTGACACTTCTCAG 602

Qy        827 ----TTACATGAAATACC--------------------------
AGTGAAAAAAGGT--- 853
                        ||  |  |||  ||  ||                       |||||    ||||
Db        601
CTGATTGCTTGAGATCCCCCAGTGTGGCCTGGGCCTTGTCCTTGAGTGAGCCCAGGTTCA 542

Qy        854 ------GAAGG---------TGCC--------
GAGCTATAAACCTCCAGAATATTATTAG 890
                        |||||        ||||       |||   |    |||||    |  | |
|
Db        541 AGCCAGGAAGGCTGGCCAGCTGCCCAAGGACTGAGGCCTTCTCCTCCT-
CCTCCTCTGTG 483

Qy        891 TCTGCATGGTTAAAAGTAGTCA------TGGATAACTACA-----
TTACCT--------G 931
                        ||  |  | | |  |  | ||        ||  | || ||       ||||
|
Db        482
TCCTCCTCGATCATCTTGGCCAGCTCCCGGGGCAGCTCCACGTCTCCACCTGCCATCTGG 423

Qy        932 TTCTTGC-CTAATAAGT----TTCTT------------
TTAATC--------------C 959
                        |||  ||  ||  ||   |||||            ||  ||
|
Db        422
ATCTGGCTCTCATCTGTCTCGTTCTTGGGTAGCCGGTATTTGTCTCGGAAGTGGCTCCGC 363

Qy        960 AAT-----CCACTAACACTTTAGTTATATTCACTGG------------------
TTTTAC 996
```

```
            | |      || ||     |||    | | |  ||||                  | ||
|
Db      362
AGTGTGGCCCGCTCTGCCTTCCTCTGTGTGAACTGTGCATCCCGCTCCATCTTCTCTTCC 303

Qy      997 ACAGAGAAATACAAAATAAAGATC--ACACATCAAGACT------------
ATCTACAAA 1042
            || |||         |||    || || | ||  | ||           || |
Db      302 AC-
GAGTTGCTTCTGATACTCCTCGTACTCCTCCCGGCTCATGCCCTGAGCTTCGGCTGC 244

Qy     1043
AATTTATTATATATTTACAGAAGAAAAGCATGCATATCATTAAACAAATAAAATACTTT- 1101
              | |    || | |    |    || ||| | ||     | | | |  | |||
Db      243 CGACTTGTCCCCATCTCCCTTATCCTCGCC-
GCCTCCCAGGCTCCCAGTGAGGTTCTTCA 185

Qy     1102 ------------------TTATCACAAAAAAAAAAA 1119
                           | ||||| |  ||    |
Db      184 GCTGGCCGCCCACCATGGTCTTCACCATGAACGCCA 149


RESULT 6
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match             41.0%;  Score 2840;  DB 1;  Length 2198;
  Best Local Similarity   36.4%;  Pred. No. 2.4e-168;
  Matches  752;  Conservative   0;  Mismatches  343;  Indels  970;
Gaps  119;

Qy        1 GCCGC-----------TGCCACCGCACCCCGCCA----------TGGAG-
CGGCCGTC-- 36
            |||||            |  ||  | ||||| |||         || | |   ||||
Db      123
GCCGCAAAGAATCAAGTTGCAATGAACCCCACCAACACAGTTTTTGATGCCAAACGTCTG 182

Qy       37 ---------------------GCTGCGCGCC---CTGCT------
CCTCGGCGCC----- 61
                              ||||    || |||  |     | | ||| ||
```

```
Db        183 ATTGGACGCAGATTTGATGATGCTGTTGTCCAGTCTGATATGAAACATTGGC-
CCTTTAT 241

Qy         62 GCTGG-----GCTGCT-----GCTCCTGCTCC------------------
TGCCC----- 88
              | |||    |  ||||    || |  |  |||                   | ||
Db        242 GGTGGTGAATGATGCTGGCAGGCCCAAGGTCCAAGTAGAATACAAGGGAGAGACCCAAAAG 301

Qy         89 ---CTCTCC----------TCTTC------
CT------------------------C 102
                 || |||        ||||||      ||
|
Db        302 CTTCTATCCAGAGGAGGTGTCTTCTATGGTTCTGACAAAGATGAAGGAAATTGCAGAAGC 361

Qy        103 CT--CTTCGGACACCTGCGGCCCCTGC----------GAGCCGGCCTCC-
TGCCCGCCCC 149
              ||  ||| |||   |||   |  |||          | ||| || | |    | |
|
Db        362 CTACCTTGGGAAGACTGTTACCAATGCTGTGGTCACAGTGCCAGCTTACTTTAATGACTC 421

Qy        150 TGCCCCCGCTGGGCTGCC-----TGCTGG-------
GCGAGACCCGCGACGCGTG----- 192
              |  | ||  |||| ||       |||||||      || | ||        | |
Db        422 T--
CAGCGTCAGGCTACCAAAGATGCTGGAACTATTGCTGGTCTCAATGTACTTAGAATT 479

Qy        193 ----------CGGCTGCTGCC-CTATGTGCGCCCGCGGCGAGGGC----------
GAGC- 230
                        |  |||||||| ||||    ||   |||| | |
||||
Db        480 ATTAATGAGCCAACTGCTGCTGCTAT---
TGCTTACGGCTTAGACAAAAAGGTTGGAGCA 536

Qy        231 --------CGTGC--------------GGGGGTGGC-----------GGCG--
CC----- 250
                      |||||              || ||||||           | |   ||
Db        537 GAAAGAAACGTGCTCATCTTTGACCTGGGAGGTGGCACTTTTGATGTGTCAATCCTCACT 596

Qy        251 -----GGCAG--------GGGG-------TACTGC-----
GCGCCGGGCATGGAGTGCGT 285
                   || |        | ||       ||| ||     | ||   | ||| |||
|
Db        597 ATTGAGGATGGAATCTTTGAGGTCAAGTCTACAGCTGGAGACACC-CACTTGG-GTG-
GA 653

Qy        286 GAAG--------AGCCGCAAG--------------
AGGCGGAAGGGTAAAGCCGGGGCAGC 324
              ||||        | ||| | |              || ||  | | ||||    |||
Db        654 GAAGATTTTGACAACCGAATGGTCAACCATTTTATTGCTGA--
GTTTAAGCGCAAGCATA 711

Qy        325 AGCCGGCGGTCCGGG-------------TGTAAG-----------
CGGCGTGTGCGTGTG 360
              || ||  || || |                 ||||||          | || ||||
|||
Db        712
```

```
AGAAGGACATCAGTGAGAACAAGAGAGCTGTAAGACGCCTCCGTACTGCTTGTGAACGTG 771

Qy        361 C-AAGAG---CCGCT--------ACCCGG--------TGTG-----------------
CG 383
                  | |||  |   || ||          |||| |          || |
|
Db        772
CTAAGCGTACCCTCTCTTCCAGCACCCAGGCCAGTATTGAGATCGATTCTCTCTATGAAG 831

Qy        384 GCAGCGACGGC---ACCACC--TACCCGAGC------------------GGCTG-
CCAGC 419
                  | | |||||  |   ||| ||  |||||| ||                  |||| ||
|
Db        832
GAATCGACTTCTATACCTCCATTACCCGTGCCCGATTTGAAGAACTGAATGCTGACCTGT 891

Qy        420 TGCGCGCCGCC----AGCCAGAGG-----GC----CGAGA-
GCCG--------------- 450
                  | || ||| |     | |||| |       ||    ||||| |||
Db        892
TCCGTGGCACCCTGGACCCAGTAGAGAAAGCCCTTCGAGATGCCAAACTAGACAAGTCAC 951

Qy        451 -----CGGGGAGAAGGCC--------------------ATCACCCAGG-
TCAG------- 477
                      |  |    | ||                    ||| || || ||||
Db        952
AGATTCATGATATTGTCCTGGTTGGTGGTTCTACTCGTATCCCCAAGATTCAGAAGCTTC 1011

Qy        478 -CAAGGGCACCTGC--------------------GAGCAAGGTCC------------
TTC 504
                   | | | ||  |                    ||||| ||
||
Db        1012
TCCAAGACTTCTTCAATGGAAAAGAACTGAATAAGAGCATCAACCCTGATGAAGCTGTTG 1071

Qy        505 C--ATAGTGACGCCCCCCAAG--GACATCTGGAATGTCACTGGTGCCCAG-------
GTG 553
                  |  || ||| ||  ||| | | |||||    ||| |||| | || |
||
Db        1072 CTTATGGTGCAGCTGTCCAGGCAGCCATCT----TGT--
CTGGAGACAAGTCTGAGAATG 1125

Qy        554 TACTTGA---GCTGT-----GAGGTCA--TCGGAATCCC--------
GACAC-------- 587
                  | |  | |   |||| |     || ||| |    | ||||        || ||
Db        1126
TTCAAGATTTGCTGCTCTTGGATGTCACTCCTCTTTCCCTTGGTATTGAAACTGCTGGTG 1185

Qy        588 ---------CTGTCCTCATCTGGAACAAGG----------
TAAAAAGGGGTCACTATGGA 628
                  ||||||||||  |  ||               || ||| | |||  |
Db        1186 GAGTCATGACTGTCCTCATCAAGCGTAATACCACCATTCCTACCAAGCAGACAC--
AGAC 1243

Qy        629 GTTCA----
AAGGACAGAACTCCTGCCTGGTG--------------------------- 656
                  ||||         |  ||   || ||||||||
Db        1244
CTTCACTACCTATTCTGACAACCAGCCTGGTGTGCTTATTCAGGTTTATGAAGGCGAGCG 1303
```

```
Qy       657 -ACCGGG---------ACAACCT--------------------GGC---
CATTCAG- 679
                 ||  |          ||||||                  |||  | | |
|
Db       1304
TGCCATGACAAAGGATAACAACCTGCTTGGCAAGTTTGAACTCACAGGCATACCTCCTGC 1363

Qy       680 -ACCCGGGGTGGCCCAGAAAAGCATGAAGTAAC---TGGC-TGGGTGC---TGGTAT-
CT 730
                 |||| |||| ||    ||  |||||| ||   || | | |||   ||||||
||
Db       1364 ACCCCGAGGTGTTCC---
TCAGATTGAAGTCACTTTTGACATTGATGCCAATGGTATACT 1420

Qy       731 C-----
CTC------------------------------------------------- 734
                 |    |||
Db       1421
CAATGTCTCTGCTGTGGACAAGAGTACGGGAAAAGAGAACAAGATTACTATCACTAATGA 1480

Qy       735 -----------
TAAGTAAGGAAG--------------------------------A 747
                      | || |||||||
|
Db       1481
CAAGGGCCGTTTGAGCAAGGAAGACATTGAACGTATGGTCCAGGAAGCTGAGAAGTACAA 1540

Qy       748 TGCTG-----GAGAATATGAGTGCCATG----CATCC---AATTCCCAAG-GAC---
AGG 791
                 ||||    |||||   ||| | | |    |||||   ||||| |  | | |
|
Db       1541
AGCTGAAGATGAGAAGCAGAGGGACAAGGTGTCATCCAAGAATTCACTTGAGTCCTATGC 1600

Qy       792 CTTCAGCAT--CAGCAA-------------AAATTACAGTG----------
GTTGATGC 825
                 ||||| |||  |||||          ||| | || |          | |||
|
Db       1601
CTTCAACATGAAAGCAACTGTTGAAGATGAGAAACTTCAAGGCAAGATTAACGATGAGGA 1660

Qy       826 CTTACATGAAAT-----ACCAGTGAAAAAAAGGTGA-----
AGG----------------- 858
                 |  ||| | ||    || |||| ||  | |  ||      ||
Db       1661
CAAACAGAAGATTCTGGACAAGTGTAATGAAATTATCAACTGGCTTGATAAGAATCAGAC 1720

Qy       859 TGCCGAG--------CTATAAACCTC--CAGAA-----
TATTATTAGTCTGCA------- 896
                 ||| |||        | | ||| ||  |||||     |        ||| ||||
Db       1721
TGCTGAGAAGGAAGAATTTGAACATCAACAGAAAGAGCTGGAGAAAGTTTGCAACCCCAT 1780

Qy       897 -----------TGGTTAAAAGT-----AGTCAT----GGATAACTAC-------
ATTACC 929
                              ||  | |||    || |||  ||| |||         |||
||
Db       1781
CATCACCAAGCTGTACCAGAGTGCAGGAGGCATGCCAGGAGGAATGCCTGGGGGATTTCC 1840
```

```
Qy        930 T---------
GTTCTTGCCTAATAAGTTTCTT--------------------------- 952
              |          | || | |||     | | |||
Db       1841
TGGTGGTGGAGCTCCTCCCTCTGGTGGTGCTTCCTCAGGGCCCACCATTGAAGAGGTTGA 1900


Qy        953 TTAATCCAA----------------------TCCAC-----
TAACACTTTAGT------T 979
              |||| ||||                      |||||     ||| || || |
|
Db       1901
TTAAGCCAACCAAGTGTAGATGTAGCATTGTTCCACACATTTAAAACATTTGAAGGACCT 1960


Qy        980 ATATTC---------ACTG-----GTTTTACACAGAGAA-
ATACAAAATAAAGATCACAC 1024
              | ||||          |||    ||||||| | ||  ||  | | | |  ||| |
Db       1961
AAATTCGTAGCAAATTCTGTGGCAGTTTTAAAAAGTTAAGCTGCTATAGTAAGTT----- 2015


Qy       1025 ATCAAGACTATCTACAAAAATTTATTAT-----ATATTTACAGAAG-----
AAAAGCA-T 1073
              | | | ||| ||| | || |||    |||| |||| |   || | ||
|
Db       2016 -ACTGGGCATTCT-
CAATACTTGAATATGGAACATATGCACAGGGGAAGGAAATAACATT 2073


Qy       1074 GCATATCATTAA----------------------------
ACAAATAAAATACTTTTTAT 1105
              ||| | || ||                         | | | || |||
||||
Db       2074
GCACTTTATAAACACTGTATTGTAAGTGGAAAATGCAATGTCTTAAATAAAACTATTTAA 2133


Qy       1106 ------CACAAAAAAAAAAAAAAA 1124
                    ||| | ||||||||||||
Db       2134 AATTGGCACCATAAAAAAAAAAAA 2158



RESULT 7
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
  Query Match            40.9%;  Score 2833.5;  DB 1;  Length 2437;
  Best Local Similarity  38.4%;  Pred. No. 1e-167;
  Matches  704;  Conservative   0;  Mismatches  390;  Indels  739;
Gaps  116;

Qy        2 CCG-----CTGCCA----CCGCA------------------
CCCCGCCA----------- 23
            |||    | || |    ||| |              || || ||
Db     1813
CCGAGCTCCAGCAATATCCCGAAGTGAAGTAAAGAGTTCATCCACGGCAATTTTGGATTT 1754

Qy       24 ------------------TGGAGCGGCC--GTC-----------GCTGC----
GCGCCCT 48
                              || || | || |||       || ||   | | |
Db     1753
GTGAAATGTCAGATTAATTGAAGAGTCCCAGTCCGTAATTTTTTGCAGCAAAGGTGACAA 1694

Qy       49 GC-----TCCTC---GGCGCCGCTGGGCTGCTGC--TCCTG-------
CTCCTGC----- 86
              |     ||||| |  | |||| ||   ||| || ||      || ||||
Db     1693 TCCAGATTCCTCACAGAAGAC-
CTGAGCCAATGCTTTCTTGACTTTTTCTTCTGCTTCAC 1635

Qy       87 ---------------CC-----CTCTCC-----------------------------
TC- 96
                            ||     ||||||
||
Db     1634
ACAGGTCTTTGTCTACCGTGAGCTCTCCAGTGACAGAATAAATATATATGAGAAGGATCA 1575

Qy       97 ----TTCC------------TCCTC-----TTC----GGACAC--------------
CT 116
                ||||            |||||     |||   || ||
|
Db     1574
GCAGTTCCTCAGGGCTGTAGTCCTCGTTGGTTCTCTGGGTTACAGGCTTAATCATGGGCA 1515

Qy      117 GCGGC--------CCCTGCGAGC----CGGCCTCC----TGCCC----------
GCCCCT 150
              || ||        | | || |   | | ||||  ||| |         |||
|
Db     1514
GCAGCTGATTTAACACAACGGACATTGCTGACTCCCCAATGCTCTGAAGAAGGAGCCTTT 1455

Qy      151 -----GCC----------CCCGCTGGGCTGCCTG--------------CTGGGC-
GAGA 179
                   |||           ||| || ||| | |||         || || |
|
Db     1454
CAAAAGCCAGAAAGTTGTCCCACTTGGCAGTCTGTGGGTGTTTCAACGTTTGAGCTGTGG 1395

Qy      180 CCCG-CGACGCGTGCGGCTGCTGCC--------------CTATG----
TGCGCCCGCGGC 220
              || | | | || | || || |              || ||    || | |
|
Db     1394
CCAGTCCAAGCTGGAGGAGGCCACAATGATTCATTAGAGCTTTGAGGTTGTTCTTGAAGA 1335
```

```
Qy        221 G--------AGGGC--GAGCCGTGCGGGGGTGGCGGCGCC-----------------
GGC 253
                |        ||| |   |||| ||  | || ||| |    |  | ||
|||
Db       1334 GCTGAATATAGGACATGAGCTGTCCCGGTGTGAC-
TCTCCCCATACTCATCTTGATTGGC 1276


Qy        254 AGGGGGT-
ACTGCGCGCC------------------------------------------G 271
                |||   |  |||| |||
|
Db       1275
AGGTTTTCTCTGCTTGCCGCTTCCACTAGATGTGTCCGAACTTCCATCACTGCCTCTTTG 1216


Qy        272 GGCATGGAGTGC-GTGAAGAGCCGCAAGAGGC---GGAAG-
GGT--------------- 310
                | || |  || | || |||    | ||    ||   | |||
Db       1215
TGCTTAGTGTTCAGTAAAGCTTCCCATAGGGCTTTGGCTGTGGTGTCACTGAATTGTGAA 1156


Qy        311 --AAAGCC-GGGGCAGCAGC---------------CGGCGGTCCGG------
GTGTAAGC- 346
                | |||| ||  ||| |    |              |  ||  ||       |||
||
Db       1155
AGACAGCCTGGTGCAACCACATTATAATTTTCCTCCTCAGTATGGAGTGCAGTGAGCGCT 1096


Qy        347 ----------------------------GGCGTGTGCG-
TGTGCAAGAGC---------- 367
                                           ||| || | ||  | ||| ||
Db       1095
ATCATGTTAACCATCACATCATTTGTGTGGCCTGGGAGCTGGGGAAGTGCTGAAATGATC 1036


Qy        368 --CGCTAC----------CC--GGTGTGCGGCAGCGACGG-------CA---------
CC 397
                | ||||        || | ||| |  | || | |       ||
||
Db       1035
TTCTCTACTAAGTTGTCTCCATGATGTCCAACTGCTCCTGTGAGATCCAGGGTTCTGTCC 976


Qy        398 ACCTACCCGAGCGGCTGCCAGCTGCGCGCCGC------CAGCCAG---------
AGGGC- 441
                || |  | |  ||||| |||| || ||       |  || |
||||
Db        975 ACAAAAACCA-CTGATGCC--
CTGCCTGCAGCAGTCTTCTTCCTGTTCTTTGCAGGGGCA 919


Qy        442 -------CGAGAGCCGCGGGGAGAAGGCCATCACCCAGG-----TCAGCAAGG-
GCACCT 488
                | ||| ||||  | || ||    ||||       ||||||   |
|||
Db        918 TAATTGGCCAGATCCGC--
AGCGATGACCTGACTTAAGGAACCTACAGCAAAACACTCCT 861


Qy        489 -GCGAGC-----AAGGTCCTTCCATAG---TGACGCC--
CCCCAAGGACATCTGGAATGT 537
                || |    || | | ||  || |   ||| |||  | | ||| ||||||
||
Db        860 CCCGTACTCCTAAATGTTCACACAGAGAACTGAGGCCTGACACTAGG-
CATCTGATCTGC 802
```

```
Qy         538 CACTGGTGCCCAGGTGTACTTGAGCTGTGAGGTCATC--------
GGAATCCCGAC---- 585
               |  |   || | || ||   | |  |  ||| |||  |         ||  ||||  |
Db         801 AGCAGCAGCTCTGGGGT--
TAGCGTAGTGGAGTCCACATCACCCAGGCTTCCCAGCTTCC 744


Qy         586 -----ACCTGTC-------------------CTCAT-CTGG---
AACAAGGTAAAAAGGG 617
                         || |||              | ||| ||||   | || |
||||||||
Db         743
TCTTGTCCGGTCGGGCGCTATTAAGGAGGTGCACATCCTGGGGTAGCAGTGGGAAAAGGG 684


Qy         618 GT-------------------CACTATGGAGTTCAA-----------------
AGGACA- 640
                   |                    ||  ||| | |||
||||||
Db         683
ATGCAAAAGCTGGAGTCAAGGCAAAGTGGGGAGCAACAGGGGCAAGCAATAACGGGACAT 624


Qy         641 -GAACTCCT--GCC----------
TGGTGACCG------------------------ 660
                |||| |||  |||            || || ||
Db         623
GGAACACCTCGGCCGTGTAGTTCATGTTGCCCATCCATTCACACAGCTTCTCCTCCAGCT 564


Qy         661 ----GGACAAC--CTG--GCCATTCAGACCCGG--GGTG--GCC-------CA-
GAAAAG 700
                   | |||| |  ||| ||| ||   ||  | ||| |  ||  |||       || ||
Db         563
GCTCGAACACCGGCTGCTGCCCCTCCATCTCGGCCGCTGCCGCCGCTGGGACATGATTAG 504


Qy         701 C-ATGAAGT----AAC-TGGCTGGGTGCTGGTATCTCCTCTAAGTA-
AGGAAGATGCTGG 753
                | ||| ||   | | |||||   | ||  | ||| | | | | |  ||||
|||
Db         503
CTGTGAGGTGGACAGCGTGGCTCACGGTTGTGACCACCACACAATACTGGAAGTGACTGC 444


Qy         754 AGAATATGAGTGCCATGCATCCAATTCCCAAGGACAGGC--TTCAGCA------
TCAG-- 803
                 | | |||| ||  | | |   || |||  || || | ||| ||||||||      ||||
Db         443 GGCAGATGATGTCC---
CGTAGGATCTCCACGGTCCGGCCTTTCAGCAGGCAGCTCAGCA 387


Qy         804 CAAAAATTACAGTGGTTGATGCCTTACATGAAATACCAGT------------
GAA----A 847
               ||||| | |  |||  | ||| | | |  | |  |  |||| |                |||
Db         386 CAAACACTGCCTTGG--GCTGCTTGGC-
TCCACCACCAATTGCGTCGGGCTCGAACTCTC 330


Qy         848 AAAGGTGAAGGTGCCGAGCTATAAA---CCTCCAGAATATTATTAG-
TCTGCA------- 896
                |||||| || |  | ||      |  ||||||||| |     | | || |||
Db         329 GCAGGTGACAGT-
CAGGGCCCCCACCGGCCTCCAGGAGACGGGTGGATCCGCAGCCCCAG 271


Qy         897 ---TGGTT--------AAAAGTAGTCATGGATAACTACATTACCTGTT---
```

```
CTT------ 936
                |   | |           |    |   | | |   | |   | | |   | | |      | |   | | |      | | |
Db       270 TGCAGGCTCTCGGCGCAGGCGGCGTCCAGGTAAACCACA--
GCCCGTTTCACTTTGGCCA 213

Qy       937 --GCCTAATAAGTTTCT-------TTTAATCCAATCCAC---TAACACT-TTAGTT--
AT 981
                | | |   |   | |   | | |         |   |   | | | | |      | | |   | | | !
Db       212 GCACCTGCTCCCATCCTTGCTGGGTAAAGGACAGTACGCCCGAGGCGCTCATGGTTGGGG 153

Qy       982 ATTCACTGGTTT----TAC-ACAGAG-AAATACAAAATAAAGATCACA---
CATCAAGAC 1032
                | | | |   |   | |         | | | | | | | |      | |      |   | | | | | |      |   | |
| |
Db       152
ATTCGCAGACTTGGGAAACTACGGTGCAGGAACTTCTTTCAGAACTCACCGCTTCCGGAA 93

Qy       1033 TAT---CTACAAAAATTTATTATA-TATTTACAGAAGA-
AAAGCATGCATATCATTAAAC 1087
                |    | | | |         | | | | | | | |   | | | | |   | |      | | | | |   | | | |
|
Db       92 ATTGGGCTCCGGGAGACTTTGACAGTCTCCACAGTACACCCAGTAGGCC-
AACAGTGCTC 34

Qy       1088 AAATAAAATAC----TTTTTATCACAAAAAAAA 1116
                |   | | | |         | | | | |   | | | |   | |
Db       33 GAG-GAATTCCGCAGCTTTTAGAGCAGAAGTAA 2


RESULT 8
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match          40.5%;  Score 2800;  DB 1;  Length 2198;
  Best Local Similarity   37.8%;  Pred. No. 9.5e-166;
  Matches  685;  Conservative   0;  Mismatches  405;  Indels  720;
Gaps  98;

Qy        1 GCCGCTG--------CCACC----------GCACC-CCGCCATGGA---------
```

```
GCGGC 32
             |||  |||        |||||          || || || ||| |            ||
Db      1881 GCC-
CTGAGGAAGCACCACCAGAGGGAGGAGCTCCACCACCAGGAAATCCCCCAGGCATT 1823

Qy        33 CGTCGCTGCGCGC--CCTGCTCCTCGGCGCCGCT-----------GGGGCTGC-----
TGC 74
             | ||    ||  ||  ||||| |   ||  | |||         ||| |||      |
                                                                         |
Db      1822
CCTCCTGGCATGCCTCCTGCACTCTGGTACAGCTTGGTGATGATGGGGTTGCAAACTTTC 1763

Qy        75 TCCTGCTCCTGC-------------------
CCCTCTC---------------------- 93
             |||  ||||| | |                       ||  ||||
Db      1762
TCCAGCTCTTTCTGTTGATGTTCAAATTCTTCCTTCTCAGCAGTCTGATTCTTATCAAGC 1703

Qy        94 -------------------CTCT--TCC---------------
TCCTCTTCG--------- 109
                             | ||  |||             ||||| |||
Db      1702
CAGTTGATAATTTCATTACACTTGTCCAGAATCTTCTGTTTGTCCTCATCGTTAATCTTG 1643

Qy       110 ----GA-------CACCTGCGGCCCCTGC----------GAGCC---
GGCCTCCTG---- 141
             ||        || | | ||   |||          || |  || ||| |
Db      1642
CCTTGAAGTTTCTCATCTTCAACAGTTGCTTTCATGTTGAAGGCATAGGACTCAAGTGAA 1583

Qy       142 -------------------CCCGCCCCTGCCC-----CCGCTGGG-------
CTGCCTGC 170
                                ||| | || |    | ||| |       | || |
                                                                         |
Db      1582
TTCTTGGATGACACCTTGTCCCTCTGCTTCTCATCTTCAGCTTTGTACTTCTCAGCTTCC 1523

Qy       171 TGGGCGAGACCCGCGACG-----
CGTGCGGCTGCTGCCCT-------------------- 205
             ||| | | ||   | | |       | |||     | |||||
Db      1522
TGGACCATACGTTCAATGTCTTCCTTGCTCAAACGGCCCTTGTCATTAGTGATAGTAATC 1463

Qy       206 ATGTGCGC-----------------CCGCGGCGAGGGC---GAG----
CCGT-------- 233
             ||| | |                  || | ||   | |    |||    || |
Db      1462
TTGTTCTCTTTTCCCGTACTCTTGTCCACAGCAGAGACATTGAGTATACCATTGGCATCA 1403

Qy       234 ---GCGGGGGTGGC----------GG--CGCC------GGCAGGGGGTA---
CTG----- 264
               |   ||| |          ||  | ||      ||||| ||||   |||
Db      1402
ATGTCAAAAGTGACTTCAATCTGAGGAACACCTCGGGGTGCAGGAGGTATGCCTGTGAGT 1343

Qy       265 -----CGCGCCGGGCATGGAGT-------------------------------
GCGTGA 287
                 | ||| ||| | ||                                        |
                                                                         |||
Db      1342
```

```
TCAAACTTGCCAAGCAGGTTGTTATCCTTTGTCATGGCACGCTCGCCTTCATAAACCTGA 1283

Qy        288 AGAGCCGCAAGAGGC--------------------------------------------
GGA 305
                 |  |  | ||  ||||
|||
Db       1282
ATAAGCACACCAGGCTGGTTGTCAGAATAGGTAGTGAAGGTCTGTGTCTGCTTGGTAGGA 1223

Qy        306 AGGG-----TAAAGCC-----GGGGCAG--------CAGCCGGCGGT-------
CCGGGT 340
                 | ||     | ||   ||    || |||     |  || || ||      ||
|
Db       1222
ATGGTGGTATTACGCTTGATGAGGACAGTCATGACTCCACCAGCAGTTTCAATACCAAGG 1163

Qy        341 GTAAGCGGCGTGTGCGTGTGCAAGAGCCGCTACCCGGTGTGCG---
GCAGCGACGGCACC 397
                 | |||| || |||    |  | ||||||| | |  | ||     |||    | |
||
Db       1162 GAAAGAGGGAGTG---ACATCCAAGAGCAGCAAATC-
TTGAACATTCTCAGACTTGTCTCC 1107

Qy        398 --AC-------CTACCCGAGCGGCTGC-----------CAGC--------------
TGCG 423
                 ||      || || |  | ||||||           ||||
|||
Db       1106
AGACAAGATGGCTGCCTGGACAGCTGCACCCATAAGCAACAGCTTCATCAGGGTTGATGCT 1047

Qy        424 CGCCGCCAG-------CC-----AGAGGGCCGAGAGCCGC-----------
GGGGAGAAG 460
                 |   |||      ||    ||| | ||| | || ||       ||||| |
|
Db       1046 CTTATTCAGTTCTTTTCCATTGAAGAAGTCTTGGAGAAGCTTCTGAATCTTGGGGATACG 987

Qy        461 ------GCCATCACCCAGGTCAG--------------------CAAG---
GGCACCTGC 490
                 ||| || ||||| ||                    | ||  |||| ||
|
Db        986
AGTAGAACCACCAACCAGGACAATATCATGAATCTGTGACTTGTCTAGTTTGGCATCT-C 928

Qy        491 GAGCAAGGTCCTTCCATAGTGACGCC------CCCC----AAGGACA----
TCTGGAATG 536
                 |  |||| ||| || || |   ||     || |     ||| ||   || |
|
Db        927 G---
AAGGGCTTTCTCTACTGGGTCCAGGGTGCCACGGAACAGGTCAGCATTCAGTTCTT 871

Qy        537 TCACTGGTGCCCAGGTGTACTTGAGCTGT-
GAGGTCATCGGAATCC-------------- 581
                 | | |||| |  ||| |||| | | || |||    || |||
Db        870 CAAATCGGGCACGG--GTAATGGAGGTATAGAAGTC----
GATTCCTTCATAGAGAGAAT 817

Qy        582 CGACACCTGTCCTCATCTGGAACAAGGTAAAAAGGGGTCACT------------
ATGGAG 629
                 |||  |  | || |   |||      ||  | ||||  | ||
| |
```

```
                 ||
Db         816
CGATCTCAATACTGGCCTGGGTGCTGGAAGAGAGGGTACGCTTAGCACGTTCACAAGCAG 757

Qy         630 TTCAAAGG------ACAGAACTC-----
CTGCCTGGTGACCGGGACAACCTGGCCATTCA 678
                  |  |  |||    |||| ||||   ||  ||| ||| ||    |  || ||  ||
       |
Db         756
TACGGAGGCGTCTTACAGCTCTCTTGTTCTCACTGATGTCCTTCTTATGCTTGCGCTTAA 697

Qy         679 GACCCG---------GGGTGGCC---CAG-----AAAAGCAT-------------
GAAGT 708
                      |  |       || || ||   | |    |||| | |              |
                 ||
Db         696
ACTCAGCAATAAAATGGTTGACCATTCGGTTGTCAAAATCTTCTCCACCCAAGTGGGTGT 637

Qy         709 AACTGGCTGGGTGCT---------GGTATC--TCCTCTA-AGTAAGGA-
AGATGCTGGAG 755
                  |  |||| |   ||          |   ||  |||||  | ||| |||| ||  |
Db         636
CTCCAGCTGTAGACTTGACCTCAAAGATTCCATCCTCAATAGTGAGGATTGACAC----- 582

Qy         756 AATATGAGTGCCATGCATCCAATTCCCAAGGACAGGC--------
TTCAGCATCAGC--- 804
                  |  |  ||||||||  |  ||| |  ||| ||   ||     ||| ||  || |
Db         581 ATCAAAAGTGCCAC-CTCCCAGGT--
CAAAGATGAGCACGTTTCTTTCTGCTCCAACCTT 525

Qy         805 --------------AAAAATTACAGTGGTTGATGCCTTACATGAAATAC------
CAGT 843
                            |  ||| ||| | | || ||     ||| |      ||
       |
Db         524
TTTGTCTAAGCCGTAAGCAATAGCAGCAGCAGTTGGCTCATTAATAATTCTAAGTACATT 465

Qy         844 GAAAAAAGGTGAAGGTGCCG-AGCTAT--AAACCT--C-
CAGAATATTATTA------- 889
                  ||  | |||    ||| | | | || | |    |||  ||  || |  | ||||
Db         464
GAGACCAGCAATAGTTCCAGCATCTTTGGTAGCCTGACGCTGAGAGTCATTAAAGTAAGC 405

Qy         890 -------GT-----CTGCATGGTTAAAAGTAGT--CATGGATAACTAC----
ATTACCTG 931
                     ||   | |||| | ||| |||  |  || ||    || |    ||| ||
Db         404
TGGCACTGTGACCACAGCATTGGTAACAGTCTTCCCAAGGTAGGCTTCTGCAATTTCC-- 347

Qy         932 TTCTTGCCTAATAAGTTTCTTTTAATCCA-ATCCACT-----
AACACTTTAGTTATATTC 985
                  ||| | | || | || | |  ||  ||| ||    |  |||| | |
                 ||
Db         346 TTCAT-CTTTGTCAGAACCATAGAAGACACCTCCTCTGGATAGAAGCTTTTGGTCTC-
TC 289

Qy         986 ACTGGTTTTACACAGAGAAAT--------------------
ACAAAATAAAGATC---- 1020
                  || || ||  ||   ||   ||                     ||  ||||||  |
Db         288
```

```
CCTTGTATTCTACTTGGACCTTGGGCCTGCCAGCATCATTCACCACCATAAAGGGCCAAT 229


Qy       1021 ---ACACATCAAGACT-ATCTACAAAAATTTATTATATATTT----
ACAGAAGAAAAGCA 1072
                        || ||| ||||| | ||| |    |  || |    |     |||| |
|||
Db        228 GTTTCATATC-
AGACTGGACAACAGCATCATCAAATCTGCGTCCAATCAGACGTTTGGCA 170


Qy       1073 TGCATA----------------TCATTAAACAAATAAAATACTTT---
TTATCACAAAA 1112
                  | || |               ||||| ||| |  || |||| |     |||||
|
Db        169 T-CAAAAACTGTGTTGGTGGGGTTCATT--GCAACT-
TGATTCTTTGCGGCATCACCGAT 114


Qy       1113 AAAAAAAAAA 1122
                  ||       |
Db        113 CAACCGTTCA 104



RESULT 9
US-10-478-914-21
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match          40.4%;  Score 2795;  DB 1;  Length 3589;
  Best Local Similarity  39.2%;  Pred. No. 1.7e-164;
  Matches  742;  Conservative   0;  Mismatches  347;  Indels  806;
Gaps  121;

Qy         1 GCC-GCT------GCCACC-----
GCACCCCGCCATGGAGCGGCCGTCGCTGCGCGCCCT 48
                |||  ||       |||| |     |||| | || | || | |||| ||
|||||||
Db         1 GCCTACTGGATTCGCCATCATTTTGCACACTGCGA-GGGGC-TCCGT--
GTGTGCGCCCT 56

Qy        49 G-CTCCTCGGCGCCG--CTGGGCTGCTGCTCCTGCTCCTGCC-CCTCT-----
CCTCTTC 99
                | ||  || |||| ||   | | ||  | ||||||| || ||     || ||
```

```
|
Db       57 GTCTTGTCTG-
GCCGTCCTCATCCCTTCCCCCACCCCCTGCCGCCACTCCGACCCGCTCC 115

Qy      100 --------CTCCTCT----TCGGACACCTGCGGCCC---CTGCGAGCCGG--CCTC-
CT- 140
                    || |     |||| | | |||     ||||| || | || |
||
Db      116 CAAAGTGGCTTCACAATAGTCGGTCCTCGGCGGTGTAGGCTGCGCACCAGGTCCACACTT 175

Qy      141 ---------------GCCCGCCC-----CTGCCCCCGCTGGG-----------
CTGC--- 166
                           | || |||    || | || ||||          |||
Db      176 AAGCGAAATCAAGGAGACC-
CCCTTCTACTTCTACCTTTGGGTTTGGTGCTCAATGCGAA 234

Qy      167 -CTGCTG-GGCG-AGACCCG-------
CGACGCGTGCGG--------------------- 195
                 ||||||   |  |||| ||        | || ||||
Db      235 GCTGCTGCAACTCAGACACGCCTAAGTCAACTCATGCAGAAAAAGGAGAAAAGTTTTGGT 294

Qy      196 ---CTGCTGCCCTATGTGC-GCCCGCGGCGAGGGCGAGCCGTGCGGGGG---
TGGCGGC- 247
                 |  ||| ||  | ||| ||  | | |    | ||||| || |  ||||
||
Db      295 ATACAAATGCTCTCAGTCCAGCCAGACAC-----
CAAGCCGAAAGGTTGTGCTGGCTGCA 349

Qy      248 GCCGG-----CAGGG---GGTA-CTGC-----GCGC----------
CGGGCATGGAG--T 281
                 |||   || || ||||| |    || |           | |||||| |
|
Db      350 ACCGAAAGATCAAGGACCGGTATCTTCTAAAGGCACTGGACAAATACTGGCATGAAGACT 409

Qy      282 GCGTGAAG---------------AGCCGCAAGAGGCGGAAGGG---------------
TA 311
                 || |||||                | ||| | || | |||
||
Db      410 GCCTGAAGTGTGCCTGCTGTGACTGTCGCTTGGGGGAGGTGGGCTCCACCCTGTACACTA 469

Qy      312 AAGC----------------CGGGGCAGCAGCCGGCGGTCC--GGGTGT------
AAGCG 347
                 ||||             || | | | |||| | ||||| ||
|
Db      470 AAGCTAATCTTATCCTTTGTCGCAGAGACTATCTGAGGCTCTTTGGTGTAACGGGAAACT 529

Qy      348 GCGTGTGCGTGT-GCAAGAGC--CGCTACC-------CGGTG-TGCG-
GCAGCGACGGC- 394
                 |||  ||| ||| | ||  |  | ||| ||        |||| |||| || | | |
|
Db      530 GCGC-TGCCTGTAGTAAGCTCATCCCTGCCTTTGAGATGGTGATGCGTGC--
CAAGGACA 586

Qy      395 ------ACCACCT-ACCCGAGCGGC-
TGCCAGCTGCG----------------------- 423
```

```
                    ||||||   | |    || || ||||| |
Db      587
ATGTTTACCACCTGGACTGCTTTGCATGTCAGCTTTGTAATCAGAGATTTTGTGTTGGAG 646

Qy      424 -CG-------CC---------------GCC--AGCCAGAGGGCCGAGAGCCGCGG--
GG- 455
                 |         ||                 ||   |||||| || |     || ||
||
Db      647 ACAAATTTTTCCTAAAGAATAACATGATCCTTTGCCAGACGGACTA----
CGAGGAAGGT 702

Qy      456 -------AGAAGGCCAT-CA-CCCAGGT---CAG------
CAAGGGCACC--------- 487
                    ||||||| || || ||||||| | |      |||   ||||
Db      703
TTAATGAAAGAAGGTTATGCACCCCAGGTTCGCTGATCTATCAACATCACCCCATTAAGA 762

Qy      488 -TGC-GAGCAAGGTCCTTCCATAGTGAC------
GCCCCCCAAGGACATCTGGAATGTCA 539
                  | | |||||  | | | | | |  | |        || || || | |||| | | ||
||
Db      763 ATACAGAGCAC--TACATTCTTT-
TATCTTTTTTGCTCCACATGTACATAAGAATTGACA 819

Qy      540 CTGGTGCC------------CAGGTGTACTTGAGCTGTGAGGTCATC-
GGAATC------ 580
                 | || ||              || || |||   || |  ||| ||  |||||
Db      820
CAGGAACCTACTGAATAGCGTAGATATAGGAAGGCAGGATGGTTATATGGAATAAAAGGC 879

Qy      581 --CCGACACCTGT--------------CCTCA--
TCTG----------------------G 601
                 | || ||||          ||  || ||  |
|
Db      880
GGACTGCATCTGTATGTAGTGAAATTGCCCCAGTTCAGAGTTGAATGTTTATTATTAAAG 939

Qy      602 AACAAGGTAA-----AAAGGG------------------------------
GTCAC--- 622
                 || || ||||      | | ||                              |||||
Db      940
AAAAAAGTAATGTACATATGGCTGGATTTTTTTGCTTGCTATTCGTTTTTGTGTCACTTG 999

Qy      623 ------------------------------------------------
TATGGAGTTCAAAG 636
                                                             | || ||
||||
Db      1000
GCATGAGATGTTTATTTTGGACTATTGTATATAATGTATTGTAATATTTGAAGCACAAAT 1059

Qy      637 G----ACAGAACTCCTG-----CC--TGGTG-
ACC------------------------ 659
                 |   |||| | ||   || ||  ||  |
Db      1060
GTAATACAGTTTTATTGTGTTACCATTTGTGTTCCATTTGCTTCTTTGTATTGTTGCATT 1119

Qy      660 -GGGACAACCTG-----------GC------------CATTCAG-----
ACCCG------ 684
                 | |||| | |               |         | ||| |    ||| |
Db      1120
```

```
TAGTACAATCAGTGTTTAAACTTACTGTATATTTATGCTTTCTGTATTTACCAGCTATTT 1179

Qy        685 ------------------------GGGTGG----------------------
CCCAG 695
                                      |  |  |                              |
|||
Db       1180
TAAATGAGCTGTAACTTTCTAGTAAAGAATTGAAAAGCAAATCTCACTAATGATACACAG 1239

Qy        696 A-----AAAGCATG----------------------------
AAGTAACTGGCTGGG-- 719
                |     ||||||  |                              |||  ||   | | |
Db       1240
ATAGATAAAGCAAGTCTATCAACATTAAAAATACTAAAAAATAAAGACACACACAGAGCA 1299

Qy        720 TGCTGGTATC-TCCTCTAAGTAAGGAAGAT----GCTGGAGAATATGAGTG-
CCATG--- 770
                | | ||  | ||| |||  || | | |   | |||  ||| |||| | ||
Db       1300
TTTTAGTGACATCCACTACTTATTGCCGCTATGAGTTAGAGTCTATCAGTGTTCTTGTTA 1359

Qy        771 ---CATCCAATTCCCAAGGACAGGCTTCAGCATCAGC----
AAAAATTACAGTGG----- 818
                  |  || ||| || |   || || |  ||||||     |||||| ||||
Db       1360 TAACCCCCTATTTTCAGG----
GGGTTAAAAATCAGCTTTAAAAAAATACATAAAAATTT 1415

Qy        819 ----TTGATGC-
CTTACATGAAATACCAGTGAAAAAAGGTGAAGGTGCCG---------- 863
                  || || ||| |||   |||||| |  ||||        |||||
Db       1416 CATCTTAAAGCACTTTCATTTTATACCAACGTGAAAA-------
GTGCCATTTTTAGAAT 1468

Qy        864 AGCTATAAACCT--CCAG----------AATA----TTATTAGTCTGC---
ATGGTTAAA 904
                | || |||| ||   |||         ||||    || || || |||     |  |||
|
Db       1469
AACTTTAAAGCTTAACAGGTTTCCTTTTAATATCCTTTTTTGTGTGCTCTTTACTTACA 1528

Qy        905 AGTAGTCATGGAT----------AACTACA----TTACCTGTTCT--
TGCCTAATAAGTT 948
                | | | |            |  || ||| | | | ||||
||
Db       1529 CAATGGCTTTGTTTTGCTTTTTCAGCCACACCCCTTATGTGAACTAGTGCCT-
TTGGGTA 1587

Qy        949 TC-------TTTTAATCCAA-----TCCACTAACACTTTAGTTA-------
TATTCACTG 989
                ||        ||| ||||||   | | ||| | | ||||      |||
||
Db       1588 TCACGTAAAATTTTTTCCAAAGGGTTACTTTAAAAATCT-
GTTACCACAATTATGAGATG 1646

Qy        990 GTTTTACACAGAGAAATACAA----------AATAA---------
AGATCACACATCAAG 1030
                  ||||  |  || |||| ||     ||||        |||||| |
||||
Db       1647
ATTTTTAAGTGATAAATTAAACTTCTTCTTGTATAAATTCTGCCCAGATCTCTCCACAAG 1706
```

```
Qy      1031 A-CTAT---CTACAAAAATTTAT-------TATATATTT---ACAGAAGAAA----
AGCA 1072
             | ||      | || || |||||      || || | |  || ||| | |    ||
Db      1707
AGCTGAGGGTTTCATAACTTTATGGCTTAATAAATGTATGACACTGAAAAGATTTGAGTG 1766


Qy      1073 TGCAT--------ATCATTAAA---
CAAATAAAA-------------------------- 1095
             || ||        |||| || |  || ||  ||
Db      1767
TGAATCTACTGAAATCACTATAATGCACATTGAAGCTATGATGGTATTTGAGTAGTGAGG 1826


Qy      1096 -TACTTTTTATC------ACAAAAAAAAAAAAAAA 1123
             |||||||| |||      ||| ||     | | ||
Db      1827 TTACTTTTGATCGGAGCAACATAATGCTCATAGAA 1861



RESULT 10
US-10-478-914-62
; Sequence 62, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 1946
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-62

  Query Match             39.7%;  Score 2747;  DB 1;  Length 1946;
  Best Local Similarity   40.7%;  Pred. No. 1.5e-162;
  Matches  667;  Conservative   0;  Mismatches  424;  Indels  548;
Gaps  88;

Qy         1 GCCGCTG----------------CCACCGCACCCCGC----
CATGGAGCGGCCGTCGCT 39
             || | ||                || | || | || |   | ||| | |      |
||
Db       259 GCAGATGGCATGTGTCTGTGACAACCTCTGCTCTCCACATCTCTTGGGCCTGTTTAC-
CT 317

Qy        40 GCGCGCCCTGCTCCTCGGCGCCGCTGGGCTGCTGCTCCTG---CTCCTGCCCC-
TCTC-C 94
             |||| ||| | |||     |||| |  | || | || |  |||| |||| ||||
|
Db       318 GCGCTCCCAGAGCCT-----CCGC----CAGCATC-
CCAGAATCTCCATCCCCATCTCTC 367
```

```
Qy         95 TCTTCCTC-CTCTTCGGACACCTGCGGCCCCT--GC-GAGCCGGCCTCCT-----
GCCCG 145
              |||   | | ||| ||| | |      || |  || | |||| | |||      ||
Db        368 ACTTATACACACATCAGTCATCGGTTATCCATTAGCTAAACCGCCTTCCTTAATAGCTTT 427

Qy        146 CCCC----TGCCCCCGCTGG----------------------------
GCTGC------ 166
              | |   ||| | ||                              | |||
Db        428 ACACTGTTTGCTTTCTCTGGAACATTTTTAGTTAAAATTTCATAATGCAGTTGCACACAA 487

Qy        167 ---------CTGCTGGGCGAGACCCGCGACGCGT--------------
GCGGCTGCTGCC 203
                       | | |||  | |   || || | |            |  | ||||| |
Db        488 ATGAAGACACAGATGGCTGCATCCTCCGTCTCTTCCCCTCGTTTACAGGAAGCTGCGGAT 547

Qy        204 CTATGTGCG------------CCCGC--GGCGAGGGC-GAGCCGTGCGGGG------
GT- 241
              |   | | |           ||| |  || ||||| ||| | | ||||
||
Db        548 CAGGGAGGGGTGTTAGGGTTACCCACATGGTAAGGGCAGAGACAAGAGGGGACCCCAGTT 607

Qy        242 -----GGCGGCGC-----CG--GCAGGGG----------
GTACTGCGCGCCGGGCATGGA 279
                   || || |    |   || ||||            | || | || | ||
Db        608 TTCCATGCTGCACATGGTCATTGCTGGGGACTGAGGTTTGCACATCAC-
CCTGCCCTGTT 666

Qy        280 GTGCGTGAAGAGCCGCAAGAGGCGGAA-----GGGTAAAGCCGGGGCAGCAGC--
CGGCG 332
                   | | |     |||| | || ||      || | ||| || || ||||| |
|
Db        667 CTCCCT------CCGC-TGGGGAGAAAGTCAGGGATGGAGC--
AAGCTGCAGCATCTTCT 717

Qy        333 GTCCGGGTGTAAGCGGC---GTGTGCGTGT------GCAAGAGCCG-CTACCC--
GGTGT 380
              |     | | | ||| || | | ||      |||| || || ||| ||
|
Db        718 GAAAAAGAAAAGGTGGCCTTGTCTCCAGGTCTCCCCTCAAGTCCCACCTTCCCATAGTTT 777

Qy        381 GCGGCAGCGAC-----------------GGCAC--------------------
CACCTA 402
              | ||  | |                  | |||                     |
||
Db        778 TCTGCCACTTCTCTTGATTTTCCTCTCTGCCACTTCTCTTGATTTTCCTCTCTGCCACTT 837

Qy        403 CCC--GA-----------GCGGCTG--------------------CCAGCTGCGCGC---
CG 428
              | |  ||             || ||||                 |||| ||| | |
|
Db        838 CTCTTGATTTTCCTCTCTGCAGCTGCTTTGAGGTGGGTTTTCTCCAGATGCACACTTTCC 897
```

```
Qy          429
CCAGCCAGAGGGCCGAGAGCCGCGGGGAGAAGGCCCATCACCCAGGTCAGCAAGGGCAC-- 486
               || ||     | ||        |   ||  |||||  ||     || |||  ||||| ||
Db          898 CCTGCTTTGCGTCCTTATTCT---
GGTAGAAGCACAATCTAAAGCTCATTAAGGGAACTA 954


Qy          487 ----CTGC-GAGCAAGGTCCTTCCATAGTGACGCCCCCCAAGGACATC-----
TGGAATG 536
                    | | |  ||| ||  ||  |  ||       | || ||  | ||  |       | | |
|
Db          955
ATCAATTCTGTGCATGGCGCTAGCTCAGCAGATCACCACACAGGCAGCACTATTAGCAAG 1014


Qy          537 TCACTGGT--GCCCAGGTGTACTTGAGCTGTGAGGTCATCGGAATCCCG------
ACA-- 586
                 ||   || |   | | |  | |||| |    |  |||      ||  | | ||||        |||
Db          1015 TCGGTGCTTAACACATG-GCACTT---
CCATGAATCGATATGGAGCCCGTGTAGAACAAG 1070


Qy          587 -CCTG-------
TCCTCATCTGGAACAAGGTAAAAAGGGGTCACTATGGAGTTCAAAG-- 636
                 | ||     | ||| ||  | ||| ||| | | ||  |   | ||| ||
Db          1071 GCATGGGTTTTTTTCTCTTCC-
CATTAAGAAAAACTGATGCCAAAAATAACTTCTCAGAT 1129


Qy          637 -----------GAC------------
AGAACTCCTGCCTGGTGACCGGGACAACCTGGC 672
                            |||            | || | |   || |  |       || ||
Db          1130 ATTTTCAAGTATGACTTTTATGAAGGGAAAAAGCATTTTTGTTTGCAAAATCATGCT-
TC 1188


Qy          673 CATTCAGACCCGGGGTGGCCCAGAAAAGCAT--------------
GAAGTAACTGGCTGG 718
                  | ||| ||| | |||       | || |             |  ||||||
||
Db          1189
AGTGCAGGCCAGTTGTGAATTGTGATGGCTTTTATTTCTCCTGGGGCTGTAACTTTAAGG 1248


Qy          719 GT------GCTGGTATCTCCTCTAAG-TAAGGAAGATGCTGGAGAATATGAGTGC-
CATG 770
                   ||       ||| | | |  | ||  ||| | ||  | | |       | |        |
||||
Db          1249
GTTTAGAATTTGGAACCACAGCCTAGCTAATCATGACACACACACACACACACACACATG 1308


Qy          771 CATCCA-ATTCCCAAGGAC-AGGCTTC----AGCATCA-
GCAAAAATTACAGTGGTT--- 820
                 || || | | || | |    | | || ||   ||| |||  |||| ||||| ||
Db          1309
CACACACATACACATACACAAAGCATCACGAAGAACCATACAAATTGTACATTATTTTAC 1368


Qy          821 -----GATGC-----CTTACATGAAATACCAGT------------
GAAAAAAGGTG---- 854
                      || || || || | | ||||||| |                ||||   |||
Db          1369 ACATGGAGGCTCACTCTAAAAT-
AGATACCATTTTAAATATTAACTAAAACTTGTGCTCA 1427


Qy          855 ----------------AAGGTGCCGAGCTATAAACCTC--------
CAGAAT-------A 883
```

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                                 | || | ||  | | |  | |       || |||
|
Db       1428
TTGTATGTTCATTCTATATGTACTGATTTGTTATTCACATTTCTTTCAAAATCGTTCAAA 1487

Qy       884 TTATTAGTCTGCATGGTTAAAAGTAGTCATGG--
ATAACTACATTACCTGTTCTTGCCTA 941
             || ||| |  |||  | ||| || | || | |  | |||||  || ||  |   |
|
Db       1488 TTTCTAGCCCACATCAATTAAA-TATTAATAGTACTTTCTACA-
AACATGAGCGCACAAA 1545

Qy       942 ATAAGT----TCTTTTAATCC--------------AATCCACTAACACTTT---
AGT-- 978
             |||| ||    ||| || |||               |  |  || | |||||  |||
Db       1546
ATAAATTCAAATCTATTTTTCCCACTGGTGTTATCAATACTGCTCATACTTTGTCAGTAA 1605

Qy       979 -TATAT-TCAC-TGGTTTTA----------CACAGAGAAATA-----------
CAAAAT- 1013
             || | |||| || | |||      |||| | || |        ||||
|
Db       1606
CTAAGTATCACATGATCTTAAAACTAATGTCACATACTAAAAAGCTTCTGAGGCAAATTG 1665

Qy       1014 ---AAAGATCACACATCA-------------
AGACTATCTACAAAAATTTATTATATATT 1057
                 ||||| | || ||                ||| |  |||| ||| ||||| || |
|
Db       1666
TAGAAAGAACTCTCAACATCATTGTTCTACTGGACAACATACATAAAATTATTTTACAGT 1725

Qy       1058 TACAGAAGAAAAGCATGCATATCAT--TAAA-----
CAAATAAAATA------------ 1097
             |  | ||| ||  | ||   |||| ||||     | || | ||
Db       1726
GATGGGAGAGAAATAGGCTCCTCATCCTAAAAGCTGCGAAGACAGTAGCGGTGCCGTGTT 1785

Qy       1098 ------------------------------------------------CTTTTT-
ATC- 1106
                                                             |||| |
|||
Db       1786
TTGGCGTTACTCCCCTGTGGATCCCAGCGACGGGTGGATTTCTCCTGTGCTTTATCATCA 1845

Qy       1107 -ACAAAAAAAAAAAAAAAA 1124
              ||| ||||  |  ||||
Db       1846 GACACAAAATGGACCAAAA 1864


RESULT 11
US-10-478-914-57
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
```

  Query Match   39.1%; Score 2704; DB 1; Length 2336;
  Best Local Similarity   36.3%; Pred. No. 2e-159;
  Matches 687; Conservative   0; Mismatches 408; Indels 796;
Gaps   97;

Qy   1 GCCGCTG----CCAC-CGCAC------CCCGC-------CATG--
GAGCGGCCGTCGCTG 40
             || || | || | |||| || | | | |||| | |
||||
Db   29
GCTGCGGAATTCCTCGAGCACTGTTGGCCTACTGGAATGCGAGCTGAGCAGACAGGGCTG 88

Qy   41 C-----------GCGC---CCTGCTCCTCGGC--
GCCGCTGGGCTGCTGCTCCTGCT--- 81
             | |||| | ||||| | || ||||| | | | || |
Db   89 CAAGGAAATCTGGCGCGGTTCAATACCTCGTCTAGC--
CTGGGTTCCAGTATCTAATTTT 146

Qy   82 ------------CCTGCCCCTCTC----
CTC---------------------------- 96
                         ||| | ||| | |||
Db   147
TTTTTTGTTTTAACTGACAAACTCATTTCTCTACTGGGACAGGATGCTGTGCTGGCTGGA 206

Qy   97 --TTCC----------------TCCTCTTCGGACA------------
CCTGCGGCCCCTG 126
               |||| ||||| | ||| | ||| ||| |
|
Db   207
AGTTCCATTTCTACAGCAAGAATCCTATCTGGAAACACAGAAGTTGTCCTCTAGCCACAG 266

Qy   127 -----CGAGC-----------------CGGCCTCCTGCC--
CGCCCCTGCCCCC------ 156
                  ||| | | || || || | |||| ||||
Db   267
CAGCTCGAACTTTTTTGATTGTCGTTGCTGCTTTCTCCCATCACCCCCATCCCCTTTTGA 326

Qy   157 --
GCT 159
             ||
Db   327
CAAAGATCCAACTGTAAAAAGTCTTACGTAACAGTTCAGGACTACTTCGGTTCTTTTACT 386

Qy   160 GGG-------------------------CT----GCC--------------------
TG 169

```
              |||                        ||    |||
         Db      387
GGGTAAGCACTTTCAATTTTTTTTTTTTTAACTAAAAGCCATTTTAAAATTGAATCTGTTG 446

Qy      170 CTGGGCGAGAC----------------------------------------
CCG--------- 183
               ||||   |||                                      | |
         Db      447
AGGGGCTTGACTAAAATCTTTTAAGTAATTTGTGTAATGGAATACTGTCAGTGGATTTTT 506

Qy      184 -CGACGCG-TGCGGCTGCTGC--CCTATGTGCGC----
CCGCGGCG-------------- 221
               || |  | | ||    ||| ||| ||| |    | |  ||
         Db      507
TCGTCTCATTTCTGCACGTGCTCCTTTGTTCTCAGAACAGAAGCTTTTTATACACATCCC 566

Qy      222 AGGGCG-AGCCGTGCGGGGGTGGCGGCGGCCGG---------------
CAGGGGGTACTGC 265
            |   || |||| | | | ||    | | ||          || || | ||
         Db      567 ATAACGCAGCTG-
GAGAGAGTTATGAAGTCAGTTATTATAAGGAACACAAAGGTTGCTTT 625

Qy      266 GC-------GCC---------------------------
GGGCATGGAGTGCGTGAAGAG 291
               |       |||                     |||||||   |
|||||
         Db      626
CCATTCTTTGCCTTTAGATAATTAATTTTTTTGTTTTCTTAAAATGGAGTATTTAAAGAA 685

Qy      292 ---------CCGCAAG----AGGCGGAAGG--------
GTAAAG---------------- 314
              | |||||    |  | |  ||         | ||||
         Db      686
GGAAGAAATTCACAAGAAATAAACTGTTGGAGAATTTAGAAAAGTTTGAAGTTTTTACCA 745

Qy      315 CC--------------------GGGGC----------AGCAGCC---
GGCGGTCCGGGTG 341
               ||                    | |||        || |||  ||||||  |||
|
         Db      746 CCTTTTCTATCTCTAGTTTTGTGTGGCCAAACACTTGTGCCGCCTGGGGCGGT--
GGGGG 803

Qy      342 TAAGCGGCGTGTGCGTGTGCA-AGAGCCGCTA--CCCGGTGTG-----CGGCA-
GCGACG 392
            | || |||    || |  || ||||   ||| || |   ||     |||| | |
|
         Db      804 T-AGAGGC--
AAGCATAGACAGAGAGGAACTAAGCCAGACATGGACAAAGGCACGAGCCA 860

Qy      393 GCACCA------CCTACCCGAGCGGCT-GCCAGCTGCGCG----------
CCGCCAGCCA 435
               ||||         ||| ||| | |||||| | |         | ||||||
         Db      861
AAACCAGACAGTCCTGGCCGTTCGATAGGCCAGCAGTGGGTGAGACAGGTCAGCCAGCTG 920

Qy      436 GAGGGCCGAGAGCCGCGGGGAG---AAGGCCATCACCCAGGTCAGCAAGG-
GCACCTGCG 491
               |||| || |||| | |||| |   | || ||| |      | |  ||| |||  |
||||
```

```
Db       921 CAGGGGCGGGAGCGGGGGGGCGGGTAGGGACAT-----
GGATGTGTGAGGTGCTCATGCG 975

Qy       492 AG---------CAAGGT----------CCTTCCATAGTGAC-GCCCC-CCAAGGAC-
ATC 529
                 |         |  | |         ||  |||| |  | || || |    |   |
                 |||
Db       976
TGCGATCGTGACTAGATTCTGAAACTGCCAGCCATTTTCCCAGCTCCGCTTTGTGCAATC 1035

Qy       530 T---GGAATG-----TCACTGGTGC-------------
CCAGGTGTACTTGAGCTGTGAG 568
                 |  ||||||     |  ||| ||             ||  |||     ||| ||
                 |
Db      1036
TAAAGGAATGCATCCCCTCTGAAGCAGTCTTGCCAGAGCCTAGTGAGGGAGAGAAGTATG 1095

Qy       569 GTCATCGGAATCCCGACACCTGTCCTCATCTGGAACAAGGTA-
AAAAGGGGTCACTATGG 627
                 || |     | | ||| ||  ||| ||| ||     || || |   || || ||
                 ||
Db      1096 GTAA---
ATACCACAACATATGGAATCAGAAAATACCGGGAACTGGAGTGGGCAAGGGGG 1152

Qy       628 AGTTCAAAGG-------------ACAGAACTCCTGCCTG------
GTGACCGGGACAACC 668
                 | | || ||| |             ||  ||  | | ||     ||||| || |
                 ||
Db      1153
AATGCAGAGGGTGTGGAAATTTTTAGTGATCTGGAATGTGTTGAGTGACAGGAAGTGCC 1212

Qy       669 TGGCCA---TTCAGACCCGGGGTGGCC---------
CAGAAAAGCATGAAGTAACTGGCT 716
                 |||    ||| |||  ||         || |||  || ||    |    |!
                 ||
Db      1213 ---CCAAGCTTCTCCCCC------ACCAACTCTTCTCAGTCGCGCCTGCTTT---
TGTCT 1260

Qy       717 GGGTGCTGGTATCTCC---------------------
TCTAAGTAAGGAAGATGCTGGAG 755
                 |  ||  ||||| |                    ||| |||    |  |     !
                 |
Db      1261
AACTCTTGTAATCTACACACTACTGCTTACAAAGCGTGTCTGAGTTTAAGACAAAAAGAAA 1320

Qy       756 AATATGAGT-GCCATGCATCCAATTCCC----------AAGGACAG-----
GC------- 792
                 || ||| || | | || | | ||          |||||  |      ||
Db      1321
CCTAAAAGTCTCCTTACTTCATAGTACCTGTGATATGGAAGGAATGTAAAAGCATGACCC 1380

Qy       793 -TTCAGCATCAG--CAAAAATTACAGT----
GGTTGATGCCTTACATGAAATACCAGTGA 845
                 || ||| |  | ||    ||   ||      |  ||    | | || | |!!
                 ||
Db      1381
TTTAAGCCTATGGACATTTTTTCAGGTATACAGGAGAAAGATAAAATAATTTTCCACAGA 1440

Qy       846 AAAAAG------------------GTGAAGGTGCC------------------
GAGCTATA 870
```

```
            ||||  |                         ||  ||||  ||                    ||  |
|
Db      1441
AAAATGAGAATTATGAATTATATAGTTCAGGTTCCAAATCTAATTTTTAAAAGAATTCTG 1500

Qy       871 AACCTCCAGAATATTA-------TTAGTCTG---
CATGGTTAAAAGTAGTCATG------ 914
             |  || |   |  |||       ||||  ||   |  |  ||  |||| || || ||
Db      1501
ATTCTGCTACACTTTACAAATGCTTAGGTTGGTTCCTAATTTGAAGGAGACTTGTTTTAT 1560

Qy       915 --GATAACTACATTACC--TGTTCTTG--CCTA----------ATAAGTTT---
CTTT-- 953
              | | | |||| |  ||  |||| |||        |||| |||   ||||
Db      1561
TTGGTTAATGCATTGCATTTGAACTTGTTTCTATTTTCTTTGCATAAATTTGGACTTTGG 1620

Qy       954 -----TAATCCAATCCACTAA--------CACTT------------
TAGTTATATTCACT 988
                 ||| |||   | |||      |||||             ||   | |||
||
Db      1621
GAGAAAAATGCAAAGTAATAAGTAGAATGCACTTGGGGGAAAAAAGGAGGATTTTTCCCT 1680

Qy       989 -----GGTT--------TTACACAGAG------
AAATACAAAATAAAGATCAC------- 1022
                 ||||      ||  | || |        |  |||| ||| || |
Db      1681
TCATGGGTTGGAAAGTATTTTAAAGGGTTGTTTTCTTGAAAAAACAAGCTCTCTCTTACT 1740

Qy      1023 ----ACATCAAGACTAT-------------CTACAAAAA----------------
TTTA 1048
                 |||| |  ||||            ||| || ||                  ||
|
Db      1741
TTCTGCATCTATGCTATAAAGATAACTATGCTATAATAAATGTAAGGTAGAAAACTTTAA 1800

Qy      1049 TTATATATTTACAG--------
AAGAAAAGCATGCATATCATTAAACAAATAAAATACTT 1100
                 | | | ||||       ||||||| | | || ||||   | ||    | ||
|
Db      1801 AGAGAAAATAACAGTGTTCTAAGTGAAAAGC-
TACTTAGCATTTTCCCAAACTCACACAT 1859

Qy      1101 TTT-------ATCACAAAAAAAAAAAAAAAA 1124
                 | |         | ||| ||||| || | |||
Db      1860 TATCAACAGAAACACTAAAAATTAAGAGAAA 1890


RESULT 12
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
```

```
  Query Match          39.0%;  Score 2697.5;  DB 1;  Length 2495;
  Best Local Similarity   34.5%;  Pred. No. 7.1e-159;
  Matches  728;  Conservative    0;  Mismatches  390;  Indels  995;
Gaps  109;


Qy        1 GCCGCTG----------CCACCGCAC---------------------
CCCGCC------- 22
            ||| ||          | || |                  |  |||
Db      349
GCCAATGTGGAACTATACTACAGAGCAATACAGTTCTACTTAGAATTCAAGCCTCTGTTG 408


Qy       23 ---------------ATGGAGCGGCCGTCGCTG------CGCGCCC-TGC--
TCC----- 53
                           |||| || | |  | | |     | | | ||| ||
Db      409
TTAAATGATTTGCTGATGGTGCTGTGTCTCCACGGTTGGATCACACTCGTGCAGTCAATTAT 468


Qy       54 -TCGGCGCCGCTGGGCTGCTGCTCCTGCT----CC-----TGC-------------
CCCT 90
             || ||   | |  | ||| |  ||| |     ||    |||              ||
|
Db      469
TTCAGCAAGGTTAAACAGCTACCACTGGTGAAACCGTATTTGCGTTCAGTTCAGAACCAT 528


Qy       91 CTCCTC----------------------------------TTCC------------
TC-- 102
              |  |                                      || |        ||
Db      529
AACAACAAATCTGTGAATGAATCATTGAACAATCTTTTTATTACAGAAGAAGATTATCAG 588


Qy      103 -CTCTTCGGACACC------TGC----GGCCCCT-------------GCGAGC-
CGGC-- 135
             |||| || ||| |      |||     | | ||            || || | ||
Db      589
GCTCTGCGAACATCAATAGATGCTTATGACAACTTTGACAATATCTCGCTTGCTCAGCGT 648


Qy      136 ---------------CTC--------------------CTGCCCGCCCCT------
GCCCC 155
                           |||                   ||||  | ||      ||
|
Db      649
TTGGAAAAACATGAACTCATTGAGTTCAGGAGAATTGCTGCTTATCTCTTCAAAGGCAAC 708


Qy      156 ---CGCTGG--GCTGCCT-----GCTGGGCGAGACCCGCGACGCGTGC--
GGCTGCTGCC 203
               ||||||   | | |       |||| || |||   | |   | |  || |||
Db      709
```

```
AATCGCTGGAAACAGAGTGTAGAGCTGTGCAAGAAAGACAGCCTTTACAAGGATGCAATG 768

Qy        204 CTATGTGCGCCCG-----------CGGCGAGGGC----GAGC-CGTGCGGGGG---
TGG 243
                 |  | |||  | |              | |    |||    || | | ||| | ||   |
|
Db        769
CAGTATGCTTCTGAATCTAAAGATACTGAATTGGCTGAAGAACTCCTGCAGTGGTTTTTG 828

Qy        244 C--GGCGCCGGCAGGGGGTACT---GCGC----------GCC----------------
GGG 273
                 | | |      || | || ||    | ||             ||
||
Db        829
CAGGAAGAAAAAGAGAGTGCTTTGGAGCTTGTCTGTTTACCTGTTACGATCTTTTAAGG 888

Qy        274 CATGGAGTGCGT--GAAGAGCCGCA-AGAGGCGGAA------
GGGTAAAGCCGGGGC--- 321
                 | |  || |||   |  | | ||| ||||| ||        || |   ||| | |
Db        889 CCAGATGT-
CGTCCTAGAAACTGCATGGAGGCACAATATCATGGATTTTGCCATGCCCTA 947

Qy        322 -AGCAGCCGGCGGTC---CGGGTGTAAGCGGC----GTG-----------
TGCGT----- 357
                 || ||  ||||    || ||||   | |    |||           ||| |
Db        948 TTTCATCC--
AGGTCATGAAGGAGTACTTGACAAAGGTGGATAAATTAGATGCTTCAGAA 1005

Qy        358 ------------------GTGCA------AGAGCCGCTACCCGGTGTGC---
GGCAGC-- 388
                                 | ||     |||| | | |||| |||      | ||||
Db        1006
TCACTGAGAAAGAAGAAGAACAAGCTACAGAGACACAACCCATTGTTTATGGTCAGCCC 1065

Qy        389 -----------GACGGCA----CCA-----------
CCTACCCGAGCGGCTGCCAGCTG- 421
                 ||| |||   |||              ||| ||| || ||   | |
Db        1066
CAGTTGATGCTGACAGCAGGACCCAGTGTTGCCGTCCCTCCCCAGGCACCTTTTGGTTAT 1125

Qy        422 --------CGCGCCGC--------CAGCCAGAG---GGC--CGAGAGCCGC----
GGGGA 456
                        ||| |||        |||||| ||   || |   |||| |        | |
Db        1126
GGTTATACCGCACCACCGTATGGACAGCCACAGCCTGGCTTTGGGTACAGCATGTGAGAT 1185

Qy        457 GAAG-GC-------------------------------CATC------
ACCCA------ 471
                 |||| ||                              |||   |||||
Db        1186
GAAGCGCTGATCCTGTAGTCACCTATTTTCGTACTGAAACATCGTCTTTACCCACTTCTC 1245

Qy        472 ---------------------GGTCAGC------------------------
AAGGGC-- 484
                                     | | |                          |||| |  |
Db        1246
AGTTTATAATGGGGGAAAACAGGCAACGTGTTCTTGTAACCTTTATTTCATGAAGGACTT 1305

Qy        485 ------------ACCTGCGAGCAAGGTCCTTCCATAGTGACGCC------
CCCCAAGGAC 526
```

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                         | ||    | |  ||  |  | ||  | |  ||      | |
||
Db       1306
CTTTTTGTTTCTAACTATAAACTTGGATCACCTATGTTAAAACCTTATTTCACATTCCAC 1365

Qy        527 ATC----TGGAATGTC------------ACTGGTGCCCAGGTGT-----
ACTTGAGCTGT 565
               |||    | ||||| |             | | ||  | | | |   ||||| |||
|
Db       1366
ATCATTTTAGAATTTATTTTCGAAGGGGAATAGTTTCAATGTTTTATTCACTTGGGCTTT 1425

Qy        566 ------------------------GAGGTCATCGGAATCCCGAC-----------
ACCTG 590
                                       || |  ||   ||| |
|||||
Db       1426
TTTTCTTCCCCCTCTTTCTTTAAAGAACTGCTCAATATTCAATCTGTTGTGAAGAACCTG 1485

Qy        591 ---TCCTCATCT------------GGAACAAGG------
TAAAAAGGGGTCAC------- 622
                  | | |  |||            | ||||| |     ||| |  | || |
Db       1486 ATTTGCAC-
TCTGTAGTGTTTAAAGAAACAAAGAAACTCTAATATTGAATCTCTTAAATT 1544

Qy        623 -----TATGGA----------------------------------------------
GTT 631
                    |||| |
||
Db       1545
TAGTGTATGTAAACAGCTTACAAATACGTATTGTCTAAATGCATTTAAATCTGTTTTATT 1604

Qy        632 CAAAGGA---------CAGAACTCCTGCCTGGTGACCGGGACAACCTG-----
GCC---- 673
               ||||| |          || ||  ||| |  ||||| |  | |||     |||
Db       1605
CAAAGAAAAGCTAAAGCAAAAACACTGGCATATGACCATGCAAGACTGTCAGTGCCAACA 1664

Qy        674 -----------ATTCAG--------ACCCGGGGTGG--------CCCAGA--
AAAGCATG 704
               | ||||      || |||    || |||| |     |||||| |  | |
Db       1665
AAGACAACACTAATCAGCACATCGTACACTGGATTGCAGTGCTTCCCAGATTATTGAAAA 1724

Qy        705 AAGTAACTGGC-------------------TGGG--------------------
TGCTG 724
               | || || | |                ||  |                    |||
|
Db       1725
ATGTTACAGACAACTTGCCTGATTTTTAAATGAGCGTAAAAGGCCCTCTAACCTATGCAG 1784

Qy        725 GTATCTCCTCTAAG--TAAGGAAGATGCTGGAG--------------AATATG-----
AG 763
               || || ||  || | || |  ||| ||||| |              |||||
|
Db       1785
GTTTCCCCATTATGCATATAGAAAATGCTAGTATGTTTTGCTCACTTCATATGTAACAGG 1844

Qy        764 TGCC-----------ATGCATCCAATTC-----CCAAGG--ACAGGC--
TTCAGCATCA- 802
```

```
                 ||||               ||  ||||  |  |       |    ||    ||  |  |||||  |
||
Db      1845
TGCCCTTATGTTGTGCTGTATCCTGTGCTTTTTCTGTGGGACCATTCCATTCAGGAGCAA 1904

Qy       803 -----GCAAAAATTACA---------GTGGTTGATG--
CCTTACATGAAATACCAGTGAA 846
                    |  |  |||  ||          |||  ||  |   ||||  |  |||  |     |||
|
Db      1905 AGAGCACCATGATTCCAATCTTGTGTGTGTTTACTAACCCTTCCCTGAGGTT--
TGTGTA 1962

Qy       847 AAAAGG----------------------TGAAGGTGC---
CGAGCTATAAACCTCCAGAA 881
                     ||                        |||  ||  |   |||  |  |  |    ||
||
Db      1963
TGTTGGATATTGTGGTGTTTTAGATCACTGAGTGTACAGAAGAGAGAAATTCAAACAAAA 2022

Qy       882 TATTATTAGTCTGCA----------TGG---TTAAAAGTAGTCATGGAT-
AACTACATTA 927
                    ||||  |  |||  ||          |||   ||  |||  ||  |||    |  || ||
||||
Db      2023
TATTGCTGTTCTTCAGTTTTGTTTGTGGAATTTGAAATTACTCAAATTTAAAATAAATTA 2082

Qy       928 C----CTGT---TCTTGCCTAATAAGTTTCTTTTAATCCAAT-
CCACTAACAC------- 972
                    |     ||||     |  |  ||  |       |||||||  |||  |||||  |  ||
Db      2083
CTGGACTGTGGAAATAACATAGAATTGAAGTTTTAATTAAATACCACTCAAACGAAAAGA 2142

Qy       973 -----------
TTTAGTTATAT------------------------------------ 983
                               |  |||||  |||
Db      2143
ACAGTAGTTTTTGTAGTTTTATATTGGATACTGAGGCATTAGGGAGGCATGAAAGGAAGA 2202

Qy       984 ----------------------------------------TCACTG------------
GT 991
                                                       |||  ||
||
Db      2203
GGAATGAGGATTGAGACATGTGAAGACATTGTGCATTATATCAATGTGCATTCCTGTAGT 2262

Qy       992 T--TTACACAGAGAAATACAAAA---TAAAGA-------TCAC---------------
AC 1024
                    |  |||   ||  |  || |||  |   ||||||        ||||
||
Db      2263
TCATTAACAAGGTACATGCAATAGTCTAAAGAACCAGAGTCACTACTATAGTGGCTTAAC 2322

Qy      1025 ATCAAGACTATCTACAAAAATTTATTATA------------
TATTTACAGAAGAAAAGC- 1071
                    ||  |  ||  ||| |||  |  |  ||||    |            |  ||||  |||| |
Db      2323
ATTTAATCTGTCTCCAATATTTTAACCAAGTGACACCGGGGTTTTTATCGAAGCATTTCA 2382

Qy      1072 -----ATG--CATATCAT----------TAAAC---
```

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AAATAAAATACTTTTTATCACAAA 1111
                    ||| || |||||       |  |||   ||||||||| ||| | ||
 |
Db      2383
CTTAAATGAACAAATCATGGCTGTTATATTAACTTGAAATAAAATATATTTAAACATGTA 2442


Qy      1112 AAAAAAAAAAAAA 1124
             |||||||||||||
Db      2443 AAAAAAAAAAAAA 2455



RESULT 13
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;    LENGTH: 2495
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match            38.3%;  Score 2653.5;  DB 1;  Length 2495;
  Best Local Similarity   35.0%;  Pred. No. 5e-156;
  Matches  686;  Conservative   0;  Mismatches  426;  Indels  847;
Gaps  103;

Qy        2 CCGCTG---CCACCGCACCC---CGCCATGGAGCGG--------
CCGTCGCT-------- 39
                || |    ||| | || |   |  || ||| ||        |   | |
Db      1977
CCACAATATCCAACATACACAAACCTCAGGGAAGGGTTAGTAAACACACACAAGATTGGA 1918

Qy       40 ------GCGCGCCCTGCTCCT--------CGGCGCCGCTG----------
GGCTGCTGCT 75
                     | || |  |||||||       || || | |         || | |
 ||
Db      1917
ATCATGGTGCTCTTTGCTCCTGAATGGAATGGTCCCACAGAAAAAGCACAGGATACAGCA 1858

Qy       76 CCT-------GCTCCTGCCCCT-----------CTCCTCTTCCT--
CCTCTTC------- 108
                |        || |||| |             |   | | || | | |||
Db      1857
CAACATAAGGGCACCTGTTACATATGAAGTGAGCAAAACATACTAGCATTTTCTATATGC 1798

Qy      109 -------GGACACCTGC-----------GGCCCCT---GC---------
```

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GAGCCGGCCTC 138
                    ||| ||||||              |||| |   ||        | | |||
Db       1797
ATAATGGGGAAACCTGCATAGGTTAGAGGGCCTTTTACGCTCATTTAAAAATCAGGCAAG 1738

Qy        139 CTGCCCG-----------------C-------CCCTGC---CC-----
CCGCTGGGCTGC 166
                    || |                    |         | |||| ||        || ||
Db       1737
TTGTCTGTAACATTTTTCAATAATCTGGGAAGCACTGCAATCCAGTGTACGATGTGCTGA 1678

Qy        167 CTGCTG-----------GGCG-----AGACCCGC---GACGCGTGC---------
GGCT- 197
                    |  ||           |||       || | ||  || |   |||
|||
Db       1677
TTAGTGTTGTCTTTGTTGGCACTGACAGTCTTGCATGGTCATATGCCAGTGTTTTTGCTT 1618

Qy        198 --GCTGCCCTATG--TGCGCCCGCGGCGAGGGC----GAGCCGTGCGGGGGTG---
GCGG 246
                    |||   || || |   | |      |  ||        | | ||     ||   ||
|
Db       1617
TAGCTTTTCTTTGAATAAAACAGATTTAAATGCATTTAGACAATACGTATTTGTAAGCTG 1558

Qy        247 --------CGC-------------------------------------------------
CGG 252
                    | |                                                        |
Db       1557
TTTACATACACTAAATTTAAGAGATTCAATATTAGAGTTTCTTTGTTTCTTTAAACACTA 1498

Qy        253 CAGGG---------GGTACTGCGCGCCGG---GCATGGAGTGC-
GTGAAGAGCCGCAAGA 299
                    ||| |      ||| |||| |  | |   || |   | || |         |
||||
Db       1497
CAGAGTGCAAATCAGGTTCTTCACAACAGATTGAATATTGAGCAGTTCTTTAAAGAAAGA 1438

Qy        300 GGCGGAAG-GGTAAAGCC------------------
GGGGCAGCAGCC------------- 328
                    || ||||||    ||||||                   |    |      ||
Db       1437
GGGGGAAGAAAAAAAGCCCAAGTGAATAAAACATTGAAACTATTCCCCTTCGAAAATAAA 1378

Qy        329 -------------------------------------------GGCGGTCCGGGT-----
GTA 343
                                                               || | ||| ||
||
Db       1377
TTCTAAAATGATGTGGAATGTGAAATAAGGTTTTAACATAGGTGATCCAAGTTTATAGTT 1318

Qy        344 AGCGGCGTG---------TGCGTG----------TGCAAGAGC-
CGCTACC--------- 374
                    ||   |           | | ||       | |||||| | || | ||
Db       1317
AGAAACAAAAAGAAGTCCTTCATGAAATAAAGGTTACAAGAACACGTTGCCTGTTTTCCC 1258

Qy        375 ----------------------------CGGTGT-------------------
GCGGCAG 387
```

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                                             ||  |||                         |
                                             |||
Db      1257
CCATTATAAACTGAGAAGTGGGTAAAGACGATGTTTCAGTACGAAAATAGGTGACTACAG 1198

Qy       388 CGACGGCAC--CACCTACCCGAGCGG------CTGCCA-GCTGCGCGCCG-
CCAGCCAGA 437
              | | | |   || | || |  ||  || |       |||| |||| || | | ||| |
|
Db      1197 GATCAGCGCTTCATCT-CACATGCTGTACCCAAAGCCAGGCTGTG-
GCTGTCCATACGGT 1140

Qy       438 GG--------------GCCGA---GAGCCGCGGGGAGAAGGCCATCAC-----
CCAG-- 472
              ||                || |   | |||  || | | | ||| |||     || |
Db      1139
GGTGCGGTATAACCATAACCAAAAGGTGCCTGGGGAGGGACGGCAACACTGGGTCCTGCT 1080

Qy       473 GTCAGCA------AGGGC--ACC-------------TGCG-------AGCAAGGTC--
CT 502
              |||||||       |||| |||              || |      ||| | ||
||
Db      1079
GTCAGCATCAACTGGGGCTGACCATAAACAATGGGTTGTGTCTCTGTAGCTTGTTCTTCT 1020

Qy       503 TC----CATAGTGACGC-----------------
CCCCCAAGGACATCTGGAATGTCACT 541
              || |  | ||||| |                ||  ||  |  || | |  ||
|
Db      1019 TCTTTTCTCAGTGATTCTGAAGCATCTAATTTATCCACCTTTG---TCAAGTAC-
TCCTT 964

Qy       542 GGTGCCCAGG-TGTACTTGAGC------------------TGTGAGGTCAT-
CGGAATC 580
               || || || | | |                       ||||   ||| | |
||
Db       963
CATGACCTGGATGAAATAGGGCATGGCAAAATCCATGATATTGTGCCTCCATGCAGTTTC 904

Qy       581 ----CCGACACCTGTCC--------TCAT--CTGG------
AACAAGGTAAAAAGGGGTC 620
               ||||| ||| ||      || |  | ||      ||||| |  ||||
|
Db       903
TAGGACGACATCTGGCCTTAAAAGATCGTAACAGGTAAACAGACAAGCTCCAAAGCACTC 844

Qy       621 ACTAT-----------------------
GGAGTTCAAAGGACAGAAC------------ 644
               || |            |||||||    | ||  |
Db       843
TCTTTTTTCTTCCTGCAAAAACCACTGCAGGAGTTCTTCAGCCAATTCAGTATCTTTAGA 784

Qy       645 ----------TCCTGCCTGGTGACC-------GG--GACAACCTGGC---------
CATT 676
                 | |||| | |   ||        ||  | |  || ||             ||
Db       783
TTCAGAAGCATACTGCATTGCATCCTTGTAAAGGCTGTCTTTCTTGCACAGCTCTACACT 724

Qy       677 CAG--ACCCGGG---GTGGCCC------AGAAAAGCATGAAGT------
```

```
AACTGGCTGGG 719
            | |   || | |   || |||     ||| ||||| || |     |||| ||
|
Db      723
CTGTTTCCAGCGATTGTTGCCTTTGAAGAGATAAGCAGCAATTCTCCTGAACTCAATGAG 664

Qy       720 TGCTGGTATCTCCT----CTAAGTAAGGAAGATGCTGGAGAATATGAGTGCCAT--
GCAT 773
             | |  || | |||    || || ||| |||| ||   || ||     |||
||||
Db       663 TTCATGTTTTTCCAAACGCTGAGCAAGCGAGATATTGTCAAAGTTGT----
CATAAGCAT 608

Qy       774 CCA-----ATTCCCAAGGACAGG-------
CTTCAG------------------------ 797
             | |       ||| ||  | | |       |||| |
Db       607
CTATTGATGTTCGCAGAGCCTGATAATCTTCTTCGTGTAATAAAAAGATTGTTCAATGATT 548

Qy       798 CAT---CAG-------------------------CAAAAAT--------
TACAGTGGTT 820
             ||| |||                         |  ||||
||||||||
Db       547
CATTCACAGATTTGTTGTTATGGTTCTGAACTGAACGCAAATACGGTTTCACCAGTGGTA 488

Qy       821 GATG-----CCTTACATGAAATACCAG--
TGAAAAAGGTGAAGGTGCCGAGCTATAA-- 871
             | ||     |||| | ||||||  |  || |  ||||     ||| |      |
Db       487 GCTGTTTAACCTTGC-
TGAAATAATTGACTGCACGAGTGTGATCCAACCGTGGAGACAGC 429

Qy       872 ACCTCCAGAATATTATTAGTCTGCATGG-------
TTAAAAGTAGTCATGGATAACT--- 921
             ||| ||| | || ||| | |   || ||  |||||| || |  ||
Db       428
ACCATCAGCAAATCATTTAACAACAGAGGCTTGAATTCTAAGTAGAACTGTATTGCTCTG 369

Qy       922 ------------ACATT----ACCTG-----------------------
TTCTTGCCT- 940
                        ||||| ||||||     |   ||||| ||
Db       368
TAGTATAGTTCCACATTGGCAACCTTGGTAATGATATCTTTGAATTGCCCTTCTTTCCAG 309

Qy       941 -AATAAGTT------------------------------
TCTTTTAATCCAATC------ 963
              || |||| ||   | || || |
Db       308
GCATCAGTTGGATGATTCATCATGGTAATTATGGCATTATCATATTCTTCATACTTGTCA 249

Qy       964 CACTAACACTTTAGTTATATTCA--------CTGGTTTTACA-----------
CAGAGAA 1004
              || |||   |||| |   ||       || ||| | ||          |   |
Db       248
TACAAAAACACCAGTTCTGCCCAAAGATGAGCTTGTTCTGCAGCTCTTAGCACCTTGGGA 189

Qy      1005 ATACAAAATAAAGATC---ACACATCAAG----------ACTATCT---
ACAAAAATTTA 1048
             ||| || |  |||| |   ||| || ||       | | |||   |
```

```
              |||||||
Db        188
ATATTCACTCTAGACCAGAACAGCTCCAGGTGCTCCCTCATTTTCTGAGGCTTAAATTTA 129


Qy       1049 TTATATA--------TTTACAGAAGAAA----------AGCATG--
CATATCATTAAACA 1088
                   ||||         | ||| | |        ||| |  ||  ||
|
Db        128
GAGTATAGAATAGCTAATTCAGTAAACATTCCCATGTGAGCTCGCTCAAGTCCCAGTGCT 69


Qy       1089 AAT---AAAATACTTTTTATCACAAAAAAAAAAAAAAA 1124
                | | || || | | | | | |||| |  | |
Db         68 GCTTCCAACATGGTGATCAGCTCTTCAAAATAGCCACGA 30



RESULT 14
US-10-478-914-3/c
; Sequence 3, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 2083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-3

  Query Match             38.3%;  Score 2653;  DB 1;  Length 2083;
  Best Local Similarity   36.4%;  Pred. No. 2.4e-156;
  Matches  680;  Conservative   0;  Mismatches  407;  Indels  780;
Gaps   99;


Qy          1 GCCGCTGCCACC-GCACCCCG---
CCATGGAGCGGCCGT--------------------- 35
               || || || ||| ||| | ||    |||  | |||| |
Db       2080 GCGGCCGCGACCTGCAGCTCGAGCACAT---
GTGGCCTTTTTTTTTTTTTTTTTATTTTG 2024


Qy         36 CGCTGCGCGCCCTG---------CTCCTCGGCGCCGCTGGG-----
CTGCTGCTCCTGC- 80
               | || |  || |||         |||||      | |     || || | |||
|
Db       2023 C-TTCTTGCTCTGGTGGTTAGTCTCCTACTATAAACATGATTTTCCTTCTTC-
CCTTCA 1966


Qy         81 ---TCCTGCCCCTCTCCTC----TTCCTCCT------------------
CTTCGGACACC 115
```

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                    |||| |  |||    |    || ||| |                      || | ||
||
Db      1965
GAGTCCTGTCAATCTTTACTTTTTTTCTCATTAATATACAGAAGTTATACTACAGATACA 1906

Qy       116 TGC--GGCCC----CTGC----------------GAGCCG----------
GCCTCCT--- 140
            | |  || |   ||||                |||||           |  || |
Db      1905
TTCAAGCTCATGACTGCTAAAAACTTCCTGAAATGAGCCTTAATTCATACGAATCATTTC 1846

Qy       141 --------------------GCCCGCCCCT---------
GCCCCCGCTGGGCTGCCTGC 170
                              | | | ||        |||| ||||| ||
|
Db      1845 TATTTGTTCTTTTTTTTTTGAGACAGACTCTTACTCTGTCGCCCAGGCTGGAGTGC--
AC 1788

Qy       171 TGGGCGAGACCCGCGACGCGTGCGGCTGCTGCCCTATGTGCGCCCGCG-
GCGAGGGCGAG 229
            |  ||| || | ||| |      |||| ||  | ||| ||| | |  | |   ||| |
||
Db      1787 T-GGCATGATCT-CGGCTC-----ACTGCAACC---TCTGC-
CTCACGAGTTAGGTCAAG 1739

Qy       230 CCGTGCGGGGGTGGCGGC--GCCG----GCAGGG------GGT-
ACTGCGCGCCGGGCAT 276
            | | |    |   | || |||    || ||     ||| |||| | || ||
|
Db      1738 CAATTCTTCTGCCTCAGCCTCCCGAGGAGCTAGGATTACAGGTCCCTGC-
CACCATGCCT 1680

Qy       277 GGAGTGCGTGAAGAGCCGCAAGAGGCGGAAGGGTAAAGCCGGGGCAGC--
AGCCGG---- 330
            |||| | |        || | |||| ||  ||| || | ||| ||| ||
Db      1679 -
GAGTAATTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTAGCCAAGCTGGTCTC 1621

Qy       331 ------CGGTC--CGGGTG-----------TAAGC--------------------
GGC 349
                     | | | | |||||        | |||
|||
Db      1620
GAATTCCTGACCTCAGGTGATCCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACGGGC 1561

Qy       350 GTGTGCGT--GTGCAAGAGCCGCTA----------------------
CCCGGTGTGC-- 382
            ||| ||   ||||  | ||| |||                      ||| |    |
Db      1560 GTGAGCCACGGTGCCTG-
GCCTCTATTTTTTATTTTAAATACCTTTTGCCCTGAAATCTA 1502

Qy       383 -GGCAGC-----GACGGCACCACCTACC--------------------------
CGAGCG 410
             | |  |        |  ||| | ||||                             |
|
Db      1501
TGTCCTCTGATTATCAACACTGCTTACCAGTTTTATTTTTGTTGGTATTTATTTCATTC- 1443

Qy       411 GCTGCCAGCTGCGCGCC--GCCAGCCAGA------GGGCCGAGAGC-------
CGCGG-- 453
```

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                  |  ||||||    |  |    ||||     |       ||   |      |        ||  |
Db       1442
AATCCCAGCTCTACAACTTACCAGTATAAAAATTTGGATCAGTTACTTAATCTTGCAGTT 1383

Qy        454 ----------GGAGAAGG-----------CCATCA---------
CCCAGGTCAGCAAGGG 483
                           |  |  ||           |  ||||      |||||  |  |
Db       1382
TCTTCCTTTTAAAAATGGAATAATATTATCTATCATATAAAATGCCCAGTTAA------- 1330

Qy        484 CACCTGCGAGCAAGGTCCTTCCATAGTGAC--GCCCCC--
CAAGGACATCTGGAATGTCA 539
                     ||  |  || |  |   ||| | ||| |||  |  || ||   |  ||| |   |  | ||||||
|
Db       1329 CAAATATGAACTAACACCTACAAT-GTGCCAGGCACCATTCTAGGGAA--
TAGAATGTAA 1273

Qy        540 CTGGTGCCCAGGTGTACTTGAGCTG--TGAGGT--CATC------
GGAATCCCGAC---- 585
                     |     |  |    || | |||| |||  | || |  |||         |||   |  |||
Db       1272 ATAAGTTCAA---
GTTCTTGACCTGAATAAGTTTACATTTTAGTGAGAAGACAGACAATA 1216

Qy        586 --------ACCTGTCC----------------
TCATCTGGAACAAGGTAAAAAGGGG--- 618
                          || |||||            | |   ||   |||| |  |||| ||||
Db       1215
AATCAATAACATGTCCATTATGCCAGATAGTTTTAAATGTCACAAAGAAAAAGGGGGAGC 1156

Qy        619 --------------------------------------------------
TCACTATGG 627
                                                               ||  ||
||
Db       1155
AATCAGATAGTGATGGAAGTTACACTCTAGAGAGGGTGGACAGAAAAAGTTTCTCTTAGG 1096

Qy        628 AGTT----------CAAAG--------GACAG------AACTCC----------
TGCCTG 653
                     ||  |           ||  ||       |||  |      ||| ||          ||
||
Db       1095
AGATGACATCTGAACAGAGATCTAAATGACTGAGTACAAACCCCAATGGAAAAGTGATTG 1036

Qy        654 GTG---------AC--
CGGGACAACC----------------------------------- 668
                           |||           ||  |    ||| ||
Db       1035
GTGTGTTGTGAAACAGCAACACAGCCAGTTTGACTAGATGAGTAGATCAGAATGACTGAG 976

Qy        669 ---------TGGCCAT--------TCAGA-------CCCGGGGTGGCC------
CAG--- 695
                           ||| |||        |||||       || ||| ||||        |||
Db        975
GTGGGACTGTGGTCATCAAAGAGATCAGAGAGGTAGCCTGGGAAGGCCACATCACAGAAT 916

Qy        696 -----------------AAAAGC---ATGAAGTAACTG-
GCTGGGTGCTGGTATCTC--- 731
                                 ||  |||    ||||  ||| |  ||| |    |||    ||
Db        915
GTCCTTTGGGCCTCTGTAAGAGCGTTTTGAAAAAACAGTTCTGAGCAAAGGTTAGTCATT 856
```

```
Qy        732 ------------CTCTAAGTAAGG----------------------
AAGATGCTGGAGAA 757
                 ||||    ||||                          ||
          |||||||||
Db        855
TAACTTGACTTACTCTTTAGAAGGATCACTTTGGCTATTGAGTGGCAAACAACTGGAGAA 796

Qy        758 -----TATGAGTGC--------
CATGCATCCAATTCCCAAGGACAGGCTTCAGCATCAGC 804
                   || | | ||     || || ||    ||    ||| || ||| | |
          |
Db        795
GTGGTTAGGGGAGCACTGTGGGCAGGAATAGAAGGAGGAAAAGCAGACTGGAGCCTAATC 736

Qy        805 AAAAATTACAG--------TGGTTGA--TGCCT--TACATGA-----
AATACC------- 840
                | | | |||      ||   ||  |||||  ||||| |      || ||
Db        735
CAGTACTTCAGATGAGAAATGACAGATTTGCCTGGTACATCATTTCCTATCCCTTTACTT 676

Qy        841 --------------------------AGTGAAAA------------------
AAGGTGA 855
                           |||| |||                           ||
          |||
Db        675
ATAACTTATTGGTGTATTTTTATTTTAAGTGTAAATTTTTATAAATGAAGCATAATTTGA 616

Qy        856 AGGT-----------GCCGAG------CTATAAAC---------
CTCCA----------- 878
                 || |         | | |    |||| | |        |||||
Db        615
AGATTGATATGTTCGGACTTGTGTTTTCTATTATCATGGTGTCTCTCCACATACCTTTTC 556

Qy        879 -----------GAATATTATTAG--
TCTGCATGGTTAAAAGTAGTCATGGATAACTACAT 925
                 |  | |||||  || || | ||   | |  | |      ||||
          |
Db        555
CCTTTAGTTCTGCTTCTTATTGTGCTCCTCAAGTCTATTTTTGTTCTTTTCCCTCTACTT 496

Qy        926 TACCTGTTCTTGCCT-AATAAG---TTTCTTTTAATCCA------
ATCCACTAACACTTT 975
                 |||||  |   || ||| |  ||||| ||   |||     | || ||
          |||
Db        495
CTACTGTTTTGAACTGTATATGCTATTTCTATTTTGCCAGGAGTTACCCCCTTCAATTTT 436

Qy        976 AGTTATATTCACT-GGTTT--TACACAGAGAAATACAAAATAAAGATC-
ACACATCAAGA 1031
                 ||| || || || ||| | ||||| |  | |  || | | | || | ||
Db        435
CGTTGTACTCTCTCAGTCTCAAACACATACCCATGCTCTCTTCTGTCCTTCTCTTCATAT 376

Qy        1032 CTATCTACAAAAATTTATTATA----------------------TATTTACAG-
AAGA 1066
                | ||||| | |||| || ||                      ||||| ||
          ||
Db        375 C-
ATCTTCTAGAATTAGTTCTACCCCGATTTCTACCAATTTATTTTATTTCCAATCAGT 317
```

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Qy      1067 A-----AAGCATGCATATCA-----
TTAAACAAATAAAATACTTTTTATCACAAAAAAAA 1116
                |    | || ||||||    ||  || |||  ||  ||||| |   |
Db       316
ACATTGATTCAGATTTATCAATATGTTTTACCAATTTTATCATTTTTTTTGGAGGCTTGT 257

Qy      1117 AAAAAAA 1123
                | | ||
Db       256 TATTTAA 250


RESULT 15
US-10-478-914-60/c
; Sequence 60, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 2022
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-60

  Query Match            38.0%;  Score 2628.5;  DB 1;  Length 2022;
  Best Local Similarity   37.4%;  Pred. No. 8.3e-155;
  Matches  654;  Conservative   0;  Mismatches  427;  Indels  667;
Gaps  95;

Qy        1 GCCGCT---GC-CA-----CC----------------------------
GCAC-----C 17
             || |||  || ||     ||                          || |
|
Db     2020
GCAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTAGATGGAGTTTTGCTCTTTTGC 1961

Qy       18 CC----------GCCATGGAGCGGCCGTCGCTGCGCGCCCTGCTCC-TCGGCGCCG-
CTG 65
             ||          || |||| ||| | ||| ||| || | |||| | || ||||
|||
Db     1960 CCAGGCTGGAGTGCAATGGCGCGATC-TCG----GCTCACTGCAACTTC--
CGCCTCCTG 1908

Qy       66 GGCTGCTGCTCCTGCTCCTGCCCCTCTCCTCTTCCTCCT------CT-----------
TC 108
             || |  ||| | |||||| |||| ||||||    ||
|
Db     1907 GGTTCAAGCTATT-CTCCTG-------
```

```
CCTCAGCCTCCTGAGTAGCTGAGGTGAGAGGAC 1856

Qy        109 GGACACCTGCGGCCCCTGC--GAGCC-----------GGCCTC------CTG----
CCCG 145
              |||  |   |  ||     |||  |||||          ||    |       |||    |
||
Db       1855 TGACGCGAGAGG--
ATTGCTTGAGCCTAGGAGGTTGAGGTTGCAGTGAGCTGTGTTCACG 1798

Qy        146 CCCCTG--CCCCC-GCTGGGCTGCCTGCTGGGCGAGACCC-
GCGACGCGTGCGGCTGCTG 201
              || ||| | ||  ||||||| ||    |    || ||||||| |    |       |       |
Db       1797 CCACTGGACTCCAGGCTGGG-TG---
ACAAAGCAAGACCCTGTCTCAAAAACAAAAACAA 1742

Qy        202 CCCTATGTGC-------------
GCCCGCGGCGAGGGC--------------------G 227
               |  |    |                      ||  |    |    |
Db       1741
ACAAACAAACAAACAAAAAAATAACCAACAAAAAAAACCCTGAGTTTAAGTTTGATTTTA 1682

Qy        228 AGCCGTGCGGGGGTGGCGG-------CGCCGGCAGGGGGTACTGCG-
CGCCGGGCATGGA 279
              || | || ||| || |         |   |    |  ||||| |||  |  |
||||
Db       1681 AGACCTGTAGGGACAGCAGATTAGTTCTACTTTAATGGGTA-TGCATCATC-----
TGGA 1628

Qy        280 GTGCGTGAAGAGCCGCAAGAGGCGGAAGGGTAAAGCCGGG-------
GCAGCAGCCGGCG 332
               ||     |||  | |   ||  | | |  |     |      |  | |         ||  |||  |
|
Db       1627 AAGC---
AAGGGTCATAAAAAGAAGATACATCTTCACTGGCACCATCACATCAGTCATCA 1571

Qy        333 GTCCGGGTGTAAGCGGCGTGTGCGTGTGCAAGAGCC--------------
GCTACC---- 374
              ||||  |  | ||   |   |  |  | | | |        ||                ||| ||
Db       1570 GTCC-----TTAGATAC-
AGAACCTTTACTGACTCCCTCAAAACTTCCATGCTTCCAAAC 1517

Qy        375 ------CGGTGTGCGGCAGCGACGGCACCA---------
CCTACCCGAGC---------- 409
                        |  || |  |  |     ||  | ||            ||| |   |  |
Db       1516
TAACCAAGCAGTTCTTCTACATTGGGATCATCGAATTTCCCTTCATGTTCCAACTCTCCT 1457

Qy        410 --GGCTGCCAGCTGCGC----GCCGCC--AGCCA---GAGGGCC------
GAGAG----- 447
                ||| | |  | |        |  || |||||   ||   ||        |||
Db       1456
CTAGCTTCAATATACACATAGACAACCTTAGCCATCTGAAAACCTACTTTTAGAATATTC 1397

Qy        448 CCGCGGGG-----AGAAGGCCATCACCCAGGT--------------------
CAGCAAGG 482
              ||| | ||       |  |  |  |  || |||| |                          |   ||
Db       1396
CCGAGTGGTTCCACGTAAGTCCTCTGCCAGATTCACATACCCATAAATTCTACTTCATAA 1337

Qy        483 GCACCTGC----------------------------------------------------
```

```
GAG 493
                    || | | |
Db      1336
GCCCATACTGTTCTTAAAAAAGAAATAGAAAAAATATATCAATATAACTTTAAAATAAGA 1277

Qy      494 CAAGGTCCTTC----------------------------
CATAGTGACGCCC-------- 517
                    ||    |||||                    ||| ||| |||
Db      1276
CACAAACCTTCATGAAAATATAGTCATCAAATTTATTTTCATTGGGATGCCATTTTTTGA 1217

Qy      518 ------CCCAAG-------------GACAT-----------
CTGGAATGTC--------- 538
                    || |||          |||||          |   ||| |
Db      1216
AGAATTCCTAAGACTAATGTTTCTTGACATGCAAGAGTTAGCATTAATAGCTTACGTTAC 1157

Qy      539 -------ACTGGTGCCCAGGTGTACTTGAGCTGT----GAG------
GTCATCGGAATCC 581
                    |||| |||   |  | | |  | |||||   |||     | |  | || |
Db      1156
TATAAATACTGCTGCTTGGAAGCAGTACAACTGTTTTAGAGTTTTAAGACTACAGACTTT 1097

Qy      582 CG--ACACCTGTCCTCATCTG------------------------GAACA--
AGGTAAAA 613
                    |   || |   || | || |                       |||||   ||| |
Db      1096
CATTACTCAAATCTTATTCAGTAAATGTAAAAATCAGAAGGTTCTGAACAGCTGGTTAGG 1037

Qy      614 AGGG--GTCACTATGGAG--------------------TTCAAAGGACAG--
AACTCCTG 649
                    | ||  | || ||| ||                   || |||| ||| |||||
Db      1036
AAGGTAGCCAAGATGCAGGAAAGATGTCTGCGCCTCCTTTTCAAGGGCAGCCAACTCTTG 977
||
Qy      650 CC----TGGTGACCGGGA---CAACCTGGCCATTCAGAC-----
CCGGGGTGGCCCA--- 694
                    |||| ||   |  | ||   |         | |  || | | || | ||
Db      976 AACAGTAGGTG-
CCAAAATATCCACATGGCCTTTATAGCTTCCACCTGCGTCACACACAA 918

Qy      695 -------------------GAAAAGCATGAAGTAAC-TGGCTG---------
GGTGC--T 723
                    || | || |||| |||| || |             || |
Db      917
|
ATAACAAAGTAATGTAAATGACATGCTTGAAATAACTTGTCAGCAATACTTTGGCTCAAT 858

Qy      724 GGTATCTCCTCTAAGTAAGGAAGATGCTGGAGAATATGAGTGCCATGCATCCAATTCCCA 783
                    |||| | || | |  | || ||| || | ||   ||| | ||
Db      857 TATATCACTTTAAACTTTGCTTGCAGCAATAAAATGT-ACTACTGGGCAAATTA-
TCTCC 800

Qy      784 AGGAC--AGGCTTCAGCATCAG------CAAAAATTACAGTG----------
GTTGATGCC 826
                    || ||   | ||| |  |  |      ||| ||| ||| |          | |
|||
```

```
Db        799
AGAACTTTGACTTTAAAAAATGTTAAATCAATTATTTCAATATAAATAAATAATTAGGCC 740

Qy        827 TTAC---ATGAAATACCA-----------------------
GTGAAAAAAGGTGAAG-- 857
              | ||    |   |  | |||               |  |  | ||   || | |
Db        739
TCACTAACAGCTGTCCCAACACCTCTACCCACCCTTGGCTCGGAAACAACTAGTTAGGCC 680

Qy        858 -------------------GTGCCGAGCTATAAA-----CCTCC-------
AGAATATTA 886
                              |  | |||||| ||    | ||||      || | ||
|
Db        679
TGAGTCTTACAATTTTTCAGGAACAAGCTAACAAAAGGGCATCCCAGGCAGAGGAAATAA 620

Qy        887 TTAGTCTGCATGGTTAAAAG----TAGTCATGGATAACTACATTACCTGTTC----
TTGC 938
              |  | | ||| ||   |   | |    ||||| |   || ||| | ||||    |
|
Db        619 TATG-CTGAATTACCACCTGAGTTAAGTCAAAGGCTTCTG-
ATTCCTTGTTCAAAATCAC 562

Qy        939 CTAATA------AGTTTCTT--TTAATCCA-------
ATCCACTAACACTTTAGTTATAT 983
              ||| ||     ||||| |  | | ||||      || ||| || ||| |  | ||
Db        561 CTATTATGCTCTTGTTTCCTAATAATTCCACAAAATGTTCAACT-
ACTCTTATGACATTA 503

Qy        984 TCACT---------GGTTTTACACAG-AGAAATACA---
AAATAAAGATCACACA----- 1025
                  ||||           |   ||  | |  ||    | ||   | | |||||||| |||||
Db        502
ACACTTCAAGAGAAAGAGCTAAGCTGAAGTCTTTCATTCACATAAAGATGACACAATTTA 443

Qy        1026 --------TCAAGAC---
TATCTACAAAAATTTATTATATATTTACAGAAGAAAAG---- 1070
                          |||| |   ||| |||||   ||| |       || || | || |
Db        442
AAAATGCTACAAGGCAGGTATGGACAAAGTACTATGAGGGTAATAAGGAGGGAATGATTA 383

Qy        1071 -CATGC-------ATATCATTAAACAAAT------
AAAATACTTTTTATCACAAAAAAAA 1116
                    || ||        |||   |||| | |||     ||| |||| | | ||| |||||
|
Db        382 ACACGCTAAAAATATACTCTTAACCTAATGAAATGAAAGTACTGCCT-
TCCCAAACCGAA 324

Qy        1117 AAAAAAAA 1124
                       ||||
Db        323 GTTCAAAA 316


Search completed: March  9, 2010, 15:51:45
Job time : 7.15787 secs

                        GenCore version 6.3
             Copyright (c) 1993 - 2010  Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2010, 15:51:16 ; Search time 1 Seconds
                                          (without alignments)
                                          1134.946 Million cell
updates/sec

Title: US-10-572-905-7
Perfect score: 17216
Sequence: 1 ttgaaatcaggaaatcaggc..........agggaaaaaattgcttgact
2901

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 417 seqs, 79705 residues

Total number of hits satisfying chosen parameters: 834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   7335755.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result   Query
   No.   Score Match Length DB ID   Description

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     1 6539.5   38.0   3210 1 US-10-478-914-4   Sequence 4,
Appli
  c 2   6447   37.4   3210 1 US-10-478-914-4   Sequence 4,
Appli
     3 6279.5   36.5   3589 1 US-10-478-914-21   Sequence 21,
Appl
  c 4 6178.5   35.9   3589 1 US-10-478-914-21   Sequence 21,
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     5   5635   32.7   2437 1 US-10-478-914-61   Sequence 61,
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  c 6 5600.5   32.5   2437 1 US-10-478-914-61   Sequence 61,
Appl
     7   5410   31.4   2495 1 US-10-478-914-20   Sequence 20,
Appl
  c 8 5366.5   31.2   2336 1 US-10-478-914-57   Sequence 57,
Appl
  c 9   5351   31.1   2495 1 US-10-478-914-20   Sequence 20,
Appl
    10   5267   30.6   2120 1 US-10-478-914-64   Sequence 64,
Appl

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Appl							
c	12	5120	29.7	2198	1	US-10-478-914-17	Sequence 17,
Appl							
	13	5066.5	29.4	2198	1	US-10-478-914-17	Sequence 17,
Appl							
	14	5053	29.4	2336	1	US-10-478-914-57	Sequence 57,
Appl							
c	15	4867	28.3	2022	1	US-10-478-914-60	Sequence 60,
Appl							
c	16	4707	27.3	2083	1	US-10-478-914-3	Sequence 3,
Appli							
	17	4686	27.2	1946	1	US-10-478-914-62	Sequence 62,
Appl							
	18	4587	26.6	2083	1	US-10-478-914-3	Sequence 3,
Appli							
	19	4447	25.8	2022	1	US-10-478-914-60	Sequence 60,
Appl							
c	20	4409.5	25.6	1946	1	US-10-478-914-62	Sequence 62,
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c	21	4176	24.3	1813	1	US-10-478-914-63	Sequence 63,
Appl							
	22	3993	23.2	1813	1	US-10-478-914-63	Sequence 63,
Appl							
	23	2295	13.3	1020	1	US-10-478-914-68	Sequence 68,
Appl							
	24	2293	13.3	889	1	US-10-478-914-5	Sequence 5,
Appli							
	25	2255	13.1	938	1	US-10-478-914-69	Sequence 69,
Appl							
c	26	2252	13.1	1020	1	US-10-478-914-68	Sequence 68,
Appl							
c	27	2245.5	13.0	938	1	US-10-478-914-69	Sequence 69,
Appl							
	28	2240	13.0	867	1	US-10-478-914-6	Sequence 6,
Appli							
c	29	2194	12.7	909	1	US-10-478-914-67	Sequence 67,
Appl							
c	30	2193	12.7	889	1	US-10-478-914-5	Sequence 5,
Appli							
c	31	2188	12.7	867	1	US-10-478-914-6	Sequence 6,
Appli							
c	32	2182	12.7	889	1	US-10-478-914-9	Sequence 9,
Appli							
	33	2176	12.6	839	1	US-10-478-914-16	Sequence 16,
Appl							
c	34	2151	12.5	816	1	US-10-478-914-15	Sequence 15,
Appl							
	35	2145.5	12.5	816	1	US-10-478-914-15	Sequence 15,
Appl							
c	36	2123	12.3	839	1	US-10-478-914-16	Sequence 16,
Appl							
	37	2097.5	12.2	794	1	US-10-478-914-13	Sequence 13,
Appl							
	38	2096.5	12.2	889	1	US-10-478-914-9	Sequence 9,
Appli							
	39	2087	12.1	816	1	US-10-478-914-38	Sequence 38,
Appl							
	40	2076	12.1	909	1	US-10-478-914-66	Sequence 66,
Appl							

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  c  42  2051.5   11.9    794  1  US-10-478-914-13       Sequence 13,
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  c  43  2045.5   11.9    845  1  US-10-478-914-18       Sequence 18,
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  c  44   2043   11.9    816  1  US-10-478-914-38       Sequence 38,
Appl
      45   2039   11.8    845  1  US-10-478-914-18       Sequence 18,
Appl
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ALIGNMENTS

RESULT 1
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match   38.0%; Score 6539.5; DB 1; Length 3210;
  Best Local Similarity   44.5%; Pred. No. 0;
  Matches 1573; Conservative   0; Mismatches 997; Indels 963;
Gaps 215;

Qy   1 TTGAAAT-CAGGAAATCAGGCCGGG----CGCAGTGGCTC--------
ATGCCT------ 41
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Db   7 TTGGCCTACTGGCC--
CAGGCCTTGCACACGCAGGTGCTCTCTTAGTGCTCCCTGGCAAG 64

Qy   42 -----GTAAGCC----CAGCACT-----TTGG--GAGGCGGAGGCG--
GGTGGATC---C 80
                    | | || ||| || | || | ||| |||| | | ||| |
|
Db   65
GATGGGAAGGCATGTTCAGTCCTAGGAGTAGGAAGGGGCAGAGGTGTTGATGGCCCCTAC 124

Qy   81 ATTGGGTC-------AGGAGC------TCAAGA---
CCAGCCTGGTCAACATGGTGAAA 124
               | | || | |||||| || | || |||| || || ||
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Db        125
AGAGCGGCCAAGGACAAGGAGCTGCTGTTCGAAACAGCCTTCCTGCTCCCCAACCTGCCT 184

Qy        125
CCCCGTCTCTACTAAAAATACAAAAAAAAAATTAGCTGGGCGTGTTGGCGGGA------- 177
          |||  | | ||       | |  || |    | | |     |||||     | ||||
Db        185 CCC--ACCCAACAGGTTTTGC----ATATACTCTACTGGG-----
AAGAGGGACACACCC 233

Qy        178 GCCTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAGAATTG-
CTTGAACCCGGGAG-- 234
          | |||| ||| ||  |||     | | ||         |  || | | ||| ||||
Db        234 GACTGCA-TCACTGCCCTCCAAGTCTCTCC-----
CTGCCCTGTCCAGCATCCAGGAGCA 287

Qy        235 ------
GCGGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTCCAGCCTGGGCGACAG 288
               |  | ||  ||       ||| || | | |      ||  |||||| |   ||
                                                                         |
Db        288 CCCCTAGTTGGGGAAGC----TTCTGTGACTCCCCCT----ACAACAGCCTAG--
GATGG 337

Qy        289
AGCAAGACTCTCTCAAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGACCACAGT 348
               ||    |          ||      || ||  ||| | ||| |     | | |
                                                                         |
Db        338 AGTGGGGTT----------
TGTGAACAAATGCAGAAGGCAGTCTTAGGGAGGTCAGCTGA 387

Qy        349 GGTAGCCACCTGGCCTAATGCTGTGTTTTTG----------------
TACC--------- 383
                  | |||| |||||||||   |||| |   | |                 | ||
Db        388 CAT-GCC-
CCTGGCCTGTGGCTGGGAAGTAGCAGAGGCTAAGGTTCTTCCCCGCTCTGGG 445

Qy        384 --TGACAGGGGT--CAC----TCATTTTAGGCACAACTC-
CTTCATTCTTTGTGAAATT- 433
                   || |||| || |||     ||| |    | |||    | | | ||| || |
Db        446 GTTGCCAGGAGTAGCACTGGATCAGTCAGGTGACAGGGCTCTCCTCTCTCTGAGCAGGTC 505

Qy        434 -AGTGAGTTTCCTTCTA---CCCGTCACCAGATTCAATATGT-
TCTATTAATACACCGAT 488
               ||| |   ||||| |    ||| |||| | | ||| | |
Db        506 CGGTG-
GCAGCCTTCAAGGTCGCCACGCCGTATTCCCTGTATGTCTGT------------ 552

Qy        489
AACCACAGGGGAAGGGCACTTGTCGCTCTCCCACCTGGTTACCACAGTCTCCATGGGTCT 548
               ||  ||||| | |   ||| ||| |         ||| |||   ||
                                                                         ||
Db        553 --CCCGAGGGGCAGAAC----GTCACCCT--CACCTG-------
CAGGCTCTTGGGCCCT 597

Qy        549 TTTGCC-----------GTGACC----
ACAAATAAAGGAAACACTCATCACTAGTATCT 592
                  |  |  |          ||||||    ||||      || |   || | | ||
                                                                         |
Db        598 GTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCG--
```

```
CAGCTCGAGGGGCG 655


Qy          593 AAGT-CGGGCTT-
TACAGTAACTATGCACCTTCTGTGTGCTTCACCTCACTCTCTA---- 646
                 | || ||| || |  ||| |   |  || ||      |   |||||| || |
Db          656 AGGTGCAGACCTGCTCAG-AGCGCCGGCCCATC------
CGCAACCTCACGTTCCAGGAC 708


Qy          647 CTTCAAACAGC-
CCATGGAGGGAGGTATTATTATACTCCTTATGTTGACAGTGAAGAATC 705
                  |||| | | ||  |||||||||            | ||  | | || ||
Db          709 CTTC-ACCTGCACCATGGAGG------------CCACC--
AGGCTGCCAACACCAGCCA 752


Qy          706 TGA---
GGCCCAGAGAGGTTGGGGACTTGAGTAAAGTCACACAGCCCTGAGAGGCAGGAC 762
                 ||   ||| ||| |        || || |||   |  | | | ||
|| 
Db          753 CGACCTGGCTCAGCGC---CACGGGCTGGAGT--CGGC-CTCCGACC-----------
AC 795


Qy          763 CAGGGTTCCAT-
TCCTGCTCTATCCAGTTCCAAGCCCTTGTGTTTTCCATTATGTTTAG- 820
                 || ||   | | |||  | || |    ||  |||| || |  |    | |
|
Db          796 
CATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCTCTACTGC 855


Qy          821 TGCCTCTTTG-------CTAACAGCAACA-TCTG----CAAGAT---TTGTG--
TTGGTT 863
                 |||||  | |        |   || || ||| |   ||  |  | | | |||    |||
Db          856 
TGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGTCCATGGTGCCATGGAG 915


Qy          864 TTGATGGAGAACTCTAGCT---------CATCCACATGC-TAGTG--
CCCAAGTGGTGGA 911
                 || || | | | ||        |||||| ||| || |||  ||||
Db          916 
CTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACTGTGTGGTGTACCCAT------- 967


Qy          912 GGGGCCACCTCAGCAGGTGGGT-----
TCTGAATGCAGCCAAGGCTGTCCCCGCAATGGG 966
                 || |||| |||| | |  | |   | | || ||   || ||||
||||
Db          968 ----CCTCCTCC-CAGGAGAGTGAAAGTAAGGGACCAACCT---CTTGCCCC-
TTTTGGG 1018


Qy          967 TGAGACTC--GCTCCAACTGCCCGC--
CCTCAGAGCAGGTGCCTAAGTCCTCCCTGGCAC 1022
                 |   ||| |  | | ||| | |  |||    ||| | | | || |   ||| |||
||
Db          1019 T---TCTCTGTTTTCTTCTGTCCTCATCCT----GCA----
CCCAGACCCTGTTTGGAAC 1067


Qy          1023 
TGGCAGGCCTTACCTCACATTGCTAAATTAAAGCAATGCAATTCCTCTTGGGTAAGAGGA 1082
                 |  | |||||| | | |              |||| | |  || | ||
Db          1068 T--CTGGCCTCATCACCC-----------CAAGCCCT-
CAGAACCCCCCGG--------- 1104
```

```
Qy        1083
ATTCCTCCTTCTTTACTAACTGATCCCCAGCAAGGAAATAAAATGTTAGGCTTTAAAAAT 1142
                  ||||||| |||| || ||| | ||| |                  || |||||
Db        1105 --TCCTCCTCCTTTTCT-GCTGCTGCACATCCC------------
TTCTGCTT------- 1142


Qy        1143 CCCTACTTTGTCATATCAGACTATATTCTAAAACTATATTTGAGCGAAACCTGTCAT-
TG 1201
                  ||| ||| ||  ||| | | | | | || ||            ||| |||
||
Db        1143 -CCTCCTTGGTGCAATC--CCCAGAAGCCCACTCT--------------
CCTTCCATCTG 1185


Qy        1202 CGTCT--AATTTCAAATATAC-
AGAATCTCCTTAAGAGCTGTTGCCTTATTTTTTTGTAA 1258
                   | ||| | | | ||   |   | || |||| |   | |||| ||||||        |
Db        1186 C-TCTGGAGTCTCTGCTCCTCTTGACTCTCTGGAGTGGCTG-TGCCTTG-------
GCAG 1236


Qy        1259 AGCCTCTCTGACATCAAATGGGGAGAAATGGTGGCACCTCCAGACA------------
CC 1306
                  | | || || |  ||   ||| |   ||| |||| |||| ||||
||
Db        1237 TGAC-CTTTGGC--CA----GGGCAA----GTG---
CCTCATGACAGGTACTGGGTGCCC 1282


Qy        1307 CT-
GAAACTACACACCATTTCTTCCCTGCTCAGCTTCTGCTCAGGAGTTCTGTGAGCTAT 1365
                  | | | ||| || |||    |||||| ||   | ||   || || |||
|
Db        1283 CAGGCAGCTAAGTGCCG------CCCTGCCCA---CCAGCCCC------CTATG-
GCT-T 1325


Qy        1366 GGGAAGGCCATTGGTTGTATTTG-
CTACTTTTACTTTCATCTTCCTCTGCTGTAG----- 1419
                  |||||||| ||| | ||| |  |            | | | |||| || |
Db        1326 GGGAAGGCTGGGGGTCCTCTTGGCCAACAGGGTGAAACCCCAT-
CTCTACTAAAAACACA 1384


Qy        1420 ------AGCCATTTAATGT----------
TATTGTCATATGCTGCTGGTGAGGTAAAGGT 1463
                  |||||  | ||      | | ||| | ||| ||   ||||
|||
Db        1385 AAAATTAGCCAGGCATGGTGGTGCGCGCCTGTAGTCCCA-
GCTACTCAAGAGGCTGAGGC 1443


Qy        1464 GGGTCCGGGTGCCTT---CCCAGGGGTTAGAGGATGTTCAAAGGGCCGATTT----
CAGC 1516
                  |    |   |||   ||| || || |||||| || ||  | ||||| |     |
|
Db        1444 AAG--AGAATCGCTTGAACCCGGGAGTCAGAGGTTG--
CAGTGAGCCGAGATCGCGCCAC 1499


Qy        1517 AGGAGTTCAGAGGGCTTATGATGGATGGTGAGAGATT---
TGACAACCACCAGAGCAC-- 1571
                  | | | ||||  |||      ||| | |  ||| |   |  ||| | | ||| |
Db        1500 TGCACTCCAGCCTGCT-------
GATAGAGCAAGACTCCATCTCAAAAAAAACAACCCAA 1552
```

```
Qy      1572 -ATGTGCTCTGACCCTCTCCTGGGCATTGGT--TCCTGCTGGTAC-
CGGGCGGTTCAGAC 1627
             || ||| ||| |    |     ||||| || ||| | | ||| |||| || |
||||
Db      1553 AATTTGC-CTGGCATGGTGGCAGGCATCTGTAATCC--
CAGCTACTCGGGAGGCTGAGAC 1609

Qy      1628 CTTCAAATAGGTTGCTTTCAAAAGAGCTTTCAGGCACTTAT-----
TGAGAATTAATGTT 1682
             |  |   | | ||||| | | |  ||||| |   |||| |       ||
Db      1610 ATGAGA----GCTGCTTGAACCTGGG-----
AGGCAGAAGTTGCAGTGAGCCGAGATCAC 1660

Qy      1683 TAAACAGACATAATAGCCTAGATGA---------AC----
TCCCAAGAGATCTATTAAAT 1729
             || | || |||||| | |||        ||    |||||| | ||| |
||||
Db      1661 ACCACTG-
CACTCCAGCCTGGGTGACAGAGCGAGACTCTGTCCCAAAAAATCAAAAAAAT 1719

Qy      1730 --CTTGTGG----GCTGAA-------TAAATATCTCGTGCAGGAC-
TGTGCAACAGTAGC 1775
             ||| |||   | | |        || | | || |||| | | ||
||
Db      1720 CACTTTTGGTAGAGATGCACTCTCGCTATGTTGCCCAGGCTGGTCTTGAACTCCTG-
GGC 1778

Qy      1776 CCA---GAGCATCCTGCCTGTGGGCATCCACCTCCCAGGTGAGGG-----
CAGTGGGAAG 1827
             || || | ||| ||| ||   |||||| | ||| ||    ||| |
||
Db      1779 TCAATTGATCTTCCCACCT-TG-------
ACCTCCAAAGTGCTGGGATTACAGGTGTGAG 1830

Qy      1828 CTGGCCCGAC-GGCAGCCAGAACTTGTT-TCTCACCTCCCACCAGCA-
ACCCCCCACCCA 1884
             |   | | |  || | | ||||| | |||    ||| | | | |
|
Db      1831 
CCACCATGCCTAGCCTCAGGGAATTCTTATAAGAACTCTATGAAGTAGGCATCACCATCT 1890

Qy      1885 ACTCTGGGCCCCAGGCACACGAAGCACAAGT--------
CTCAGGGGACCATTCCCACAT 1936
             |||||  || || |  || || | ||        || |  | ||| |
|||||
Db      1891 TCTCTGTATCCATGGAAAGAGAGGC-
CTAGAGATGTATGCTAACTTGCCCAAGCTCACAT 1949

Qy      1937 TG----GGGGATC----CTGAGG----GAGC-----CC---------
ATCACCGCCTCTT 1970
             |  ||| | |   ||| |    |||| ||         | | |
||
Db      1950 
AGCCCCAGGGTAGCATAGCTGGGATGTTGAGCTGAGGCCGGAGGAGAAGTAGCAGTCGCTG 2009

Qy      1971 GCATA-CA-ACTGTC--CACTAGG------------------AGGCAC--
GCC------ 1999
             ||| | || || | | | || ||                   ||| || |||
Db      2010 
GCAGAGCACACAGGCTGCTCTGGGGGATGAGCTGGTGCGTTTAAGGAACAGGCCAGCACT 2069
```

```
Qy       2000 ------------CAGTG-----TGGGAGAGATGT----ATGGTCT------
TGCCTTCCA 2032
                          |||||      ||||||||||     |||||      || |||
||
Db       2070
GGCATTCGCAAGCAGTGGGGAAGGGGAGAGATGCCGAGGTGGTCAGTATCCTGACTTTCA 2129

Qy       2033 ----
CCTGTAAAAACTGCACATATGCAAGCCATTTGCACTCTGGAACTGCATGCCGTGAA 2088
                  ||| |        || | | |    ||||| ||| |       |
||
Db       2130 GAGGCCTTTTTT---TGTTTGTTTTAAT---TTTTGCTAGATTGATAT--------
TAAA 2175

Qy       2089 AACTCCTAATGGTGTGGAACTTA--
GTTTGAATTTGAAATCACGCCGCATGCACAAAGGG 2146
                  |||||    ||| | |||||| |   ||  || |||      || | | | |
|
Db       2176 AACTC---ATGTGGAGGAACTCAAGGAATG-TTTAGAAG----
ACCAAAAGTCCCCAATG 2227

Qy       2147 ACAGGCCCAGGCCCGAC--------------CTCAGGTCA-TCC--------------
GC 2177
                  |||||  ||    | ||             |||  ||| |||
|
Db       2228
ACAGGAACAAAAGCAACCAATTTTTAACTTTCTCTTCTCATTCCTGTTTTCATTGATTTC 2287

Qy       2178 CCGCTGGCTGCAGAGCAT---CCCTGGGAG-CCAAGGCGA-------
GGCCCGTGGAGC- 2225
                  || |    || || | |   | | || || |  || ||      |  |  ||
|||
Db       2288 CCAC---
ATGTAGTCCTTTTGCTCAGGAAGTCTTTGGGGAAATTAAGGATCTTTGAAGCT 2344

Qy       2226
CTGAGCTTTGTGTAGCTCGAGCTTTGTGTAGCTCGTGCACTTATTATGC----------- 2274
                  |||| ||| |||||  ||| ||  || |||| |
Db       2345 CTGAAATAGGT---GATC-
AGGTTAGTGGTGTCTGTCAGCTGTCTAAGAGGTTGGAAAAT 2400

Qy       2275 -ACCACCTCCCTTCAGTCAC--CACTCCT---------CTTCCTC-CGCCAT------
CC 2315
                  | |  ||| ||||||  | | |   |              || || |||| ||||
Db       2401
GAACTACTCAAGATAGTCACGAAAATACTGAAAGTTTGATTTTTCTTTCCATATTTGAAT 2460

Qy       2316 TCATTTATACTGATTGC-----------------------
ACACCCCCCGCTCAAACA-- 2350
                  | |||| | ||| |||                        | | | ||| || || |
Db       2461
TAATTTTTTCTGTTTGACTGGAAGGGGTTTTTGTATAACTAAAACCTCAGCGCATAAAGG 2520

Qy       2351 ------ACAATGTCC-------TTATTATGATGACCAT----CTCG----------
TAGT 2383
                  | ||| |      ||| |   | ||||   || |                  |
|
Db       2521
AGATTTAAAAGGAGCACATGATTTAGTGGGTGGGCCATGAAACTAGAGATGGGATTTGGG 2580
```

```
Qy       2384 GGTACAT---TCCATTCCT--ATTTAAGGTAAGCC-------CAA---
AGCC------- 2420
              ||| ||   || || || ||||  |  || |     | |   ||||
Db       2581
GGTGAATTTGTCAATATCTGGATTTTAATCCAGACATCTCTGCTAACGAGCCTTTGGTAA 2640

Qy       2421 --CACTTTTGG---ATTTTCTC----------------
GACTGTCCGAGAAAAGTTGTGT 2459
              ||||| |   ||| ||| |     | ||| | || | |||
Db       2641 GTCACTTCAGATACTTTTCCTCCTTTTTACAAAGAGAGGGCTGGCTTAGTTAT-
TTGCCA 2699

Qy       2460 AAGC---------GCCTGCGTTCTTCTGG---
GTTTGGCTAGATAGGGTTGTGTCCCTCT 2507
              ||||       ||||| ||| |   | ||  ||   ||| || | ||
||||
Db       2700 AAGCCCCTTCCAGGCCTGAATTCCACAAGTACGATTTACT--
GTAGTGTCTTATCACTCT 2757

Qy       2508 -----------ATGGAATGGAG----
AGTGATGTGGGCAAGGGTGTCATTTTCTCGCACA 2552
                        || | ||||   || ||    | | || | | |  | ||   | ||
||
Db       2758 TTCATGTCACAATAGCGTGGAGCATTAGAGA-AAAGCCTAGACTTTTAGTTGATAGC-
CA 2815

Qy       2553 AT--
ACAACTCACTGAGGATGCTTCTGTAGAAGTGAGAAACACGATGAGTACATTCAGAA 2610
               | |  ||| |||        || ||    || | ||      ||| | |    |
Db       2816 GTTGAAATATCATTGATAGAATTTTAGTTTTAGGAAAAATTGGTTTGATTTCTAGCTTTA 2875

Qy       2611
TTACAATAACTCACTCTCACTGGGTAACTTCTCATGATAGATTTGTATGATCAATACGGG 2670
              |||| ||           | ||||| |  || | | | |  | | |||| | |
|
Db       2876 TTACTAT-------------TAGGTATGTGAGCTTGGGCAAATCGCTTAATCTTT--
GAG 2920

Qy       2671 TCTATTTTTATGTC-AACTGAACACTGTAGGGTA--------CC----
TTCCAGTCTTTT 2717
              |||| |||| | || || ||| ||  || |||| ||         ||   |||||| ||
|
Db       2921 TCTAGTTTTCTCTCAAAATGAGAACATTAGGCTAAATGATTTCCGAGTTTCCAG-
CTAGT 2979

Qy       2718 TCAAGATTGTTAAATTGAGACAAGTAATTGAA-
TAATTTGTCCTATTTTTATTTTAAAAA 2776
               | ||| | ||| |  | | ||||||| || ||| | | | |   |  | || |
||
Db       2980 CCTAGAGTTCTATATTTCTACA--
TAGTTGAATTATTTTATCATGCTGTTGCTGGGGAAT 3037

Qy       2777 AAG----------TGAATGGACTGA---AATGTTAAATGTGAATGTACAT--
TTCTTAA 2820
               | |         |||| ||| |     |||| |  | || || ||| ||
|||
Db       3038
```

```
ATGACTAACCCTTTTGAAGCTACTAATTTTATGTCGAGCTTTAAAGTCCATAATTGTTAT 3097

Qy      2821 TTGCA------ATTTTT----CTACTGAGTGT---TTGCACTATA---------
CTTT-- 2856
             | ||      ||| ||    |||| |  |||      || | ||          ||||
Db      3098
CTTCAGAAAATATTATTTGACCTACAGTATGTCCAAATCAATTTAATAAAATCGCTTTAT 3157

Qy      2857 --CTGGAATCTTATTTAACAAAAATAAAGGGAAAAAA--------TTGCTTGA 2899
               | ||||    |   || ||||| |||  ||||||        |||| ||
Db      3158 AACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCCACATGTGCTCGA 3210


RESULT 2
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match            37.4%;  Score 6447;  DB 1;  Length 3210;
  Best Local Similarity   44.4%;  Pred. No. 0;
  Matches 1548;  Conservative    0;  Mismatches 1029;  Indels  911;
Gaps  219;

Qy         1 TTGAAATCAGGAAATCAGGC---------
CGGGCGCAGTGGCTCATGCCTGTAAGCCCAG 51
             ||    ||  | || | ||               |   ||| |||  ||||| | |
|
Db      3170 TTTTTTTCCTGTTATAAAGCGATTTTATTAAATTGATTTGG-ACAT-
ACTGTAGGTCAAA 3113

Qy        52 CACTTTGGGAGGCGGAGGCGGGTGGATCCATTGAGGTC--
AGGAGCTCAAGACCAGCCTG 109
               | | |      | ||  |      | | ||| || |     ||||| | |  |
|
Db      3112 TAATAT---TTTCTGAAG-----
ATAACAATTATGGACTTTAAAGCTCGACATAAAATTA 3061

Qy       110 G-----TCAACATGGT------GAAACCCCGTC-
TCTACTAAAAATACAAAAAAAAAATT 157
                |     |||| | |||       | |||| | | | |  ||| || ||   ||
|
```

```
Db      3060 GTAGCTTCAAAAGGGTTAGTCATATTCCCCAGCAACAGC--
ATGATAAAATAATTCAACT 3003

Qy       158 AGCTGGGCGTGTTGGCGGGAGCCTGTAGTCCCAGCT----ACACGGG--------
AGGCT 205
              |  |   |   |  |       ||  ||| | ||||    || ||          ||
||
Db      3002 ATGTAGAAATATAG------
AACTCTAGGACTAGCTGGAAACTCGGGAAATCATTTAGCCT 2949

Qy       206 AAGGTGGGAGAATTGCTTGAACCCGGGAGGCGGAGGTT--GCAGTGAG-
CTGAGATTGC- 261
              || ||        |||    ||| | ||  || ||  |  ||  |   |  || |
|
Db      2948
AATGTTCTCATTTTGAGAGAAAACTAGACTCAAAGATTAAGCGATTTGCCCAAGCTCACA 2889

Qy       262 -ACC--
ATTGCACTCCAGCCTGGGCGACAGAGCAAGACTCTCTCAAAAAAAAAAAAAAAG 318
              |||  || | | | ||| | |    || | |||   |  || ||| ||||    |
Db      2888 TACCTAATAGTAATAAAG-
CTAGAAATCAAACCAATTTTTCCTAAAACTAAAATTCTATC 2830

Qy       319 AAAGA-AAGAAATCAGAAAATCGACCACAGTGGTAGCCACCTGGC-CTAATGCT--
GTGT 374
              || ||  |     | | |   ||| || |     |||    | |  |||||||||
|
Db      2829 AATGATATTTCAACTGGCTATCAACTAAAAGTCTAG--
GCTTTTCTCTAATGCTCCACGC 2772

Qy       375 TTTTGT-ACCTGACAGGG------GTCACTC--------------------
ATTTTAGGC- 407
              |  |||| || ||| || |      | ||||                   |  ||
||||
Db      2771
TATTGTGACATGAAAGAGTGATAAGACACTACAGTAAATCGTACTTGTGGAATTCAGGCC 2712

Qy       408 ------------------ACAACT-------
CCTTCATTCTTTGTGAAAT---------- 432
                                | ||||      || || |||||||| |||
Db      2711 TGGAAGGGGCTTTGGCAAATAACTAAGCCAGCCCTC--
TCTTTGTAAAAAGGAGGAAAAG 2654

Qy       433 ------TAGTGAGTTTCCTTCTACCCGTCACCAG----------------
ATTCAATATGT 471
                    ||||| || ||    | ||| | |||                | || | ||
|
Db      2653
TATCTGAAGTGACTTACCAAAGGCTCGTTAGCAGAGATGTCTGGATTAAAATCCAGATAT 2594

Qy       472 T--CTATTAATACACCGATAACCACAGGGGAAGGGCACTTG--TC---
GCTCTCCCACCT 524
              |   | | |  ||| |   ||| |   ||| | ||| ||    || | ||||||
Db      2593 TGACAAATTCACCCCCAAATCCCAT-----------
CTCTAGTTTCATGGCCCACCCACTA 2544

Qy       525 GGT----TACCAC-----AGTCTCCAT---------GGGTC----
TTTTGCCGTGACCAC 562
              |    |   | |     | ||||| |         |||     || | |    |||
|
```

```
Db       2543
AATCATGTGCTCCTTTTAAATCTCCTTTATGCGCTGAGGTTTTAGTTATACAAAAACCCC 2484

Qy        563 -----AAATAAAGGAAACACTCATCACTAGTAT------
CTAAGTCGGGCTTTACAGTAA 611
                        || |||| | | | ||||| |       || ||   ||||
           |||||
Db       2483 TTCCAGTCAAACAGAAAAAATTAATTCAAATATGGAAAGAAAAATCAAACTTT-
CAGTAT 2425

Qy        612 CTATGCACCT-TC-TGTGTGCTTCA----CCTCACTCT----CTACT-
TCAAACAGCCCA 660
                | |  || || || || |||| ||      || |||| | || ||||| |
           |
Db       2424
TTTCGTGACTATCTTGAGTAGTTCATTTTCCAACCTCTTAGACAGCTGACAGACACCAC- 2366

Qy        661 TGGAGGGAGGTATTATTATACTCCTTATGTTGA-CAGTGAAGAATCTGAGG---
CCCAGA 716
                        || |  || | |||  |   || |     |||| || |      ||||
           |
Db       2365 ----------TAACCTGAT-
CACCTATTTCAGAGCTTCAAAGATCCTTAATTTCCCCAAA 2317

Qy        717 --------GAGGTTGGGGACT---TGAGTAAAGTC-----
ACACAGCCCTGAGAGGC--- 757
                        |||     ||||| || | || ||     | |||| ||||| |
Db       2316
GACTTCCTGAGCAAAAGGACTACATGTGGGAAATCAATGAAAACAGGAATGAGAAGAGAA 2257

Qy        758 ----AGGACCAGG--------GTTCCATTC----------------CTGCT---
CTATCC 786
                        | |  | |     ||||| ||        || ||    |
           |||
Db       2256
AGTTAAAAATTGGTTGCTTTTGTTCCTGTCATTGGGGACTTTTGGTCTTCTAAACATTCC 2197

Qy        787 ---AGTTCCAAGCCCTTGTGTTTTCCAT-TATGTTTAGTGCCTCTT--
TGCTAACAGCAA 840
                ||||||   | | ||  |||||  || |   | |||       ||    | ||||
           ||
Db       2196 TTGAGTTCCTC-
CACATGAGTTTTTAATATCAATCTAGCAAAAATTAAAACAAACAAAAA 2138

Qy        841 ----CATCTGCAAGATTTGTGTTGGTTTTGA-----
TGGAGAACTCTAGCTCATCCACA- 890
                | |||| ||   || ||| | |  | |    | | |||| | | |||
           ||
Db       2137 AAGGCCTCTGAAA-----GTCAGGATACTGACCACCTCGGCATCTCTC-
CCCTTCCCCAC 2084

Qy        891 ----TGCTAGTGCCCAAGTGGTGG-AGGGGCC---
ACCTCAGCAGGTGGGTTCTGAATGC 942
                        ||| |||| ||||  |||| |||   |  ||   | | ||| |     | |
           ||
Db       2083 TGCTTGCGAATGCC--
AGTGCTGGCCTGTTCCTTAAACGCACCAGCTCATCCCCCAGAGC 2026

Qy        943 AGCC--AAGGCTGTCCCCGCAATGGGTGAGACTCGCTCCAACTGC-
CCGCCCTCAGAGCA 999
```

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              ||||      ||| | || ||        |||| ||| |  || | ||| |||||
||
Db      2025 AGCCTGTGTGCTCTGCCAGC---------GACT-
GCTACTTCTCCTCCGGCCTCAGCTCA 1976

Qy      1000 GGTGCCTAAGT---CCTCCCT-GGCACTG---GC--AGGCC--
TTACCTCACATTGCTAA 1048
               || |  |  || || | ||  | ||   ||| | |  ||| | |||| ||
Db      1975
ACATCCCAGCTATGCTACCCTGGGCTATGTGAGCTTGGGCAAGTTAGCATACATCTCT-- 1918

Qy      1049 ATTAAAGCAATGCAATTCCTCTTGGGTA---AGAGGA-----
ATTCCTCCTTCTT----T 1096
               | || || | | | ||| ||  ||| ||     || ||| |||| |
|
Db      1917 ----AGGCCT--CTCTTTC-
CATGGATACAGAGAAGATGGTGATGCCTACTTCATAGAGT 1865

Qy      1097 ACTAACT--GATCCCCAGCAAGGAAATAAAATGTTAGGCTTTAA----AAATCCCT--
AC 1148
               || |     || ||| | ||| |  | |  |             |   ||||||
||
Db      1864 TCTTATAAGAATTCCCTG--AGGCTAGGCATGGT--
GGCTCACACCTGTAATCCCAGCAC 1809

Qy      1149 TTT----GTCAT-
ATCAGACTATATTCTAAAACTATATTTGAGCGAAACCTGTCATTGCG 1203
               ||| |     |||| | || ||  | | | |      | | | ||| | |
Db      1808 TTTGGAGGTCAAGGTGGGAAGATCAATTGAGCCCAGG--
AGTTCAAGACCAGCCTGGGCA 1751

Qy      1204 TCTAATTTCAAATATACAGAATCT-CCTTAAGAGCTGTTGCCTTATTTTTTG---
TAAA 1259
                | || | || |||  ||| | ||| || |  || ||||||| |
|
Db      1750 AC--ATAGCGAGAGTGCA-TCTCTACCAAAAGTGATTTT--
TTTGATTTTTTGGGACAGA 1696

Qy      1260 GCCT--CTCTGACATCAA--
ATGGGGAGAAATGGTGGCACCTCCAGACACCCTGAAACTA 1315
               | || ||||| ||| | |     | | | ||||| | ||| | | ||
||||
Db      1695 GTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGGTGTGATCTC--
GGCTCACTGCAACTT 1638

Qy      1316 C--ACACCAT--TTCT------TC-CCTG-CTCAGCTTC------
TGCTCAGGAGTTCTG 1357
               |  | ||   ||   |||      | |      || ||  || |  ||| ||| | |
|
Db      1637 CTGCCTCCCAGGTTCAAGCAGCTCTCATGTCTCAGCCTCCCGAGTAGCT-
GGGATTACAG 1579

Qy      1358 TGAGCTATGGGAAGGCCA---------TTGGTTGTATTT----------
GCTACTTTTACT 1399
               ||      | ||||        | ||||||| |||       |   |||
||
Db      1578
ATGCCTGCCACCATGCCAGGCAAATTTTGGGTTGTTTTTTTTTGAGATGGAGTCTTGCTCT 1519
```

```
Qy      1400 TTCATCTTCCT---CTGCTGTAGAGCCATTTAATGTTATTG--TCATATG-
CTGCTGGTG 1453
                |||  |    ||     ||| || | || || |    | | ||   | | || ||  | |
Db      1518
ATCAGCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCTCTGACTCCCG--- 1462


Qy      1454 AGGTAAAGGTGGGTC-CGGGTGCCT---TCCCAGGGGTTAGAGGATGTTCAAAGGGC-
CG 1508
                |||  | |  || |  |||||    | | |||     ||   | || |||
||
Db      1461 -GGTTCAAGCGATTCTC--TTGCCTCAGCCTCTTGAGTAGCTGGGACTACA---
GGCGCG 1408


Qy      1509 ATTTCAGCAGGAGTTCAGAGGGCTTATGATGG-----
ATGGTGAGAGATTTGACAACCAC 1563
                 || || |  |    |||| || |    | || |||||||   |
|
Db      1407 C-ACCACCATGCCT------GGCTAATTTTTGTGTTTTTAGT-
AGAGATGGGGTTTCACC 1356


Qy      1564 CAG--AGCACATGTG---
CTCTGACCCTCTCCTGGGCATTGGTTCCTGCTGGTACCGGGC 1618
                | |   || ||  | |   || |  | ||| ||   ||| |||   |
||||
Db      1355 CTGTTGGC-CAAGAGGACCCCCAGCCTTC-CCAAGCCATAGGGGGCTGGTGG-
GCAGGGC 1299


Qy      1619 GGTTCAGACCTTCAAATAG------
GTTGCTTTCAAAAGAGCTTTCAGGCACTTATTGAG 1672
                || | | || |    |       || || ||| || ||   | || ||
|
Db      1298 GGCACTTAGCTGCCTGGGGCACCCAGTACCTGTCATGAG-GC--
ACTTGCCCTGGCCAAA 1242


Qy      1673 AATTAATGTTTA--AACAGACA----TAATAGCCTAGATGAAC----
TCCCAAGAGATCT 1722
                 | | ||  |   |||| ||      | || ||| |||| |    | | ||||
Db      1241
GGTCACTGCCAAGGCACAGCCACTCCAGAGAGTCAAGAGGAGCAGAGACTCCAGAGCAGA 1182


Qy      1723 ATTAAATCTTGTGGGCT----GAATAAATATCTCG--------
TGCAGGACTGTGCAACA 1770
                 ||  |||||||  |      | | |           | |||  |||||
||
Db      1181
TGGAAGGAGAGTGGGCTTCTGGGGATTGCACCAAGGAGGAAGCAGAAGGGATGTGCAGCA 1122


Qy      1771 GTA------------GCCCAGAGCATCCT----GCCTGTGG----GCATCCA-----
CCT 1805
                | |            | || | | ||    || || ||   |   |||
||
Db      1121
GCAGAAAAGGAGGAGGACCGGGGGGTTCTGAGGGCTTGGGGTGATGAGGCCAGAGTTCCA 1062


Qy      1806 CCCAGG--------------TGAGGGCAGTGGGAAGCTG---
GCCCGACGGCAGCCAGAA 1848
                ||||              ||||| |||  | || |    ||| |  |   ||
|||
Db      1061
AACAGGGTCTGGGTGCAGGATGAGGACAGAAGAAAACAGAGAACCCAAAAGGGGCAAGAG 1002
```

```
Qy      1849 CTT-GTTTCTCAC---CTCCCACC------------
AGCAACCCCCCACC---------- 1882
             || ||  || ||  | | ||              |  || || |||
Db      1001
GTTGGTCCCTTACTTTCACTCTCCTGGGAGGAGGATGGGTACACCACACAGTTGGATGGT 942


Qy      1883 -CAACTCTGGGCCCCAG---GCACACGAAGCACAAGTCTCAGGGGACCAT--
TCCCACAT 1936
             || || ||   || |   |||| | ||| |    || || ||||| |||
Db       941 GCATCTTTG----CCTGTCTGCACCTGCAGCTC------
CATGGCACCATGGACCCT--- 895


Qy      1937 TGGGGGATCC---TGAGGGAGCCC-ATCACCGCCTCTTGCATACAACTGT-----
CCACT 1987
                  | | ||||   || || ||| ||| || || |   || || || ||      ||
Db       894 ---GTGCTCCGAGTGGTGGTGCCTGATCTCCACCAC---
CAGGCAGCAGTAGAGGCCGCT 841


Qy      1988 AGGAGGCA-----------CGCCCAGTGTGGGAG-AGATGT----ATGGTC--
TTGCC-- 2027
             |   |||         ||| | ||| |||| || ||     ||||| |||
Db       840
ATCCAGCAGGGTCAGGTTGCGCATGGTGATGGAGAAGTTGCCATGGTGGTCGGAGGCCGA 781


Qy      2028 TTCCA-
CCTGTAAAAACTGCACATATGCAAGCCATTTGCACTCTGGAACTGCATGCCGTG 2086
             |||| || ||      || | || | | | |     |||| || |||
|
Db       780 CTCCAGCCCGTG------GCGCTGAGCCAGGTCGTG-----
GCTGGTGTTGGCAGCCTGG 732


Qy      2087 AAAACTCC----TAATGGTGTGGAACTTAGTT--
TGAATTTGAAATCACGCCGCATGCAC 2140
             ||||     |   ||||  | | | |    ||| |||       ||||   ||
|
Db       731 TGGCCTCCATGGTGCAGGTGAAGGTCCTGGAACGTGAGGTTGCGGATGGGCCG-
GCGCTC 673


Qy      2141 AAAG--GGACAGGCCCAGGCCC------------GACCTC----------AGGT--
CATC 2174
             ||  || ||  |  || ||||            ||| |          ||||
||||
Db       672
TGAGCAGGTCTGCACCTCGCCCCTCGAGCTGCGGTACCACGTCTTGTAGAAGGTCACATC 613


Qy      2175 -CGCCCGCTGGCTGCAGAGCATCCCTGGGAGCC--AAGGCGAG-----------
GCCCGT 2220
             ||||  || | ||| |    ||  ||||| |||  ||| |||               ||||
|
Db       612 GTGCCCTTTGTCCACAGGG----
CCCAAGAGCCTGCAGGTGAGGGTGACGTTCTGCCCCT 557


Qy      2221 GGAGCCTGAGCTTTGTGTAGCTCGAGCTTTGTGTAGCTCGTGCA--
CTTATTATGCACCA 2278
             | | | || | || | |    ||  ||| | | ||| |    ||           |
                                                                       |||
Db       556 CGGGACAGACATACAGGGAATACG-GC---
GTGGCGACCTTGAAGGCTGCCACCGGACCT 501
```

```
Qy       2279 CCTC-------------CCTTCAGTCACC--AC---TCCTCTTC--CTCC-
GCCATCCTC 2317
             |||              || |  ||||||  ||   ||||  | |  |||| | || ||
|
Db        500 GCTCAGAGAGAGGAGAGCC--
CTGTCACCTGACTGATCCAGTGCTACTCCTGGCAACCCC 443

Qy       2318 A--------------
TTTATACTGATTGCACACCCCCCGCTCAAACAACAATGTCCTTAT 2363
              |                 ||| ||  |||     ||| || ||| |   || | | |
Db        442 AGAGCGGGGAAGAACCTTAGCCT--CTGCTACTTCCCAGC-
CACAGGCCAGGGGCAT--G 388

Qy       2364
TATGATGACCATCTCGTAGTGGTACATTCCATTCCTATTTAAGGTAAGCCCAAAGCCCAC 2423
                 |  | ||||| || |  ||    || || ||   |   |  |   | ||||
||||||
Db        387 TCAGCTGACC-TCCCTAAG----AC-TGCCTT--CTGCATTTGTT---
CACAAACCCCAC 339

Qy       2424 TTTTGGATTTTCTCGACTGTC-CGAGAAAAGTTGTGTAAGCG---CCTGC-----
GTTCT 2474
                   |          | || | |||| |    |  |||     |||| |  || |      ||
Db        338 T-----
CCATCCTAGGCTGTTGTAGGGGGAGTCACAGAAGCTTCCCCAACTAGGGGTGCT 284

Qy       2475
TCTGGGTTTGGCTAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAGG 2534
                 |||| |  ||| ||||| |    ||  |    |||||  || ||||||| | |
|
Db        283 CCTGGAT---GCTGGACAGGGCAGGGAGAGACT-TGGA--
GGGCAGTGATGCAGTCGGGT 230

Qy       2535 GTGTCATTTTCTC-GCACAATACAACTCACTGAGGATGCTT---
CTGTAGAAGTGAGAAA 2590
                 |||||       |||   | || || |         |    ||||    |||| |   ||| ||
Db        229 GTGTCC----CTCTTCCCAGTAGA-------GTATATGCAAAACCTGTTG-
GGTGGGAGG 182

Qy       2591
CACGATGAGTACATTCAGAATTACAATAACTCACTCTCACTGGGTAACTTCTCATGATAG 2650
                 || | || |   ||| |  | |   | ||         | | ||| |  |
Db        181 CAGGTTGGGGA---GCAGGAAGGCTGTTTCGAAC-----------AGCAGCTCCT--
TGT 138

Qy       2651
ATTTGTATGATCAATACGGGTCTATTTTTATGTCAACTGAACACTGTAGGGTACCTTCCA 2710
                 ||| | || ||  ||  | |     ||||| | | ||      |
||||||
Db        137 CCTTGGCCGCTCTGTAGGGGCC---------ATCAAC--ACCTCT-----
GCCCCTTCC- 95

Qy       2711
GTCTTTTTCAAGATTGTTAAATTGAGACAAGTAATTGAATAATTTGTCCTATTTTTATTT 2770
                 | |                                                 |||||
Db         94 ------TAC-------------------------------------
TCCTA--------- 87
```

```
Qy       2771
TAAAAAAAGTGAATGGACTGAAATGTTAAATGTGAATGTACATTTCTTAATTGCAATTTT 2830
                         ||||||||              |||  | |  | |  |||| |
Db         86 --------------GGACTGAA------------CATG-
CCTTCCCATCCTTGCCAGGGA 54


Qy       2831 TCTACTGAGTGTTTGCACTATACTTTCTGGAATCTTATTTAA---
CAAAAATAAAGGGAA 2887
              | ||| || |  ||||         |||   | | | ||  |      |  ||
Db         53 GC-ACTAAGAG--AGCAC--------CTG----
CGTGTGCAAGGCCTGGGCCAGTAGGCC 9


Qy       2888 AAAATTGC 2895
              || | |||
Db          8 AACAGTGC 1



RESULT 3
US-10-478-914-21
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match              36.5%;  Score 6279.5;  DB 1;  Length 3589;
  Best Local Similarity    42.9%;  Pred. No. 0;
  Matches 1607;  Conservative    0;  Mismatches 1125;  Indels 1015;
Gaps  215;

Qy          2 TGAAATCAGGAAATCAGGCCGGGCGC----
AGTGGCTCATGCCTGTAAGCCCAGCACTTT 57
               || | || |  ||||    | |   || ||||| | |||  |||| |
|||
Db          7 TGGATTC--GCCATCATTTTGCACACTGCGAGGGGCTCC-GTGTGTGCGCCCTG-
TCTT- 61

Qy         58
GGGAGGCGGAGGCGGGTGGATCCATTGAGGTCAGGAGCTCAAGACCAGCCTGGTCAACAT 117
                        | | ||    ||     |||    |||| || ||   | |
|
Db         62 ----------GTCTGG-----CC------GTC-----CTCAT-
CCCTTCCCCCACCCCCT 94
```

```
Qy        118 GGTGAAACCCCGTCT--CTACTAAAAATACAAAAAAAAAATTAG--CTGGGC-
GTGTTGG 172
              |  |  || ||| |   || | |||   |   | || | |  |  || ||| ||||
||
Db         95 GCCGCCACTCCGACCCGCTCCCAAAGTGGCTTCACAATAGTCGGTCCTCGGCGGTGTAGG 154

Qy        173 CGG-GAGCCTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAGA------
ATTGCTTGA 225
              | | |  || | |||| | || | | | | |     |||||       | |||
Db        155 CTGCGCACCAG--GTCCACACTTAAGCGAAATCAA-----
GGAGACCCCCTTCTACTTCT 207

Qy        226
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTCCAGCCTGGGCGA 285
              ||| | |   | | || || |  |    ||| |    |||| |||| |
||
Db        208 ACCTTTGGGTTTGGTGCT-CAATGCGAAGC---TGC-----TGCAACTCAGAC---
ACGC 255

Qy        286 CAGAGCAAGACTCTCTCAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATC---
GAC 342
              |  || | |||| || ||||| | |||||      | | ||  |  || |
|
Db        256 CTAAGTCA-ACTCATGCAGAAAAGGAGAAAAGTT--
TTGGTATACAAATGCTCTCAGTC 312

Qy        343 CACAGTGGTAGCCACCTGGCCTAA------TGCTG------------
TGTTTTTGTACCT 384
              ||   |  || |||| ||| ||       |||||           | |   |
|||
Db        313 CA----
GCCAGACACCAAGCCGAAAGGTTGTGCTGGCTGCAACCGAAAGATCAAGGACCG 368

Qy        385 G-----ACAGGGGTCACT----
CATTTTAGGCACAACTCCTTCATTCTTTGTGAAATTAG 435
              |      |    | |||| | |  |||| |  || | | |   ||||
|
Db        369 GTATCTTCTAAAGGCACTGGACAAATACTGGCATGAAGACTGCCTGAAGTGTGCCTGCTG 428

Qy        436 TGAGTTTC----------------CTTCTACCCGT-
CACCAGATTCAATATGTTCTATTA 478
              ||| | ||                 || |  || || ||| |  |   ||| |  ||
||
Db        429 TGACTGTCGCTTGGGGGAGGTGGGCTCCACCCTGTACACTAAAGCTAATCTTATCCTTTG 488

Qy        479 ATACACCGA-TAAC-----CAC----------AGGGGAAGGGCACT---TGT----
CGCT 515
               ||  || || |     | |          ||| || || ||   |||
|||
Db        489 TCGCAGAGACTATCTGAGGCTCTTTGGTGTAACGGGAAACTGCGCTGCCTGTAGTAAGCT 548

Qy        516 C-TCCC-ACC-------TGGT------TACCACAGTC-------TCCA-TGGGTCT--
TT 550
              | |||| ||       ||||      | ||| | |       ||| || ||
||
Db        549
```

```
CATCCCTGCCTTTGAGATGGTGATGCGTGCCAAGGACAATGTTTACCACCTGGACTGCTT 608

Qy        551 TGCC----------GTGACCACAAA-----TAAAGGAAACA--------CT----
CATCA 583         |||           || | || |    |   ||| |||        ||      ||
|
Db        609
TGCATGTCAGCTTTGTAATCAGAGATTTTGTGTTGGAGACAAATTTTTCCTAAAGAATAA 668

Qy        584 CTAGTATCT----AAGTCGGGC-----------TTTACAGTAA-----
CTATGCACCTTC 623            |  |  ||    || ||| |        |||| | ||    |||||||||
|
Db        669
CATGATCCTTTGCCAGACGGACTACGAGGAAGGTTTAATGAAAGAAGGTTATGCACC--C 726

Qy        624 TGTGTGCTTCACCTCACTCTCTACTTCAAACAGCCCATGGAG-----
GGAG--------- 669                 |  |||| |   || || || |||    ||||| ||      |||
Db        727 CAGG---TTCGCTGATCTATCAACATCAC----
CCCATTAAGAATACAGAGCACTACATT 779

Qy        670 ---GTAT-TATTATACTCCTTATG----------TTGACAGTGAAGAAT-CTGA--
GGCC 712              ||| | || ||| |||      ||||| | || ||
||
Db        780
CTTTTATCTTTTTGCTCCACATGTACATAAGAATTGACACAGGAACCTACTGAATAGCG 839

Qy        713 CAGAG----------AGGTTGGGGACTTG--AGTAAAGTCACACAGCC-CTG-----
AGA 754               |||         ||| ||| |  || |  |||| | || || |||
Db        840
TAGATATAGGAAGGCAGGATGGTTATATGGAATAAAAGGCGGACTGCATCTGTATGTAGT 899

Qy        755 GG--------CAGGACCAGGGTTCCATTCCTGCTCT-----------
ATCCAGTTCCAA-- 794              |        |  |   | ||| |    |     |   | || | |
Db        900
GAAATTGCCCCAGTTCAGAGTTGAATGTTTATTATTAAAGAAAAAAGTAATGTACATATG 959

Qy        795 GC-----CCTTGTGTTTTCCATTATGTTTAGTGCCTCTTTGC----------
TAACAGCA 839              ||      || |   ||| || |      |  |       ||
Db        960
GCTGGATTTTTTGCTTGCTATTCGTTTTTGTGTCACTTGGCATGAGATGTTTATTTTGG 1019

Qy        840
ACATCTGCAAGATTTGTGTTGGTTTTGATGGAGAACTCTAGCTCATCCACATGCTAGTG- 898              || | |   ||| |||    |   || || |      |    |    | |
Db   1020
ACTATTGTATATAATGTATTGTAATATTTGAAGCACAAATGTAATACAGTTTTATTGTGT 1079

Qy        899 -CCCAAGTGGTGGAGGGGCCA----CCTCAGCAGGTGGGTTC--
TGAATGCAGCCAAGGC 951              ||| ||     |  ||| | ||    |   | || | | || ||
|
Db   1080 TACCATTTG-----
```

```
TGTTCCATTTGCTTCTTTGTATTGTTGCATTTAGTACAATCAGTGT 1134

Qy        952 TGTCCCCGCAATGGGTG---AGACTCGCTCCAACTGCCCGCCCT-----
CAGAGCAGGTG 1003
              | |    |   | || |      |  || ||  |  | || ||  |       |||| |
Db       1135 T-
TAAACTTACTGTATATTTATGCTTTCTGTATTTACCAGCTATTTTAAATGAGCTGTAA 1193

Qy       1004 C---CTA-----------------AGTCCTCCCTG-----GCACTG---------
GCAGG 1029
              |   |||                 |   ||| |     ||| |         |||
|
Db       1194
CTTTCTAGTAAAGAATTGAAAAGCAAATCTCACTAATGATACACAGATAGATAAAGCAAG 1253

Qy       1030 CCTTACCTC----ACATTGCT--AAATTAAAG-------CAATGCAAT---------
TCC 1067
                 || |   |     | | || ||| ||||||     ||  ||| |
|||
Db       1254
TCTATCAACATTAAAAATACTAAAAAATAAAGACACACACAGAGCATTTTAGTGACATCC 1313

Qy       1068 TCT--------------TGGGTAAGAGGAATTCCTCCTTCTT-
TACTAACTGATCCCCAG 1112
                 ||                || || ||||    ||   ||||| | |||| |||||
Db       1314 ACTACTTATTGCCGCTATGAGTTAGAGTCTATCAGTGTTCTTGTTATAAC----
CCCCTA 1369

Qy       1113 ----CAAGGAAATAAAATGTTAGGCTTT--AAAAATCCCTAC----
TTTGTCATATCAGA 1162
                  || || |||||  | ||||| ||||||| | ||     || || ||
|
Db       1370 TTTTCAGGGGGTTAAAA--
ATCAGCTTTAAAAAAATACATAAAAATTTCATCTTAAAGCA 1427

Qy       1163 CTATATTCTAAAACTATATTTGAGCGAAACCTGTCATTGCGTCTAATTTCAAATATACAG 1222
              || |  | | | || |   ||| |||    ||  | |        || |  |
||||
Db       1428 CTTTCATTTTATACCA-
ACGTGAAAAGTGCCATTTTTAGAATAACTTTAAAGCTTAACAG 1486

Qy       1223 ----------AATCTCC-----TTAAGAGCTGTTGCCTTA----------
TTTTTTTG-- 1255
                        ||| |||      ||  | ||| ||  ||||          || |||||
Db       1487
GTTTCCTTTTAATATCCTTTTTTTGTGTGCTCTTTACTTACACAATGGCTTTGTTTTGCT 1546

Qy       1256 --TAAAGCCTCTCTGACATCAAATGGGGAGAAAT-------
GGTGGCAC----------C 1296
               |  ||||| |   | |  | | | |  | |      ||| |||
Db       1547 TTTTCAGCCAC----
ACCCCTTATGTGAACTAGTGCCTTTGGGTATCACGTAAAATTTTT 1602

Qy       1297 TCCA----GACACCCTGAAAC-----
TACACACCAT----------------------- 1323
              ||||    |  ||  |    |||  ||| ||| ||
Db       1603 TCCAAAGGGTTACTTTAAAAATCTGTTAC-
CACAATTATGAGATGATTTTTAAGTGATAA 1661
```

```
Qy        1324 -------TTCTTC----------CCTGCTCAGCT-
TCTGCTCAGGAGTTCTGTGAG---- 1361
               ||||||          |||| ||| | ||| | || ||| ||| | |
Db        1662 ATTAAACTTCTTCTTGTATAAATTCTGCCCAGATCTCTCCACAAGAG--
CTGAGGGTTTC 1719


Qy        1362 ------CTATGG----------GAAGGCCATTGGTTGTATTTGC---
TACTTTTACTTTC 1402
               |||||          | | || ||    ||||||    |   | |||| 
Db        1720 ATAACTTTATGGCTTAATAAATGTATGACACTGAAAAGATTTGAGTGTGAATCTACTGAA 1779


Qy        1403 ATCTTCCTCTGCTGTAGAGCCATTTAATGTTATTGTCATATGCTGCTGGTGAGGTAAAGG 1462
               |||         || || ||   || | ||| | ||        | ||||||| |
Db        1780 ATC-------
ACTATAATGCACATTGAAGCTATGATGGTATTTGAGTAGTGAGGTTACTT 1832


Qy        1463 TGGGTCCGGGTGCCTT----CCCAGGGGTT--------
AGAGGATGTTCAAAGGGCCGAT 1510
               | | || | |  | |    | || |  |       ||| ||     ||||||
|||
Db        1833 TTGATCGGAGCAACATAATGCTCATAGAATCTTCTAGAAGAAGAGAAACAAAGG---
GAT 1889


Qy        1511 TTCAGCAGGAGTTCAGAGGGCTTATGAT----GGATGGTGAGAGATT---
TGACA----- 1558
               |   |   | | | ||| || ||||       |   | |   ||   |||||
Db        1890 T---
GATAAAATGCTGAGAACTAGTGATTATATATTTTTCTGTATTTACCTGACATTTAT 1946


Qy        1559 --------ACCACCAG--AGCAC----------
ATGTGCTCTGACCCTCTCCTGGGCATT 1598
                      | |  || | |||          ||||| | | || ||||| | |
                                                                          |
Db        1947 TTTAATGTTCAAAAAGTAAACACTTTAAGTTTGATGTGTTTT-
ACTCTCTCATTGTTTTA 2005


Qy        1599 GGTTCCTGCTGGTACCGGGCGGTTCAGA--CCTTCA--
AATAGGTTGCTTTCAAAAGAG- 1653
               || | |||        |  ||||| | ||| ||||| ||     |||
                                                                          |
Db        2006 AGTAATTGC----------CAACTCAGAATACATCATTCTTAGGCTG-----
AAATTTGT 2050


Qy        1654 CTTTCAGGCACTTATTGAGAATTAAT-GTTTAAACAGACATAATAGCCT----
AGATGAA 1708
               |||||   || || || ||    ||| ||   | | || | ||||| |    |||
                                                                          |||
Db        2051 CTTTC---
CATTTTTAAGGTGAAATAGTACTACCTTACGTGATAGCATACAAAGAAGAA 2107


Qy        1709 CTCCCAAGAGATCTATTAAATCTTGTGGGCTGA----
ATAAATATCTCGTGCAGGACTGT 1764
               | | ||| |    |||| || | |||     ||||| |   | |
                                                                          ||
Db        2108 AGCTCTAGAAA---
GAGAAATTATGGAGAATGATTATTTAAATTACAATTAAGGAAATGA 2164


Qy        1765 GCAACAGTAGCCCAGAGCATCC----TGCCTGTGGGCAT-
```

```
CCACCTCCCAGGTGAGGGCA 1819
        | |   ||   ||    | |||    ||||      | | | |  |    ||
|
Db      2165 GAATATGATCCCCT---
CTTCCGAGTTGCCCACAAACTTGCTTCTTTGCTTTTGCTCCCT 2221


Qy      1820 GTGGGAAGCTGGCCCGAC--GGCAGCCAGAACTTGTTTCTCAC--CTCC---
CACCAGCA 1872
             ||       | |  | ||     ||  || | ||  |||  |||  | ||    ||||
Db      2222 GT-----AATAGAACTACTTTTCA-
ACAAATCTAATTTTGCACGGCACCGTTAACCATAT 2275


Qy      1873 ACCCCCCAC--CCAACTCTGGGCCCCAGGCACAC------------------
GAAGCAC 1911
                   | | ||| | |||| | || |  ||   | |                        |
|||
Db      2276
TTTCACTACAGCAAACTTAGTGCTATGGGTTTTCTTTTTCTTTGTTTTTTTCTTGATCAC 2335


Qy      1912 AAGTCTCAGGGGAC--CATTCCCACATTGGGGGATCCTGAGGGA----
GCCCATCACCGC 1965
               || | |||  || |||| | |||  | ||  | |  | |  | || |
Db      2336 TTGTAT-AGGAAACAACATTTTC-CAGTGTTATTTGCATATATATTTTGTCCTT--
CCAA 2391


Qy      1966 CTCTTGCA--------------------TACAACTGTCCACTAG----
GAGGC------ 1994
                 ||||              || | |||    || |    | |||
Db      2392
TATATGCATTACAGATGAAAATTAAATGTTATACCTGAATTCTTGGGTTGGGGCCAAAAT 2451


Qy      1995 ---ACGC-----------CCAGTGTGGG-------------AGAGAT---
GTATGGTCTT 2024
              | ||           |  ||||||         | ||| |   |||| |
|
Db      2452
ATTAAGCTGAAAATAATGCTGGTGTGGATTTGTTTTAAAACAAAGCTTTATTATGAACAT 2511


Qy      2025 GCCT-TCCACCTGTA-AAAACTGCACATATGCAAGCCATTTGCACTCTGGAAC-
TGCATG 2081
              || | |  | ||| | |   |  | ||  |||  | | | | | || ||  ||
|||
Db      2512
GCATGTGAATCTGGATATTGCCTCTTATTTTTAAGAAAATGGTTCTGTGAAAAGTGAATG 2571


Qy      2082 CCGTG--------AAAACTCCTAATGGTGTGGA-ACTT--AGTT---TG-------
AATT 2120
                ||        ||| | | ||||| ||| ||| |||| ||
|||
Db      2572
ATATGTATTTTTCCAAATGCTTCATGGTTAGGAGTCTTCAAGTTCCATGTTCCCCAGATT 2631


Qy      2121 TGAAATC-AC-GCCGCATGCA---CAAAGGGA-C------
AGGCCCAGGCCCCGA------ 2162
              ||| || ||   | ||  | |||| | | ||||| |   |
Db      2632 TGAGATATACTAAAGAAAGAAATTCAAAAGTAGCTATTTGGGGCCCA--
CAAAAATAACT 2689


Qy      2163 ----------CCTCAG-GTCATCCGCCCGCTGGCTGCAGA----------GCAT--
CCCT 2199
```

```
                    ||| || | | | | | |  | |   || |||          |||| ||
Db      2690
ATTATTTTAGCCTTAGAGCCTTACACTTGTTTCATGAAGAGAAAGGACTTGCATAACCAA 2749

Qy      2200
GGGAGCCAAGGCGAGGCCCGTGGAGCCTGAGCTTTGTGTAGCTCGAGCTTTGTGTAGCTC 2259
                    |  ||| || || |     |   |    | | ||||| |  | ||| |  ||| |
Db      2750 AATAAACAAAGCAAGACAAATTAA-----AAATATGTGGGG-GAGAGATCAGTGAA--
AA 2801

Qy      2260 GTGCACTTATT-ATGCACCAC-------CTCCCTT--CAGTCAC--------
CAC----- 2296
                    |||   || || ||||| |      | || || | |        |||
Db      2802
GTGGTTTTCTTAATGCAGCCCTGCTGGTCCCCATTAACAATTGCTTGAAATTCACATGGA 2861

Qy      2297 ----------------TC---CTCTTCCTCCGCCATCCTCATTTA------
TACTGATTG 2331
                            ||  |||| || |  ||  || |||||         ||||
||
Db      2862 TGTAAAATTATAATTGTCAGGATCTTATTCAG--
ATGATCTTTTAAGGTTTAACTGGTTT 2919

Qy      2332 CACACCCCCCGCTC-AAACAACAATGTCCTTATTA--TGATGAC-------------
CAT 2375
                      |         || | |   ||| | ||| | | |  ||   ||            |
Db      2920
TGCTTTTGTTTATCTATATGTCAAAATACTTGTAAATTGGGAACAAACTTCTCTCAGCTT 2979

Qy      2376 CTCGTAGTGGT---ACATTCCATTCCTATTTAAGGTAAGCC---CAAAG-----
CCCACT 2424
                      || | ||| ||  || | || || |  || || | ||| |          |
||
Db      2980 CTTGAAGTTGTTCAACTATCCTTGCCACT----
GGAAGACCAAACAAGGTTTTCACTGCT 3035

Qy      2425 TTTGGATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGC----
GCCTGCGT--------- 2471
                      |||  ||| |  | |    | |||||  ||  || ||     || |
Db      3036
TTTTCTTTTACATAATATGCTGAGAATTATTTCTTATGCTTTTTACTACAAACAAAATTA 3095

Qy      2472 -TCTTCTGGGTTT---------GGCTAGATAGGGTTG---TGTC-----
CCTCTATGGAA 2513
                      ||  |||| ||          | |||  || | ||    | ||      ||| |||
||
Db      3096
CTCACCTGGATTAAAGATTAAGGCCTTAATCTGTTTAGATTATCTTTAATCTCCATGAAA 3155

Qy      2514 TGGAGAGTGATG--TGGGCAAGGGTGTCATTTTCTCG-
CACAATACAACTCACTGAGGAT 2570
                      | | ||  | |     |  || || ||| |    | ||  |||| || | ||
||
Db      3156
TCGTGAAATAAGACAAGAATAGTGTTTCAGCTGTAGGCCATTTTACAGCTAATTGCCCAT 3215

Qy      2571
GCTTCTGTAGAAGTGAGAAACACGATGAGTACATTCAGAATTACAATAACTCACTCT--- 2627
                      | |||||| | |   || ||  |||||       |||     | ||| ||||
```

```
Db        3216 AAAT-TGTAGCATTTATTGACCTGA--AGTACTAAGCTAATTGTCTTGACT-
ACTCAAAG 3271

Qy        2628 -CACTGGGT-------AAC-
TTCTCATGATAGATTTGTATGATCAATACGGGTCTATT-- 2676
               |  |||   |       ||| ||| |  |  | |  |||| |   |   ||  |||  ||
Db        3272 CCCCTGAATTGTTGTCAACTTTCCCCT--TTGTGTTGTGTAGCCCTAAC--
GTCATTTAG 3327

Qy        2677 -TTTATGTCAACTGAACACTGTAGGGTACCTTCCAGT----CTT---TTTC------
AAG 2722
                  ||  ||||   ||   |||||  ||| ||| |    ||| ||||
|
Db        3328 CTTGTTGTCTGATGCCTCCAGTAGGACACC-
TCCGATGGAGCTTTGATTTCTGAGCAGCG 3386

Qy        2723 ATTGTTAAATT-----
GAGACAAGTAATTGAATAATTTGTCCTATTTTA---------- 2767
               |  |  ||   ||      ||  ||     | | |||   || ||||| | |
Db        3387 AAAGCTCCCTTCCTAAGATGCA---TCTCGCATAGGCTG-
CCTATGATGAAGGACCGTGC 3442

Qy        2768 ------TTTTAAAAAAAGTGAATGGACTGAAATGTT-
AAATGTGAATGTACATTTCTTAA 2820
                  |  || ||||  ||   | ||| ||| |  ||||  |||| |||||
|
Db        3443 ACCTCCACTCCAACAGAGTG-CTGAGTTTAAAAGTTGACCTGTGTTTGTA-ATTTC--
AC 3498

Qy        2821 TTGCAATTTTTCTACTGAGTGTTTGCACTATACTTTC-----
TGGAATCTTATTTAACAA 2875
                  || || ||   || | | | |||  || |||||        ||   |   ||
||
Db        3499
TTTCATCTTGCTTAATAAATATCTGCTGGATTCTTTCAAAAAAAAAAAAAAAAAAAAAAAAA 3558

Qy        2876 AAATAAAGGGAAAAAATTGCTTGA-CT 2901
               ||| ||| || | | |||| ||| |
Db        3559 AAAAAAAAGGCCACATGTGCTCGAGCT 3585


RESULT 4
US-10-478-914-21/c
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
```

```
;    LENGTH: 3589
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match              35.9%;   Score 6178.5;  DB 1;  Length 3589;
  Best Local Similarity    43.3%;   Pred. No. 0;
  Matches 1590;  Conservative    0;  Mismatches 1170;  Indels  909;
Gaps  209;

Qy        1 TTGA---AATCAGGAA-------ATCAGGCCGGGCG-CAGTG---------
GCTCATG-- 38
            ||||   |||| | |       || | || |  |  ||||        | || |
Db     3537
TTGAAAGAATCCAGCAGATATTTATTAAGCAAGATGAAAGTGAAATTACAAACACAGGTC 3478

Qy       39 --CCTGTAAGCCCAGCACTTTG-------GGAGG----CGG-----------
AGGCGG-- 72
              | | ||| | ||||||| ||      |||||    |||        |||| |
Db     3477
AACTTTTAAACTCAGCACTCTGTTGGAGTGGAGGTGCACGGTCCTTCATCATAGGCAGCC 3418

Qy       73 ---GTG-GATCCAT-
TGAGGTCAGGAGCTCAAGACCAGCCTGGTCAACATGGTGAAACCC 127
               | | ||| ||| | ||| ||||||  | | ||   | | ||      || |
|
Db     3417 TATGCGAGATGCATCTTAGGAAGGGAGCTTTCG--CTGCTCAGAAATCA-----
AAGCTC 3365

Qy      128 CGTC--------TCTACTAAAAATA-
CAAAAAAAAAATTAGCTGGGCGTGTTGGC----- 173
               | ||        |||||| |   | | || | || || || | ||   |||
Db     3364 CATCGGAGGTGTCCTACTGGAGGCATCAGACAACAAGCTAAAT-
GACGTTAGGGCTACAC 3306

Qy      174 -------GGGAGCCTGTAGTCCCAGCTACACGGGAGGCTAAG-GTGG----
GAGAATT-G 220
               || |    || |   || | | | || |||| | || |    || ||||
|
Db     3305 AACACAAAGGGGAAAGTTG--ACAACAATTCAGG-
GGCTTTGAGTAGTCAAGACAATTAG 3249

Qy      221 CTT-GAAC--CCGG------GAGGCGGAGGTT-----
GCAGTGAGCTGAGATTGCACCAT 266
               ||| | || | ||      | | || |   ||| | ||||| |
|
Db     3248 CTTAGTACTTCAGGTCAATAAATGCTACAATTTATGGGCAATTAGCTGTAA-------
AA 3196

Qy      267 TGCACTCCAGCCTGGGCGACAGAGCAAGAC---TCTCTC-
AAAAAAAAAAAAAAAGAAAG 322
               || |||| ||| |||    ||    | | |  | |||| |    |  || | |
|
Db     3195 TGGCCTACAG-
CTGAAACACTATTCTTGTCTTATTTCACGATTTCATGGAGATTAAAGAT 3137

Qy      323 AAAGAAATCAGAAAATCGACCACAGTGGTAGCCACCTG--
GCCTAATGCTGTGTTTTTGT 380
               ||   || |||| |  | | || | |   || |  | |||| ||| || |
||
```

```
Db      3136 AATCTAAACAGATTA-AGGCCTTAAT-CTTTAATCCAGGTGAGTAATTTTGT-
TTGTAGT 3080

Qy       381
ACCTGACAGGGGTCACTCATTTTAGGCACAACTCCTTCATTCTTTGTGAAATTAGTGAGT 440
          |  || |   ||| |  | ||| |   || |    |   | ||| |||| |||||
Db      3079 AAAAAGCATAAG-AAATAATT-----
CTCAGCATATTATGTAAAAGAAAAAGCAGTGAAA 3026

Qy       441 TTCCT------TCTACCCGTCAC-------------
CAGATTCAA--------------T 467
             | |    ||| || || |         ||  |||||
                                              |
Db      3025
ACCTTGTTTGGTCTTCCAGTGGCAAGGATAGTTGAACAACTTCAAGAAGCTGAGAGAAGT 2966

Qy       468 ATGTTC--------------
TATTAATACACCGATAACCACAGGGGAAGGGCACTTGTCG 513
             |||||         | | || ||  ||||| || |  | ||   || ||
Db      2965 TTGTTCCCAATTTACAAGTATTTTGACATATAGATAAACA-
AAAGCAAAACCAGTTAAAC 2907

Qy       514 CTCTCC----CACCTGGTTA----CC--ACAGT-----------
CTCCATGGGTCTTT-- 550
             ||      || ||| ||   || |           |||||| | |||
Db      2906
CTTAAAAGATCATCTGAATAAGATCCTGACAATTATAATTTTACATCCATGTGAATTTCA 2847

Qy       551 TGCCGT----------GACCA-CA-------
AATAAAGGAAACACTCATCACTAGTATC- 591
             || |         ||||| ||      | |||   || |||| ||||| |
|||
Db      2846
AGCAATTGTTAATGGGGACCAGCAGGGCTGCATTAAGAAAACCACTTTTCACTGATCTCT 2787

Qy       592 -----------------TAAGTCGGGC----
TTTACAGTAACTATGCACCTTCTGTGTGC 630
                              | ||| ||  |||| |  |||||| | || |
Db      2786
CCCCCACATATTTTTAATTTGTCTTGCTTTGTTTATTTTGGTTATGCAAGTCCTTTCT-C 2728

Qy       631 TTCACCTCACT---------CTCTACTTCAAACA------------------
GCCCATGG 663
             ||||  ||       ||||| ||| |                     ||||
Db      2727
TTCATGAAACAAGTGTAAGGCTCTAAGGCTAAAATAATAGTTATTTTTGTGGGCCCC--- 2671

Qy       664 AGGGAGGTATTATT-
ATACTCCTTATGTTGACAGTGAAGAATCTGAGGCCCAGAGAGGTT 722
             |  || || | |  | | ||||| |   |   |||||| || || ||
||
Db      2670
AAATAGCTACTTTTGAATTTCTTTCTTTAGTATATCTCAAATCTGGGGAACATGGAACTT 2611

Qy       723 GGGGAC-----------------TTGAGTAAAGTCA--------------
CACAGCCC-- 749
             | |||             ||| ||| ||              ||||| |
Db      2610
GAAGACTCCTAACCATGAAGCATTTGGAAAAATACATATCATTCACTTTTCACAGAACCA 2551
```

```
Qy        750 ------------TGAGAGGCAGGACCAGGGTTC-
CATTCCTGCTC-------------- 781
                     | | ||||| | |  | |||  ||| | || ||
Db       2550
TTTTCTTAAAAATAAGAGGCAATATCCAGATTCACATGCATGTTCATAATAAAGCTTTGT 2491


Qy        782 ---TATCCAGTTCCAAGCC--CTTGTGTTTTC--
CATTATGTTTAGTGCCTCTTTGC--- 831
                     |  || |||| ||| | |||| | | ||| ||| | |||  |
Db       2490 TTTAAAACAAATCCACACCAGCAT-TATTTTCAGCTTAATATTTTG-
GCCCCAACCCAAG 2433


Qy        832 ----------TAACAGCAA-----CATCTGCAAGATTTGTGTTGG----------
TTTTG 866
                       ||||| |   ||||||| ||   | | ||||          | |
Db       2432
AATTCAGGTATAACATTTAATTTTCATCTGTAATGCATATATTGGAAGGACAAAATATAT 2373


Qy        867 ATG--GAGAACTCTAGCTCA------TCCACATGCTAGTGCCCAAG---------
TGGTG 909
                     |||   | ||| || |   |          | |  || | ||||  ||||         |
Db       2372
ATGCAAATAACACTGGAAAATGTTGTTTCCTATACAAGTGATCAAGAAAAAAACAAAGAA 2313


Qy        910 GAGGGGCCACCTCAGCAGGTGGGTT-CTG-AATGCAGCCAAGG----CTGT-
CCCCGCAA 962
                       | |       || ||||   | || ||| || |   | ||     | || ||
||||
Db       2312
AAAGAAAACCCATAGCACTAAGTTTGCTGTAGTGAAAATATGGTTAACGGTGCCGTGCAA 2253


Qy        963 --------TGGGTGAGAC-TCGCTCCA--ACTGCCCGC-----
CCTCAGAGCAGGTGCCT 1006
                     | | ||| |  ||| ||  |           |      |    |||| |
|
Db       2252 AATTAGATTTGTTGAAAAGTAGTTCTATTACAGGGAGCAAAAGCAAAGAAGCAAGT--
TT 2195


Qy        1007 AAGTCCTCCCTGGCACTGGCAGGCCTTACCTCA---CATTGC---
TAAATTAAAGCA--A 1058
                     | |   || | || ||     | |  |||| | ||     ||| ||||| |
|
Db       2194
GTGGGCAACTCGGAAGAGGGGATCATATTCTCATTTCCTTAATTGTAATTTAAATAATCA 2135


Qy        1059 TGC-----
AATTCCTCTTGGGTAAGAGGAATTCCTCCTTCTTTACTAACTGATCCCCAGC 1113
                     | |    |||| |||| |||    ||||   | | ||||||   || ||| |
|
Db       2134 TTCTCCATAATTTCTCTT--TCTAGAG-----CTTTCTTCTTTGTATGCT-ATCAC--
GT 2085


Qy        1114 AAGGAAATAAAATGTTAGGCTTTAAAAATCCCTACTTTGTC--
ATATCAGACTA------ 1165
                     ||||| ||  || ||    ||| |||||||     |    | |  || |||| |||
Db       2084 AAGGTAGTACTAT-TTCACCTTAAAAAATGGAAA----
GACAAATTTCAGCCTAAGAATG 2030


Qy        1166 ---TATTC----------------
```

```
TAAAACTATATTTGAGCGAAACCTGTCA-------- 1198
                            |||||   ||    |||  ||||   |||
Db      2029
ATGTATTCTGAGTTGGCAATTACTTAAAACAATGAGAGAGTAAAACACATCAAACTTAAA 1970


Qy      1199 ----TTGCGTCT--------------AATTTCAAAT--ATACAG-
AATCTCCTTAAGAGC 1237
             ||  | |          |||  |||   |  |||||| ||   |||
                                                               |
Db      1969
GTGTTTACTTTTTGAACATTAAAATAAATGTCAGGTAAATACAGAAAAATATATAATCAC 1910


Qy      1238 T-GTTGCCTTATTTTTTTGTAAAGCC-------
TCTCTGACATCAAATGGGGAGAAATGG 1289
             |  |||  || |   |||| | || ||       |||||  | ||           |
Db      1909 TAGTT--CTCAGCATTTTATCAATCCCTTTGTTTCTCT-TCTTC-------------
TAG 1866


Qy      1290 TGGCACCTCCAGACACCCTGAAACTACACACCA---
TTTCTTCCCTGCTCAGCTTCTGCT 1346
             |   ||     ||     ||    || |   |   |  | || || |||| ||
                                                               |
Db      1865 AAGATTCTATGAGCATTATGTTGCTCCGATCAAAGTAACCTCACTACTCAAATACC-
AT 1807


Qy      1347 CAGGAGTTCTGTGAGC--TATGGGAAGGCCATTGGTTGTATTTGCT-
ACTTTTACTTTCA 1403
             ||    ||| ||| || | |  ||  || |    ||| | ||   |
|||||
Db      1806 CATAGCTTCAATGTGCATTATAGTGATTTCAGTAG----
ATTCACACTCAAATCTTTTCA 1751


Qy      1404 TCTTCCT-CTGCTGTAGAGCCATTTAATGTTATTGTCATATGCTGC---
TGGTGAGGTAA 1459
             ||| |   | |  |  |||||| | |  |     | |  ||| |   ||| ||| |
Db      1750 GTGTCATACATTTATTAAGCCATAAAGTTATGAAACCCTCAGCT-
CTTGTGGAGAGATCT 1692


Qy      1460 AGGTGGG------TCCGGGTGC----------------------CTTCCCA-----
GGG 1485
             ||  |        |  |   |                        | || ||     |
Db      1691 GGGCAGAATTTATACAAGAAGAAGTTTAATTTATCACTTAAAAATCATCTCATAATTGTG 1632


Qy      1486 GTTAGAGGATGTTCAAAGGGCC---------
GATTTCAGCAGGAGTTCAGAGGGCTTATG 1536
             ||| | || | || ||   ||         | ||   | ||   | | |||
                                                               |
Db      1631 GTAACAGATTTTTAAAGTAACCCTTTGGAAAAAATTTTACGTGATACCCAAAGGCACTAG 1572


Qy      1537 AT---GGATGGTGAGAGATTTGACAACC--ACCAGAGCACATGTGCTC-
TGACCCTCTCC 1590
             |     | || || ||| |   | ||| |  | || |||   ||||   | |     |
Db      1571 TTCACATAAGGGGTGTGGCTGAAAAAGCAAAACAAAGCCATTGTGTAAGTAAAGAGCACA 1512
```

```
Qy       1591 TGGGCATTGGTTCCTGCT--GGTACCGG----GCGGTTCAGACCTTC--
AAATAGGTTGC 1642
                 |  || |   |    | ||| |   || |  | ||   ||| |||  ||
Db       1511
CAAAAAAGGATATTAAAAGGAAACCTGTTAAGCTTTAAAGTTATTCTAAAAATGGCACT 1452

Qy       1643 TTTCA--------------AAAGAGCTTTCAG--
GCACTTATTGAGAATTAATGTTTAA 1685
                  |||||           |||| ||||| ||  | | ||| ||  | ||| | ||
||
Db       1451 TTTCACGTTGGTATAAAATGAAAGTGCTTTAAGATGAAATTTTTATGTATTTTT-
TTAAA 1393

Qy       1686 ACAGACATAATAGCCTAGATGAACTCCCAAGAGATC---
TATTAAATCTTGTGGGCTGAA 1742
                 | || |       | ||| ||| | ||      ||| | |   |
||||
Db       1392 GCTGATTT-----------
TTAACCCCCTGAAAATAGGGGGTTATAACAAGAACACTGAT 1344

Qy       1743 TAAATAT--CTCGT-
GCAGGACTGTGCAACAGTAGCCCAGAGCATCCTGCCTGTGGGCAT 1799
                 | | | ||| ||| |  |   | |   || |   | || |  ||||| |
|
Db       1343 AGACTCTAACTCATAGCGGCAATAAGTAGTGGATGTCACTAAAATGCT--
CTGTGTGTGT 1286

Qy       1800 C--CACCTCCCAG-GTGAGGGCAGTGGGAAG-CTGGC---------CCG----
ACGGCAG 1842
                 |   |   |  || |       || |  || || ||        | |     |
||
Db       1285
CTTTATTTTTTAGTATTTTTAATGTTGATAGACTTGCTTTATCTATCTGTGTATCATTAG 1226

Qy       1843 CCAGAACTTGTTTCTCACCTC-CCACCAGCAACCCCCCACCCAACT-------
CTGGGCC 1894
                 |||  |||  ||| ||     ||  || ||| |  |         |||| 
Db       1225 TGAGAT-
TTGCTTTTCAATTCTTTACTAGAAAGTTACAGCTCATTTAAAATAGCTGG--- 1170

Qy       1895 CCAGGCACACGAAGCACAAGTCT-CAG-
GGGACCATTCCCACATTGGGGGATCCTGAGGG 1952
                 |   ||| ||||| | |  ||  |    |  | |  |||      | ||  |
|
Db       1169 -TAAATACAGAAAGCATAAATATACAGTAAGTTTAAACACTGATTG-----
TACTAAATG 1116

Qy       1953 AGCC----CATCACCGCCTCTTGCATACAACTG--TCCACTAGGAGGC---
ACGCCCAGT 2003
                 |   |||     || | | | |||| ||    ||| |  |  |   |
|
Db       1115 CAACAATACAAAGAAGCAAATGGAACACAAATGGTAACACAATAAAACTGTATTACATTT 1056

Qy       2004 GTGGGAGAGATGT--
ATGGTCTTGCCTTCCACCTGTAAAAACTGCACATATGCAAGCCAT 2061
                 |||   | || |   |  |  |    | ||   ||  ||| |||  | |
||||
Db       1055 GTGCTTCAAATATTACAATACATTATATACAATAGTCCAAAATAAACATCT-
CATGCCAA 997
```

```
Qy       2062 TTGCACTCTGGAAC----TGCATGCCGTGAAAACT--
CCTAATGGTGTGGAACTTAGTT- 2114
                 || || |   |||    ||| ||   ||| |   || ||| |     ||||
||
Db        996 GTG-ACACAAAAACGAATAGCAAGCAAAAAAATCCAGCCATAT-
GTACATTACTTTTTTC 939

Qy       2115 TGAATTTGAAATCACGCCGC-ATGCACAAAGG---------GACAGGCCCAGGC---
CCG 2161
                 |  |  | |||| |   | | ||| ||   || |           ||| |  | |||
|||
Db        938
TTTAATAATAAACATTCAACTCTGAACTGGGGCAATTTCACTACATACAGATGCAGTCCG 879

Qy       2162 ACCT------CAGGT---CATCC-GCC------------
CGCTGGCTGCAGAGCATCCCT 2199
                 | |        || |   |||||| |||          |||| | |||    |
|||
Db        878 CCTTTTATTCCATATAACCATCCTGCCTTCCTATATCTACGCT--
ATTCAGTAGGTTCCT 821

Qy       2200 GGGAGCCAAGGCGAG---GCCCGTGGAGC--
CTGAGCTTTGTGTAGCTCGAGCTTTGT-- 2252
                 | | ||| |  |   | |||||||    || |    | |  | | ||| |||
Db        820 --
GTGTCAATTCTTATGTACATGTGGAGCAAAAAAGATAAAAGAATGTAGTGCTCTGTAT 763

Qy       2253 -------------------GTAGCTC-
GTGCACTTATTATGCACCACCTCCCTTCAGTCA 2292
                 ||| || | || |    |||| |||| | |||| |
|
Db        762
TCTTAATGGGGTGATGTTGATAGATCAGCGAACCTGGGGTGCATAACCTTCTTTCATTAA 703

Qy       2293 CCACTCCTCTTCCTCCGCCATCC------TCAT-TTATACTGATTGCACAC-----
CCCC 2340
                 |  ||||| |  |||| |   |   |     |||| |||| ||   | | |       |
||
Db        702 ACCTTCCTCGTAGTCCGTCTGGCAAAGGATCATGTTATTCTTTAGGAAAAATTTGTCTCC 643

Qy       2341 CGCTCAAACAACAATGTCCTTATTATGATGACCATC-------TCGTAGTGGT--
ACAT- 2390
                 | |||| | || |   |||  | | |||| |       ||  |||||
||||
Db        642 AACACAAA-ATCTCTG--
ATTACAAAGCTGACATGCAAAGCAGTCCAGGTGGTAAACATT 586

Qy       2391 -TCCAT----------TCCTATTTAAGGTAAGCCCAAAGCCCACTTTTGG------
ATTT 2433
                 ||| |          ||  | ||| |      ||| |||  ||        |
||
Db        585 GTCCTTGGCACGCATCACCATCTCAAAGGCAGGGATGAGCTTACTACAGGCAGCGCAGTT 526

Qy       2434 TCTCGACTGTCCGAGAA-----
AAGTTGTGTAAGCGCCTGCGTTCTTCTGGGTTTGGC-- 2486
                 || || | ||| | |   |    | | ||| ||| |    |  | ||  ||
Db        525 TCCCGTTACACCAAAGAGCCTCAGATAGTCTCTGCGACAAAG----
```

```
GATAAGATTAGCTT 470

Qy       2487 TAG---ATAGGGTTGTGTCCCTCTATGGAATG-GAGAGTGA-TGTGGGCA------
AGGG 2535
             |||    |  | |||||  | | ||  ||      | | || ||| |  |  ||||
|||
Db        469
TAGTGTACAGGGTGGAGCCCACCTCCCCCAAGCGACAGTCACAGCAGGCACACTTCAGGC 410

Qy       2536
TGTCATTTTCTCGCACAATACAACTCACTGAGGATGCTTCTGTGTAGAAGTGAGAAACACGA 2595
             |||    ||| ||  || ||         || |  |   |||  || ||||    ||| ||
||
Db        409 AGTC---TTCATGC-CAGTATTTGTC-CAG----TGC--CTTTAGA----AGATAC-
CGG 366

Qy       2596 T--GAGTACATTCAGAATTACA---ATAACTCACTCTC-ACTGGGTAACT-TCT--
CATG 2646
             |    |   | ||| |  || ||  |  ||   || || || ||| |||   ||  ||
||
Db        365 TCCTTGATCTTTCGG--
TTGCAGCCAGCACAACCTTTCGGCTTGGTGTCTGGCTGGACTG 308

Qy       2647 ATAG-ATTTGTATGATCAATACGGGTCT-
ATTTTTATGTCAACTGAACACTGTAGGGTAC 2704
             |  || ||||||||  | ||   |||    | ||   |   ||| |  || | ||
Db        307 AGAGCATTTGTAT-ACCAAAACTTTTCTCCTTTTTTCTG-
CATGAGTTGACTTAGGCGTGT 250

Qy       2705 C----TTCCAGTCTTTTTCAAGATTGTTAAATTGAGACA-----
AGTAATTGAATAATTT 2755
             |    || ||| |   ||| ||||   |     |  ||       || | | |||
|
Db        249 CTGAGTTGCAG-CAGCTTCGC-
ATTGAGCACCAAACCCAAAGGTAGAAGTAGAAGGGGGT 192

Qy       2756 GTCCTATTTTTATTTTAA------
AAAAAGTGAATGGACTGAAATGTTAAATGTGAATGT 2809
             ||||  ||| ||||   |   |||    | || |        | | |
Db        191 CTCCTTGATTTCGCTTAAGTGTGGACCTGGTGCGCAGCCTACACCG----
CCGAGGACCG 136

Qy       2810 ACATTTCTTAATTGCAATTTTTCTA------
CTGAGTGTTTGCA---------------- 2847
             || || | ||  || |||  || |    |    | ||||| |||
Db        135 ACTATTGTGAA--
GCCACTTTGGGAGCGGGTCGGAGTGGCGGCAGGGGGTGGGGGAAGGG 78

Qy       2848 ----------CTATACTT-TCTGGAATCTTATT---
TAACAAAAATAAAGGGAAAAA--A 2891
                             | | ||    | || |  |        |      |  | | ||||
|
Db        77
ATGAGGACGGCCAGACAAGACAGGGCGCACACACGGAGCCCCTCGCAGTGTGCAAAATGA 18

Qy       2892 TTGCTTGAC 2900
             | ||    |
Db        17 TGGCGAATC 9
```

RESULT 5
US-10-478-914-61
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match   32.7%; Score 5635; DB 1; Length 2437;
  Best Local Similarity   44.1%; Pred. No. 0;
  Matches 1360; Conservative   0; Mismatches 887; Indels 838;
Gaps 183;

Qy   2 TGAAATCAGGAAATCAGGCCGGGCGCAGTGGCTCATGC-CTGTAAGCCCA------
GCAC 54
              | | || | | || ||| | | ||| || |||| ||| | |
  ||
Db   2 TTACTTCTGCTCTAAAAGCT--
GCGGAATTCCTCGAGCACTGTTGGCCTACTGGGTGTAC 59

Qy   55 TTTGGG---AGGCGGAGGCGGGTGGATCC--ATT----GAGGTCAGGAGCTC---
AAGAC 102
              | ||| | | || | ||| || ||| || | ||| ||
  ||||
Db   60
TGTGGAGACTGTCAAAGTCTCCCGGAGCCCAATTTCCGGAAGCGGTGAGTTCTGAAAGAA 119

Qy   103
CAGCCTGGTCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAAAAAATTAGCT- 161
                |||| || | | | ||| ||| | ||| | | || | |
  ||
Db   120 GTTCCTG--CACCGTAGT---TTCCCAAGTCTGC---
GAATCCCCAACCATGAGCGCCTC 171

Qy   162 GGGCGTGTTGGCGGGAGCCTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAG-
AATTG 220
              ||||||| || ||| || |||| || | | ||||||| |
  ||
Db   172 GGGCGTACTG------TCCTTTA--CCCA------------
GCAAGGATGGGAGCAGGTG 211

Qy   221
CTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTCCAGCCTG 280
              || | | || ||| |||| | || ||| || || ||

```
                 ||||
Db        212 CTGGCCAAAGTGAAACGG------------GCTGTGGTT-TACC--TGGACGCC-
GCCT- 254

Qy        281 GGCGAC-
AGAGCAAGACTCTCTCAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATC 339
                   ||| | ||||| |   | |||                          | |
                 |||
Db        255 -GCGCCGAGAGCCTG---CACT-----------------------
GGGGCTGCGGATC 285

Qy        340 GACCACAGTGGTAGCCACCTGGCCTAATGCTGTGTTTTTGTACCTGACAGGGGTCACTCA 399
                   |||           | | ||||| | || |||            |||| | ||
                 |
Db        286 CACC--------CGTCTCCTGG----AGGCGGTG---------------
GGGGGCCCTGA 318

Qy        400 TTTTAGGCACAACTCCTTCATTCTTTGTGAAATTAGTGAGTTTCCTTCTA-
CCCGTCACC 458
                   | |        | |||| |           | |||    ||| | |||| |
Db        319 CTGT--------CACCTGC----------------GAGAG-----
TTCGAGCCCGACG-- 347

Qy        459 AGATTCAATATGTTCTATTAATACACCGATAACCACAGGGGAAGGGCACTTGTCGCTCTC 518
                   |||| || |        || | ||| || || |      || |
                 ||
Db        348 -----CAATTGGTGGTG-----GAGCCAAGCAGCCCA-
AGGCAGTGTTTGTGCTGAGCTG 396

Qy        519 CCACCTGGTTACCACAGTCTCCATGGGTCTTTTGCCGTGACCACAAATAAAGGAAACACT 578
                   || ||| | | | ||      || | || |   | | |||| |       | |
                 ||||
Db        397 CCTGCTGAAAGGC-CGG--ACCGTGGAGATCCT-
ACGGGACATCATCTGCCGCAGTCACT 452

Qy        579 CATCACTAGTATC-
TAAGTCGGGCTTTACAGTAACTATGCACCTTCTGTGTGCTTCACCT 637
                   | ||||| | | ||| || | |     || | ||||         |
                 |||||
Db        453 ----TCCAGTATTGTGTGGTGGTCACAACCGTGA----GCCAC-GCTG-----
TCCACCT 498

Qy        638 CACT-CTCTACTT---CAAACAGC--------CC---
ATGGAGGGAGGTATTATTATACT 682
                   ||| ||  | |   | | ||           ||   ||||||||
                 |
Db        499 CACAGCTAATCATGTCCCAGCGGCGGCAGCGGCCGAGATGGAGGGG---------
CAGCA 549

Qy        683 CCTTATGTT------GACAGTGAAGAATCTGAGGCCCAGAGAGGTTGGG-
GACTTGAGTA 735
                   | | |||         |     | |||| ||| |     || || |||| || ||| |
Db        550 GCCGGTGTTCGAGCAGCTGGAGGAGAAGCTGTG----
TGAATGGATGGGCAACATGAACT 605

Qy        736
AAGTCACACAGCCCTGAGAGGCAGGACCAGGGTTCCATTCCTGCTCTATCCAGTTCCAAG 795
```

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                   |||| |||     |||| |  |||  || || ||  ||||    || ||| |
Db        606 -----ACACGGCC----GAGG-TGTTCCA-
TGTCCCGTTATTGCTTGCCCCTGTTGCTCC 654


Qy        796 CCCTTGTGTTTTCCATTATG-
TTTAGTGCCTCTTTGCTAACAGCAACATCTGCAAGATTT 854
               || | || ||  |  | |||| | |||| | || || || | |
Db        655
CCACTTTGCCTTGACTCCAGCTTTTGCATCCCTTTTCCCACTGCTACCCCAG-------- 706


Qy        855
GTGTTGGTTTTGATGGAGAACTCTAGCTCATCCACATGCTAGTGCCCAAGTGGTGGAGGG 914
                    ||||         || | ||  | |  ||| ||||
|
Db        707 -----------GATG---------TGCACCTC--
CTTAATAGCGCCC------------G 732


Qy        915
GCCACCTCAGCAGGTGGGTTCTGAATGCAGCCAAGGCTGTCCCCGCAATGGGTGAGACTC 974
               ||        || | ||   ||| | |||| |          |||||||
Db        733 ACCG----GACAAGAGGAAGCTGG--GAAGCC-----------------
TGGGTGATGTGG 770


Qy        975 GCTCCAACTGC-CCGCCCTCAGAGCAGGTGCCTAAGTCC---
TCCCTGGCACTGGCAGGC 1030
               |||| ||| |  |   || |||||| | |||    ||  |    | ||| |    ||
|||||
Db        771 ACTCC-ACTACGCTAACCCCAGAGCTGCTGCTGCAGATCAGATGCCTAG---
TGTCAGGC 826


Qy       1031 CTTACCTCACATTGCTAAATTAAAGCAATGC----------AATTCCT--------
CTTG 1072
               || |  || | || ||  || | | |||| |            || ||
|||
Db        827
CTCAGTTCTCTGTGTGAACATTTAGGAGTACGGGAGGAGTGTTTTGCTGTAGGTTCCTTA 886


Qy       1073 GGTAAGAGGAATTCCTC-CTTCTTTACTAACTGAT----CCCCAGCA------
AGGAAAT 1121
               || ||      || || || |     || |  ||     |||| |        |||||
Db        887 AGTCAGG-----
TCATCGCTGCGGATCTGGCCAATTATGCCCCTGCAAAGAACAGGAAGA 941


Qy       1122 AAAATGTT--
AGGCTTTAAAAATCCCTACTTTGTCATATCAGACTATATTCTAAAACTAT 1179
               | | ||| |  ||||       |  | |  |||| |  | ||| | || |  | ||
Db        942 AGACTGCTGCAGGC------
AGGGCATCAGTGGTTTTTGTGGACAGAACCCTGGATCTC- 994


Qy       1180 ATTTGAGC-
GAAACCTGTCATTGCGTCTAATTTCAAATATACAGAATCTCCTTAAGAGCT 1238
               |  |||| |    |||| | | |   ||| | | ||    || ||||  || ||
|||
Db        995 ACAGGAGCAGTTGGACATCATGGAGACAACTT-----AGTAGAGAAGATCATTTC-
AGCA 1048


Qy       1239
GTTGCCTTATTTTTTTGTAAAGCCTCTCTGACATCAAATGGGGAGAAATGGTGGCACCTC 1298
               || ||            || ||| | | | || |  | |  |||||    ||
|
```

```
Db      1049 CTTCCC------------CAG-CTCCCAGGCCACACAAATGATGTGATGGT-
TAACATG 1093

Qy      1299
CAGACACCCTGAAACTACACACCATTTCTTCCCTGCTCAGCTTCTGCTCAGGAGTTCTGT 1358
          |  |    |||  ||| |||              | |||  |||| |      |
                                                                 |
Db      1094 ATAGCGCTC----ACTGCACTCCA-----------------
TACTGAGGAGGAAAATTAT 1132

Qy      1359
GAGCTATGGGAAGGCCATTGGTTGTATTTGCTACTTTTACTTTCATCTTCCTCTGCTGTA 1418
           |  | |||     |||  || ||| |||      || |  || | ||
                                                                 |
Db      1133 AA--TGTGGTTGCACCA--GGCTGTCTTT-CACAATTCAGTGACA----CCACAGC--
CA 1181

Qy      1419 GAGCCATTT----AATGTTATTG-TCA-TATGCTGCTGGTGAGGTAAAGGTGG--
GTCCG 1470
           |||| | |    |   ||| ||  || || ||        |||| |  | ||| ||
                                                                 |
Db      1182 AAGCCCTATGGGAAGCTTTACTGAACACTAAGC--
ACAAAGAGGCAGTGATGGAAGTTC- 1238

Qy      1471
GGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGGGCCGATTTCAGCAGGAGTTCAGAGGG 1530
           || | | ||          ||| ||| |       || ||     | | |    ||| ||
Db      1239 GGAGACATC--------TAGTGGAAG--CGGCAAGCAGAGAAAACCTGCCAATCA-
AG-- 1285

Qy      1531 CTTATGATGGATGGTGAGAGATTTGACAACCACCAG---AGCACATGT----------
GC 1577
               |||| | |||| |||      | || |||| |  ||| |||||
                                                                 ||
Db      1286 ---ATGA-GTATGGGGAGA-----GTCA--
CACCGGGACAGCTCATGTCCTATATTCAGC 1334

Qy      1578 TCT--------GACC------CTCTCCTGGG-CATTGG------
TTCCTGCTGGTACCGG 1616
               |||         |||    |||| ||  |||||        ||| ||| | ||
                                                                 ||
Db      1335
TCTTCAAGAACAACCTCAAAGCTCTAATGAATCATTGTGGCCTCCTCCAGCTTGGACTGG 1394

Qy      1617 --GCGGTTCAGACCTT------CAAATAGGTTGCTTTCAAAAGAG----
CTTTCAGGCAC 1664
               | | |||| ||  |||     ||  ||| ||  | |    |||||| |||
Db      1395 CCACAGCTCAAACGTTGAAACACCCACAGACTGC---
CAAGTGGGACAACTTTCTGGC-- 1449

Qy      1665 TTATTGAGAATTAATGTTTAAACAGACATAATAGCCTAGATGA-ACTCCCAAG--
AGATC 1721
               | |||    || | |   | | | |||| | | || | | | |    |
                                                                 |
Db      1450 -TTTTGA-----AAGGCT----
CCTTCTTCAGAGCATTGGGGAGTCAGCAATGTCCGTTG 1499

Qy      1722
TATTAAATCTTGTGGGCTGAATAAATATCTCGTGCAGGACTGTGCAACAGTAGCCCAGAG 1781
               |  |||||||    ||||              || | || || | || | |||
```

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|||||||
Db          1500 TGTTAAATC-----AGCTG---------CT-GCCCATGATTAAGC--
CTGTAACCCAGAG 1542

Qy          1782 CATCCTGCCTGTGGGCATCCACCTCCCAGGTGAGGGCAGTGGGA-
AGCTGGCCCGACGGC 1840
                 | ||  |  | || |  |  ||            |  | || |  |||| |  ||  |
Db          1543 -AACCAAC--GAGGACTACAGCC-------------
CTGAGGAACTGCTGATCCTTC--- 1583

Qy          1841 AGCCAGAACTTGTTTCTCACCTCCCACCAGCAACCCCCC-----
ACCCAACTCTGGGCCC 1895
                    || |   | | | |   || ||| | | | |      || |   ||| |
Db          1584 --TCATA---
TATATTTATTCTGTCACTGGAGAGCTCACGGTAGACAAAGACCTGTG--- 1635

Qy          1896
CAGGCACACGAAGCACAAGTCTCAGGGGACCATTCCCACATTGGGGGATCCTGAGGGAGC 1955
                    |   || |||| ||| |||  ||| | | |||| |  |       ||  | ||| | |
Db          1636 -TGAAGCA-GAAGAAAAAG--TCAAGAAAGCATTGGCTCA----
GGTCTTCTGTGAGGAA 1687

Qy          1956 CC---ATCACCGCCTCT--
TGCATACAACTGTCCACTAGGAGGCACGCCCAGTGTGGGAG 2010
                    | | ||   | ||| ||||| | |  ||| ||| | | | |
Db          1688 TCTGGATTGTCACCTTTGCTGCAAAAAATTACGGACTGGGA--
CTCTTCAA--------- 1736

Qy          2011 AGATGTATGGTCTTGCCTTCCACCTGT-AAAAACTGCACATATGCAAGCCATTTG---
CA 2066
                    |  ||| | || ||  |  |||| ||| |      | |  |||
||
Db          1737 ------TTAATCTGACATTTCACAAATCCAAAATTGC-
CGTGGATGAACTCTTTACTTCA 1789

Qy          2067 C-TCTGGA-ACTGCATGC-
CGTGAAAACTCCTAATGGTGTGGAACTTAGTTTGAATTTGA 2123
                    | | ||| ||| |  | |  | | | | ||||      || ||| ||||| | |
Db          1790 CTTCGGGATATTGCTGGAGCTCGGAGTCTCC--------TGAAAC--
AGTTTAAGTCTGT 1839

Qy          2124 AATCACGCCGCATGCACAAAGGGA-
CAGGCCCAGGCCCGACCTCAGGTCATCCGCCCGCT 2182
                    |            ||| |  | ||  |||| || | | ||   | ||  |||
|
Db          1840 AT---------ATGTTCCTGGAAATCATACCCA--CCAGGCATC---TTATAAGCC--
AT 1883

Qy          2183
GGCTGCAGAGCATCCCTGGGAGCCAAGGCGAGGCCCGTGGAGCCTGAGCTTTGTGTAGCT 2242
                    | || ||    |   ||| | |        |||| |  ||| ||
Db          1884 TGTTGAAGCAAGT-
TGTGGAGGAAATATTTCATCCCGAGAGGCCAGA------------- 1929

Qy          2243
CGAGCTTTGTGTAGCTCGTGCACTTATTATGCACCACCTCCCTTCAGTCACCACTCCTCT 2302
                    | |  ||  ||| | ||| |  ||||||| |  ||||
|||
Db          1930 ------------------
```

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TTCCGTTGATATTGAACACATGTCTTCAGGCCTCACTGATCT 1971


Qy       2303 TCCT----
CCGCCATCCTCATTTATACTGATTGCACACCCCCCGCTCAAACAACAATGTC 2358
                  | |     | |     |   ||| |  | ||| |   || |  ||||
||
Db       1972 CCTTAAAACTGGATTTAGCATGT-TCATGAAGGTGAGCCGGC--CTCA----------
TC 2018


Qy       2359
CTTATTATGATGACCATCTCGTAGTGGTACATTCCATTCCTATTTAAGGTAAGCCCAAAG 2418
                | | ||| ||| |||               | ||||| ||| ||||| |
Db       2019 C---TAGTGACTACCCCCTC-------------
CTGATCCTCTTTGTGGTAGG------- 2055


Qy       2419 CCCACTTTTGGATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGC-
GCCTGCGTTCTTCT 2477
                           |||       || || |||   |||      ||| ||   | |   | ||||
|
Db       2056 --------TGGGG----TC-ACAGTCTCTGAA-----
GTGAAAATGGTCAAAGATCTTGT 2097


Qy       2478
GGGTTTGGCTAGATAGGGTTGTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAGGGTG 2537
                     || | |    |||    |||| ||    ||||        | |||
Db       2098 GGCAT---C--------GTTGAAGCC-----AGGAAC---------------
CCAGGTAA 2126


Qy       2538 TCATTTTCTCGCACAATACAACT-----
CACTGAGGATGCTTCTGTAGAAGTGAGAAACA 2592
                     || |  | ||||| || ||       |||| | || | |  | |   | |
|||
Db       2127 TCGTGCTGTC-
CACACGACTCCTGAAGCCACTTAACATTCCTGAGCTGTTATTTGCAACT 2185


Qy       2593 CGATGAGTACATTCAGAATTACAAT----AACTCACTCTCACTGGGTAA---
CTTCTCAT 2645
                    || | ||| |||| |    |      | |   | || |   | ||| ||
||||
Db       2186 GACCGACTGCATCCAGACCTTGGCTTCTGAGCATCCGCTAAGAAGATAAGACCTACTCAA 2245


Qy       2646
GATAGATTTGTATGATCAATACGGGTCTATTTTTATGTCAACTGAACACTGTAGGGTAC- 2704
                  | | || ||      |  |     | |||| | ||  | ||  |   || |   |
|
Db       2246 GCTGGAAATG-----CCGATGC------AATTTTCTGCCACC---
ACTCCAAATACTCCT 2291


Qy       2705 ---CTTCCA--
GTCTTTTTCAAGATTGTTAAATTGAGACAAGTAATTGAATAATTTGTCC 2759
                      |  ||| ||| | |||          ||||| || || | || |||| | ||
||
Db       2292 CCACAACCAGCGTCCCTGTCAC-------TAATTGCGAGAA-TGATGGAAT--TCTG-
CC 2340


Qy       2760 TATTTTTATTTTAAAAAAAGTGAATGGAC-
TGAAATGTTAAATGTGAATGTACATTTCTT 2818
                                   |||| || | ||| |  |     |||| |||| ||
|||
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Db      2341 --------------------TGAAGGGTCTTGATACCTACTCAGTGAG-
GTACTTTGCTT 2379

Qy      2819 -
AATTGCAATTTTTCTACTGAGTGTTTGCACTATACTTTCTGGAATCTTATTTAACAAAA 2877
                 ||||| |  ||||                              | |    ||
||||
Db      2380 GGATTGCTGTGATTCT------------------------------
TAAAAAAAAAAA 2408

Qy      2878 ATAAAGGGAAAAAATTGCTTGA-CT 2901
                 | ||| ||  | | |||| ||| ||
Db      2409 AAAAAAGGCCACATGTGCTCGAGCT 2433


RESULT 6
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match            32.5%;  Score 5600.5;  DB 1;  Length 2437;
  Best Local Similarity  45.5%;  Pred. No. 0;
  Matches 1348;  Conservative   0;  Mismatches  862;  Indels  753;
Gaps  191;

Qy         8 CAGGAAATCAGGCCGGGCGCA-GTGGC---------TCATGCCTGTAAG---
CCCAGCAC 54
                 | |    ||| || || || |||||        |  |   | |||| |
|||||
Db      2437 CTG-----
CAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTAAGAATCACAGCAA 2383

Qy        55 TTTGGGAGGCGGAGGCGGGTGGATC-
CATTGAGGTCAGGAGCTCAAGACCAGCCTGGTCA 113
                 |    | || |    | | | || |||   |||   ||||||||
|
Db      2382 TCC---AAGCAAA-------GTACCTCACTGAG--TAGGT-ATCAAGACC--------
CT 2344

Qy       114
ACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAAAAAAATTAGCTGGGCGTGTTGGC 173
```

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                || ||    ||   || ||                             |||   |
Db      2343 TCA-GGCAGAATTCCATC----------------------
ATTCTC------------- 2321


Qy        174
GGGAGCCTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAGAATTGCTTGAACCCGGGA 233
                  ||   ||||  |||   || ||  |       |||| ||  ||| |
Db      2320 ----GCAATTAGTGACAGGGACGCTGGTTGT-------
GGAGGAGTATTTGGA------- 2279


Qy        234 GGCGGAGGTTGCAGTGAGCTGAGATTGCACCATTGCA-
CTCCAGCCTGGG---------- 282
                 | |||| ||||    |  | |||||| |   |||   |||||| || |
Db      2278 ----GTGGTGGCAG------AAAATTGCATCG--
GCATTTCCAGCTTGAGTAGGTCTTAT 2231


Qy        283
CGACAGAGCAAGACTCTCTCAAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGAC 342
                 |  |  |||  ||  |||        | ||   || |  | | | |||| |   | | |
Db      2230 CTTCTTAGC-GGATGCTC-------
AGAAGCCAAGGTCTGGATGCAGTCGGTCAGTTG-- 2181


Qy        343 CACAGTGGTAGCCAC-
CTGGCCTAATGCTGTGTTTTTGTACCTGACAGGGGTCACTCATT 401
                  || |    || | | | |   |||        ||  ||   ||   |||| |||
|
Db      2180 CAAA----TAACAGCTCAGG---AATG------TTAAGTGGCT-
TCAGGAGTCG-----T 2140


Qy        402 TTAG---GCACAACT-CCTTCATTCTTTGTGAAATTAGTGAGTTTCCTTCTAC-
CCGTCA 456
                   | |   |||| | | |||   ||| | |                     |||| ||   |
Db      2139 GTGGACAGCACGATTACCTGGGTTCCTGG------------------
CTTCAACGATGCCA 2097


Qy        457 CCAGATTCAATATGTTCTATTAATACACCGATAACCACAGGGGAAGGGCACT-
TGTCGCT 515
                  | ||||   | || | | ||          | ||  |||  |        ||| ||  ||  |
Db      2096 CAAGAT---CTTTGACCATTT----------TCACTTCAGAG-------
ACTGTGAC--- 2060


Qy        516 CTCCCACCTGGTTACCACA------GTCTCCATGGGTCTTTTGCCGTGACCACAA--
ATA 567
                  |||||  |||||||        ||  | |||          ||   ||| |
||
Db      2059 --CCCACC----TACCACAAAGAGGATCAGGAGGGG---------
GTAGTCACTAGGATG 2015


Qy        568 AAG--GAAACACTCATCACTAGTAT-CTAAGTCGGGCTTTACAGT-
AACTATGCACCTTC 623
                  | |  |   ||| | |  |  | ||||| ||  | |||  |   | | ||   |
|
Db      2014 AGGCCGGCTCAC-
CTTCATGAACATGCTAAATCCAGTTTTAAGGAGATCAGTGAGGC--C 1958


Qy        624
TGTGTGCTTCACCTCACTCTCTACTTCAAACAGCCCATGGAGGGAGGTATTATTATACTC 683
                  ||    | |   ||| | || ||   |    ||| |   |||| | | |||| |
|||
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```
Db      1957 TGAAGACATGTGTTCAATATCAACGGAATCTGGCCTCT--CGGGATGAAATATT-
TCCTC 1901

Qy       684 CTTATGTTG-----
ACAGTGAAGAATCTGAGGCCCAGAGAGGTTGGGGACTTGAGTAAAG 738
             |  |  |||   ||| ||  || | |||| | |    |  |     |
Db      1900
CACAACTTGCTTCAACAATGGCTTATAAGATGCCTGGTGGGTATGATTTCCAGGAACATA 1841

Qy       739 TCACACAGCCCTGAGAGGCAGGACCAGGGTTCCATTCC-
TGCTCTATCCAGTTCCAAGCC 797
             |  |||| | |   | ||   |||| |   |  ||| |||| | || | ||
||
Db      1840 T---ACAGACTT---AAACTGTTTCAGGAGAC---TCCGAGCTCCAGCAATATC----
CC 1794

Qy       798 CTTGTGTTTTCCATTATGTTTAGTG--
CCTCTTTGCTAACAGCAACATCTGCAAGATTTG 855
               |||    | ||   || | || || | |       ||  |||| | ||
||||||
Db      1793 GAAGTG---------AAGTAAAGAGTTCATC------CACGGCAA-TTTTG---
GATTTG 1753

Qy       856 -----
TGTTGGTTTTGATGGAGAACTCTAGCTCATCCACATGCTAGTGCCCAAGTGGTGG 910
                 |||  | ||  || ||| | ||    ||| |  |  ||| |  | |||
|
Db      1752 TGAAATGTCAGATTAATTGAAGAGTCCCAG----
TCCGTAATTTTTTGCAGCAAAGGT-G 1698

Qy       911 AGGGGCCA----CCTCAGCAGGTGGGTTCTG----
AATGCAGCCAAGGCTGT-------- 954
             |  |||  ||||| |||    | |||     ||||| |  | ||| |
Db      1697 ACAATCCAGATTCCTCA-CAG--
AAGACCTGAGCCAATGCTTTCTTGACTTTTTCTTCTG 1641

Qy       955 CCCCGCAATGG------------GTGAGACTCGCTCCAACTGCCCGCC-------
CTCAG 995
             |  |  ||  ||           ||||| | ||||| | | |           |
|
Db      1640 CTTCACACAGGTCTTTGTCTACCGTGAG---CTCTCCAG-
TGACAGAATAAATATATATG 1585

Qy       996 AGCAGGTGCCTAAGTCCTCCCTGGCACTGGCAGGCCTTACCTCACATTG-----
CTAAAT 1050
             || |||  |  | ||| |  | |||    | || |||        | |||
||
Db      1584 AGAAGGATCAGCAGTTCCTCAGGGCT---GTAGTCCT-------
CGTTGGTTCTCTGGGT 1535

Qy      1051 TAAAGCAATGCAATTCCTCTTGGGTA--AGAGGAATT----
CCTCCTTCTTTACTAACTG 1104
             || ||    || ||  || || ||     |   || ||    |   | || || ||
Db      1534 TACAG----GC--
TTAATCATGGGCAGCAGCTGATTTAACACAACGGACATTGCTGAC-- 1483

Qy      1105 ATCCCCA--GCAAGGAAATAAAATGTTAGGCTTTAAAAATCCC-TACTTTGT----
CATA 1157
             ||||||  ||  |||  |      || |||| |||| || |   |  |||    |
|
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```
Db      1482 -TCCCCAATGCTCTGAAGAAGG-----
AGCCTTTCAAAAGCCAGAAAGTTGTCCCACTTG 1429

Qy      1158 TCAGACTATATTCTAAAACTATATTTGAGC-
GAAACCTGTCATTGCGTCTAATTTCAAAT 1216
              ||| || |   |     |   | |||||||| |   || ||| ||        | |
Db      1428 GCAGTCTGTGGG-TGTTTCAACGTTTGAGCTGTGGCCAGTCCAAGC-------
TGGAGGA 1377

Qy      1217 ATACAGAAT-CTCCTTAAGAGCTGTTGCCTTATTTTTTTGTAAAGC---
CTCTCTGACAT 1272
              || |||  | | | ||||| |||  | || ||| | ||| | |  |||
Db      1376 GGCCACAATGATTCATTAGAGCT-TTGAGGT-
TGTTCTTGAAGAGCTGAATATAGGAC-- 1321

Qy      1273 CAAATGGGGAGAAATGGTGGCAC-
CTCCAGACACCCTGAAACTACACACCATTTCTTCCC 1331
              ||| |  | |   |||| || |||| ||  || |    | |   || | |||
                                                                     |
Db      1320 ---ATGAGCTGTCCCGGTGTGACTCTCC--
CCATACTCATCTTGATTGGCAGGTTTTCTC 1266

Qy      1332 TGCT--CAGCTTCTGCTCAGGAGTTCTGTGAGCTATGGGAAGGCCAT---
TGGTTGTATT 1386
              |||| | ||||| | | || ||  || ||        |||| ||  | |
                                                                     |
Db      1265 TGCTTGCCGCTTC--CACTAGATGTCTCCGAACTT--------
CCATCACTGCCTCTTTG 1216

Qy      1387 TGCTACTTTTACT-
TTCATCTTCCTCTGCTGTAGAGCCATTTAATGTTATTGTCATATGC 1445
              |||| | | | ||||  |   || ||| |   | |    |  ||||
                                                                     |
Db      1215 TGCTTAGTGTTCAGTAAAGCTTC-----CCATAGGGC--
TTTGGCTGTGGTGTCA----C 1167

Qy      1446 TG-
CTGGTGAGGTAAAGGTGGGTCCGGGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGG 1504
              || | |||| | ||  |   ||    |  ||| | ||| || ||||
Db      1166 TGAATTGTGAAAGACAG------CCTGGTGCAACCACA----TTATA--
ATTTTCCT--- 1122

Qy      1505 GCCGATTTCAGCA-GGAGTTCAGAGGGC-
TTATGATGGATGGTGAGAGATTTGACAACCA 1562
              ||    |||| | |||| || | || ||| ||                    ||
|||||
Db      1121 -CC----TCAGTATGGAGTGCAGTGAGCGCTATCATG------------TT---
AACCA 1083

Qy      1563 CCAGAGCACATGTGCTCTGACCCTCTCCTGGGCATTGGTTCCTGCTGGTACCGGGCGGTT 1622
              || | || |||| ||       ||||||          ||||| | || |
Db      1082 TCACATCATTTGTG---TGG------CCTGGG----------
AGCTGGGGAAGTGCTGAA 1042

Qy      1623 CAGACCTTCAAATAGGTTGCTTTCAAAAGAGCTTTCAGGCACTTATTGAGAATTAATGTT 1682
              || |||           || |    || | ||
Db      1041 ATGATCTTC-------------
TCTACTAAGTTGTCT----------------------- 1018
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```
Qy       1683 TAAACAGACATAATAGCCTAGATGAACTCCCAAGAGATCTATTAAATCTTGTGGGCTGAA 1742
              |||  ||| || |  || ||||    ||||||| |                    ||| |
Db       1017 -------CCATGATGTCC--AACTG--CTCCTGTGAGATCCA-----------
GGGTT--- 982

Qy       1743 TAAATATCTCGTGCAGGACTGTGCAACAGTAGCC-CAGA-
GCATCCTGCCTGTGGGCATC 1800
                                           |||| | ||| | || | || ||  |||||||||  |||
Db        981 ------------------CTGT-CCACAAAAACCACTGATGC--CCTGCCTGC-
AGCAGT 944

Qy       1801 CACCTCCCAGGTGAGGGCAGTGGGA-AGCTGGCCCGA-
CGGCAGCCAGAACTTGTTTCTC 1858
                      |   || || | |     |||| ||| |   ||||| || | ||||| |  || ||  |
Db        943 CTTCTTCCTGTTCTTTGCAGGGGCATAATTGGCCAGATCCGCAGCGATGACCTGACT-
TA 885

Qy       1859 ACCTCCCACCAGC--AACCCCCCACCC---------------AACTCTGGGCCCC-
AGGC 1900
                      |    ||  ||||  ||| | ||||                     || | |||  |
              ||||
Db        884 AGGAACCTACAGCAAAACACTCCTCCCGTACTCCTAAATGTTCACACAGAGAACTGAGGC 825

Qy       1901 ---ACACGAAGCA-CAAGTCT-CAGGGGACCATTCCCACATTGGGGGATCCTGAG-
GGAG 1954
                         |||| | ||| |   ||| ||| |        |  |  |||||    |  ||
              ||||
Db        824 CTGACACTAGGCATCTGATCTGCAGCAG-------
CAGCTCTGGGGTTAGCGTAGTGGAG 772

Qy       1955 --CCCATCACC---GCCT-CTTGCATACAACTGTC--------CACT----AGGAG--
GC 1994
                        | |||||||  || | |  || |  |      ||||    | ||    |||||
              ||
Db        771 TCCACATCACCCAGGCTTCCCAGCTTCCTCTTGTCCGGTCGGGCGCTATTAAGGAGGTGC 712

Qy       1995 ACGCCCAGTGTGGGAGAGATGTATGGTCTTGCCTTCCAC--
CTGTAAAAACTGCACATAT 2052
                        || ||    |||| ||  || |      |  |  | |||  |  ||| |
Db        711 ACATCC----
TGGGGTAGCAGTGGGAAAAGGGATGCAAAAGCTGGAGTCAAGGCAAAGTG 656

Qy       2053 GCAAGC--CATTTGCACTCTGGAACTGCATGCCGTGAAAACTCCT-
AATGGTGTGGAACT 2109
                        |  ||| ||   ||| |    ||| |   | | ||  ||| |||          |||| |
              |
Db        655 GGGAGCAACAGGGGCAAGCAATAACGG---GACATG-
GAACACCTCGGCCGTGTAGTTCA 600

Qy       2110 TAGTTTGAATTTGAAATCACGCCGC-----------ATGCACAAAGGGACAGGCC-
CAGG 2157
                        |   |||    |  | |||| |                   ||| | ||    || ||| |
              |
Db        599 TG--TTGCCCATCCATTCACACAGCTTCTCCTCCAGCTGCTCGAA--
CACCGGCTGCTGC 544
```

```
Qy        2158 CCCGACCTCAGGTCATCCGC-----CCGCTGGCTGCAGAGCATCCCTGGGA----
GCCAA 2208
               |||  |  ||   ||  ||||     ||||||  |   |   ||| ||   |
||
Db         543 CCCTCCATC---TCGGCCGCTGCCGCCGCTGG--
GACATGATTAGCTGTGAGGTGGACA- 490

Qy        2209 GGCGAGGCCCGTGG----
AGCCTGAGCTTTGTGTAGCTCGAGCTTTGTGTAGCTCGTG-C 2263
               ||| ||| |  ||       ||   |   |   |  | |  |  | ||| |  ||
|
Db         489 -
GCGTGGCTCACGGTTGTGACCACCACACAATACTGGAAGTGACTGCGGCAGATGATGTC 431

Qy        2264 ACTTATTATGCACCA----CCTCCCTT----
CAGTCACCACTCCTCTTCCTCCGCCATCC 2315
               | || || | |||    ||  ||||    ||| || |  |  |    | | |||
Db         430 CCGTAGGAT-
CTCCACGGTCCGGCCTTTCAGCAGGCAGCTCAGCACAAACACTGCC---- 376

Qy        2316 TCATTTATACTGATTGCACACCCCCCGCTCAAACAACAATGTC---
CTTATTATGATGAC 2372
                ||   ||| ||| | || ||  |       |    |    ||   ||        |
||||
Db         375 ----TTGGGCTGCTTG-
GCTCCACCACCAATTGCGTCGGGCTCGAACTCTCGCAGGTGAC 321

Qy        2373 CATCTCGTAGTGGTACATTCC-ATTCCTATTTA-
AGGTAAGCCCAAAGCCCACTTTTGGA 2430
                ||   || |  |  ||   |||       |  |||    ||  |||||    ||
|
Db         320 AGTC----AGGGCCCCCCACCGCCTCCAGGAGACGGGTGGATCCGCAGCCCC--
AGTGCA 267

Qy        2431 TTTTCTCG--ACTGTCCGAGAAAAGTTGTGTAAGCGCCTG--
CGTTCTTCTGGGTTTGGC 2486
                |||||   |  |  |  |    ||    ||||  |  | |  ||||    |
||||||
Db         266 GGCTCTCGGCGCAGGCGGCGTCCAG----GTAAACCACAGCCCGTTTCAC----
TTTGGC 215

Qy        2487
TAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAGGGTGTCATTTTCT 2546
                ||      ||   ||  || | ||                |||| || |  | || |
Db         214 CAGCAC---CTGCTCCCATCCTTG--------------CTGGGTAAAG--
GACAGT---A 177

Qy        2547 CGCACAATACAACTCACTGAGGATGCTTCTGTAGAAGTGAGAAAC-ACGATG-
AGTACAT 2604
                ||| |  |   |  ||| | |    | |  |  ||| || ||||| ||| || |
|
Db         176 CGCCCGAGGC-GCTCATGGTTGGGGATTC-
GCAGACTTGGGAAACTACGGTGCAGGAACT 119

Qy        2605 TCAGAATTACAATAACTCACTCTCACTGGGTAACT--
TCTCATGATAGATTTGTATGATC 2662
                ||      ||  || |  ||||||||  ||   ||    ||    |      |||| |
||
Db         118 TC----TTTCAG-AACTCAC-CGCTTCCGGAAATTGGGCTCCGGGAGACTTTGACAG-
```

TC 66

Qy   2663
AATACGGGTCTATTTTTATGTCAACTGAACACTGTAGGGTACCTTCCAGTCTTTTTCAAG 2722
                 || | | || | |||| | | | | | | || ||| ||||
Db   65 TCCACAGTACACCCAGTAGGCCAACAGTGCTC-GAGGAATTCCG--CAG-
CTTT------ 16

Qy   2723 ATTGTTAAATTGAG-ACAAGTAA 2744
                        | ||| | |||||| |
Db   15 ---------TAGAGCAGAAGTAA 2

RESULT 7
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match   31.4%; Score 5410; DB 1; Length 2495;
  Best Local Similarity   45.7%; Pred. No. 0;
  Matches 1375; Conservative   0; Mismatches 956; Indels 678;
Gaps 181;

Qy   4 AAATCAGGAAATCAGGC------CGGGCGCAGTGGCTCATGCCTGTA-
AGCCCAGCACTT 56
             | || | ||| | | | |||||| | || | ||| | |||
Db   2 ACTGTTGGCCTACTGGCTACTATCAGGATC-GTGGCTATT--
TTGAAGAGCTGATCACCA 58

Qy   57 TG--
GGAGGCGGAGGCGGGTGGATCCATTGAGGTCAGGAGCTCAAGACCAGCCTGGTCAA 114
             || ||| || | | | ||| | |||| | ||||| || | ||
Db   59 TGTTGGAAGCAGC-AC---TGGGAC--TTGAG--C--GAGCTC---ACATG---
GGAATG 102

Qy   115 CATGGTGAA--
ACCCCGTCTCTACTAAAAATACAAAAAAAAAATTAGCTGGGCGTGTTGG 172
             | |||| | | ||| |||| |||| || || | |
|
Db   103 TTTACTGAATTAGCTATTCTATACTCTAAATTTAAGC----------
CTCAGAAAT--G 150

```
Qy         173
CGGGAGCCTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAGAATTGCTTGAACCCGGG 232
           ||||||  | |    |||  | ||  ||| || ||  || |||      |||
Db         151 AGGGAGCACCTGG----AGCTGTTCTGGT--CTAGAGT--GAATATT-------
CCC--- 192


Qy         233
AGGCGGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTCCAGCCTGGGCGACAGAGCA 292
                    | | |||  |||||  ||| |||  || |  |    |||| |    ||||
|
Db         193 ------AAGGTGCTAAGAGCTGC---AGAACAA--GCTCATCT--TTGGG---
CAGAACT 236


Qy         293
AGACTCTCTCAAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGACCACAGTGGT- 351
                  |  | | |  |  | || |  ||||  ||| | |||  |  |    |||| ||
Db         237 GGTGTTTTTGTATGACAAGTATGAAGAATATGATAATGCCATAATT--
ACCATGATGAAT 294


Qy         352 -AGCCACCTG--GCCT--AATGCTGTGTTTTTGTA------
CCTGACAGGGGTCACTCAT 400
                  | ||| |||  |||| ||  ||  | |  || |     | | ||   ||| |
||
Db         295 CATCCAACTGATGCCTGGAAAGAAGGGCAATTCAAAGATATCATTACCAAGGTTGC-
CAA 353


Qy         401 TTTAGGCACAACTCCTTCATTCTTTGTGAAATTAGTGAGTT-TCCTTCTAC--
CCGTCAC 457
               |  || || || | |  ||     | | |||     |||| | ||| |    |    |
Db         354 TGT-GGAACTA-TACTACA------GAGCAATAC---
AGTTCTACTTAGAATTCAAGCCT 402


Qy         458
CAGATTCAATATGTTCTATTAATACACCGATAACCACAGGGGAAGGGCACTTGTCGCTCT 517
               ||  | | | | ||| | | || | |  | ||||  | |    |||| || ||
|
Db         403 CTGTTGTTAAATGATTTGCTGATGGTGCTGTCTCCACGGTTGGATCACACTCGT-
GCAGT 461


Qy         518
CCCACCTGGTTACCACAGTCTCCATGGGTCTTTTGCCGTGACCACAAATAAAGGAAACAC 577
                |     ||| |||  ||| |||  || | || | | |     |   |  ||||||
Db         462 C------AATTATTTCAG----CAAGG---TTAAACAGCTACCACTGGT----
GAAAC-- 502


Qy         578 TCATCACTAGTATCTAAGTCGGGCTTTACAGTAACTATGCACC--TTCTGTG--
TGCTTC 633
                         ||||  |   ||  | |  ||| |    || |  |||||| ||
||
Db         503 --------CGTATTTG---
CGTTCAGTTCAGAACCATAACAACAAATCTGTGAATGAATC 551


Qy         634
ACCTCACTCTCTACTTCAAACAGCCCATGGAGGGAGGTATTATTATACTCCTTATGTTGA 693
               |   || ||| ||  |||      || | |||  ||| | ||  ||
|
Db         552 ATTGAACAATCTTTTTATTACA-------GAAGAAG--ATTATCAGGCTC----
TGCGAA 598
```

```
Qy         694 CAGTGA-AGAATCTGAGGCCCAGAGAGGTTGGGGACTTGAGTAAAGTCACAC-
AGCCCTG 751
                   ||    | |||  || |  |                 ||||    ||  || | |  || |
|
Db         599 CATCAATAGATGCTTATGAC-------------
AACTTTGACAATATCTCGCTTGCTCAG 645


Qy         752 AG-------AGGCAGGACC----AGGGTTC-----
CATTCCTGCTCTATCCAGTTCCAAG 795
                   |     |  || ||  | ||||    ||| ||||| ||||   |||
|||
Db         646 CGTTTGGAAAAACATGAACTCATTGAGTTCAGGAGAATTGCTGCT-TATCTC-
TTCAAAG 703


Qy         796 CC--CTTGTGTTTTCCATTATGTTTAGTGCCTCTTTGCT--
AACAGCAACATCTGCAAGA 851
                   | |    | |   |   || |||  || |||   ||   || | | | |||
Db         704 GCAACAATCGCTGGAAACAGAGTGTAGAG---
CTGTGCAAGAAAGACAGCCTTTACAA-- 758


Qy         852
TTTGTGTTGGTTTTGATGGAGAACTCTAGCTCATCCACATGCTAGTGCCCAAGTGGTGGA 911
                   || |  ||| || || | || || | | || |  || |  ||| | ||| ||  || |||
||
Db         759 --------GGATGCAATGCAGTATGCTT-CTGAATCTAAAGATACTG---
AATTGGCTGA 806


Qy         912 GGGGCCACCTCAGCAGGTGGGTTCTGAATGCAG--
CCAAGGCTGTCCCCGCAATGGGTGA 969
                   |  | |||| ||| |||| ||| | | | |     ||| ||   || |||
Db         807 -AGAACTCCT--GCA-GTGGTTTTTGCAGGAAGAAAAAAGAGAGT----
GCTTTGG---- 854


Qy         970 GACTCGCTCCAACTGCCCG---CCCTCAGAGCAGGTGCCT-
AAGTCCTCCCTGGCACTG- 1024
                   || | ||    | | | |  |  || |    || |||  | ||| | ||| ||| |
||||
Db         855 AGCTTG-TCTGTTTACCTGTTACGATCTTTTAAG--
GCCAGATGTCGTCCTAGAAACTGC 911


Qy         1025 --GCAGGCCTTACCTCACATTGCTAAATTAAAGCAATGC---
AATTCCTCTTGGGTAAGA 1079
                    | ||||  |  |||     |  |  | ||  |  ||||   | ||| ||  ||  |
||
Db         912 ATGGAGGCACAATATCA------TGGATT-
TTGCCATGCCCTATTTCATCCAGGTCATGA 964


Qy         1080 GGAATTCCT---------------
CCTTCTTTACTAACTGATCCCCAGCAAGGAAATAAA 1124
                    |  |  |        ||   | ||  | ||  | | | |  ||  || |||
Db         965 AGGAGTACTTGACAAAGGTGGATAAATTAGATGCT-TCAGAATCACTG--
AGAAAAGAAG 1021


Qy         1125 ATGTT-AGGCTTTAAAAATCCCTA--CTTTGTCAT--ATCAGAC----
TATATTCTAAAA 1175
                    | |   | |||   | | | | | |  ||||       |||| |     |  || || |
|
Db         1022 AAGAACAAGCTACAGAGA-
CACAACCCATTGTTTATGGTCAGCCCCAGTTGATGCTGACA 1080
```

```
Qy       1176  --------CTATATTTGAGCGAAACCTGTCATTGCGTC---
TAATTTCAAATATACAGAA 1224
                             |  |  |   |||  |   ||  |  ||     |||||  |
                                                                     |
Db       1081  GCAGGACCCAGTGTT---
GCCGTCCCTCCCCAGGCACCTTTTGGTTATGGTTATACCGCA 1137

Qy       1225  TCTCCTTAAGAGCTGTTGCCTTATTTTTTTGTAAAGCCT--CTCTG---
ACATCAAATGG 1279
                     | || || |  |     |||           |  ||||| || ||   ||| ||
                                                                       ||
Db       1138  CCACCGTATGGAC---AGCC------------
ACAGCCTGGCTTTGGGTACAGCATGTGA 1182

Qy       1280  GGAGAAATGGTGGCACCTCCAGACACC----------
CTGAAACTACACACCATTTCTTC 1329
                     |  |||  | |  |||  || ||||        |||||||   |  ||| |
                                                                      |
Db       1183  GATGAAGCGCT-GATCCTGTAGTCACCTATTTCGTACTGAAAC--ATCGTCTTTAC-
CC 1238

Qy       1330
CCTGCTCAGCTTCTGCTCAGGAGTTCTGTGAGCTATGGGAAGGCCATTGGTTGTATTTGC 1389
                       || ||||| ||| |  ||       |  |       |||| |    |||
                                                                      |||
Db       1239  ACTTCTCAGTTTATAATGGGG------GAAAAC-------AGGCAAC---
GTGTTCTTGT 1282

Qy       1390  TACTTTTACTTTCATCTTCCTCTGCTGTAGAGCCATTTAATGTTATTGTC-
ATATGCTGC 1448
                         || |||| |||||      || || |    || |||| |  | ||| ||
Db       1283  AACCTTTA-TTTCA------------
TGAAGGACTTCTTTTTGTTTCTAACTATAAACT-- 1328

Qy       1449
TGGTGAGGTAAAGGTGGGTCCGGGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGGGCC- 1507
                                 ||| |||       |||            ||||| |||
                                                                      ||
Db       1329  --------------TGGATC-----ACCT-----------------ATGTTAAAA---
CCT 1350

Qy       1508  GATTTCA------
GCAGGAGTTCAGAGGGCTTATGATGGATGGTGAGAGATTTGAC---- 1557
                       ||||||        || | ||| |||| | || || ||     ||| |
Db       1351  TATTTCACATTCCACATCATTTTAGA--
ATTTATTTTCGAAGGGGAATAGTTTCAATGTT 1408

Qy       1558  --
AACCACCAGAGCACATGTGCTCTGACCCTCTCCTGGGCATTGGTTCCTGCTGGTACCG 1615
                       | |||  || |   | |  | |   ||| |||         ||| |      ||
                                                                       |
Db       1409  TTATTCACTTGGGCTTTTTTTCT---TCCCCCTCT----------TTCTT-----
TAAAG 1450

Qy       1616
GGCGGTTCAGACCTTCAAATAGGTTGCTTTCAAAAGAGCTTTCAGGCACTTATTGAGAAT 1675
                      |  | ||| | |  ||| |||  |||| |    ||   ||| |||||   ||
Db       1451  AACTGCTCA-ATATTC-AATCTGTTG-TGAAGAACCTGATTT---GCACT--
CTG----- 1497
```

```
Qy        1676
TAATGTTTAAACAGACATAATAGCCTAGATGAACTCCCAAGAGATCTATTAAATCTTGTG 1735
          ||  ||||||| |  ||| |        ||||| |    | |||| |||||
Db        1498 TAGTGTTTAAAGAAACAAAG----------AAACTCTAA-------
TATTGAATCT---- 1536

Qy        1736
GGCTGAATAAATATCTCGTGCAGGACTGTGCAACAGTAGCCCAGAGCATCCTGCCTGTGG 1795
          || ||      || ||||  |   |||  ||| |    | |   | |  || ||
Db        1537 --CTTAA-----ATTTAGTGTA----TGT-
AAACAGCTTACAAATACGTATTGTCTAAAT 1584

Qy        1796
GCATCCACCTCCCAGGTGAGGGCAGTGGGAAGCTGGCCCGACGGCAGCCAGAACTTGTTT 1855
          ||||  |    |      || |     || ||||||   | |          ||| |
Db        1585 GCATTTAAAT--CTGTTTTATTCAAAGAAAAGCTAAAGCAAAAAC-------
ACTGGCAT 1635

Qy        1856 CTCACCTCCCAC------CAGCAACCCCCCACCCAACTCTGGGCCCCAGGCACA-
CGAAG 1908
            | |||  ||      ||| | |  |||| |  |        ||||| ||
Db        1636 ATGACCATGCAAGACTGTCAGTGCCAACAAAGACAACACTAATC----
AGCACATCGTA- 1690

Qy        1909 CACAAGTCT-CAGGGGACCATTCCCACATTGGGGGATCCTGAGGGAGCCCATCACCG-
CC 1966
            ||| |  ||| |      |||||| |||   |  |   ||           | || |
Db        1691 CACTGGATTGCAGTG----CTTCCCAGATTATTGAAAAATG----------
TTACAGACA 1736

Qy        1967 TCTTGCATAC-----AACTGTCCACTAGGAGGCACGC---
CCAGTGTGGGAGAGATGTAT 2018
            ||||| |      ||| |  | ||  |||| |    || ||   |
Db        1737 ACTTGCCTGATTTTTAAATGAGCG-
TAAAAGGCCCTCTAACCTATGCAGG---------- 1785

Qy        2019 GGTCTTGCCTTCCA-----
CCTGTAAAAACTGCACATATGCAAGCCATTTGCACTCTGGA 2073
            || || ||  ||  | || || |||  ||||   |||||| | ||
Db        1786 ----TTTCC--CCATTATGCATATAGAAAATGCTAGTATG------
TTTTGCTCACTTCA 1833

Qy        2074
ACTGCATGCCGTGAAAACTCCTAATGGTGTGGAACTTAGTTTGAATTTGAAATCACGCCG 2133
            || |  |||      ||| ||| |||  || ||          ||| |
Db        1834 TATGTAACAGGTGC-----CCTTATGTTGTG---CT--GT-----------ATCCTG-
TG 1871

Qy        2134
CATGCACAAAGGGACAGGCCCAGGCCCGACCTCAGGTCATCCGCCCGCTGGCTGCAGAGC 2193
            || |   | |||||    ||| | ||| ||   ||| | | | |
Db        1872 CTTTTTCTGTGGGACCATTCCATTCAGGAGCAAAG------AGCAC-
CATGATTC----C 1920
```

```
Qy        2194
ATCCCTGGGAGCCAAGGCGAGGCCCGTGGAGCCTGAGCTTTGTGTAGCTCGAGCTTTGTG 2253
            |  | ||| |    | |  |||   |||||| |||||||| | |  | |
            |||||
Db        1921 AATCTTGTGTGTGTTTACTA-ACCCTT---
CCCTGAGGTTTGTGTATGTTGGATATTGTG 1976


Qy        2254 TAG--CTCGTGCACTTATTATGC--ACCACCTCCCTTCAGTCACC--
ACTCCTCTTCCTC 2307
                |   | |  |||| | | | |  | |     |||| || | | || |||
||
Db        1977
GTGTTTTAGATCACTGAGTGTACAGAAGAGAGAAATTCAAACAAAATATTGCTGTTCTTC 2036


Qy        2308
CGCCATCCTCATTTATACTGATTGCACACCCCCCGCTCAAACAACAATGTCCTTATTATG 2367
             |   |   |||  |||    ||| |    | |    | |  || | ||| |  | |
||
Db        2037 AGTTTT----
GTTTGTGGAATTTGAAATTACTCAAATTTAAAATAAATTACTGGACTGTG 2092


Qy        2368 ATGACCATCTCGTAGTGG----
TACATTCCATTCCTATTTAAGGTAAGCCCAAAGCCCAC 2423
                |  | | || | |  ||  || | ||  |        || |  | ||||
||
Db        2093 GAAATAACATAGAATTGAAGTTTTAATTAAATACCACT------
CAAACGAAAAGAACA- 2145


Qy        2424
TTTTGGATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGCGCCTGCGTTCTTCTGGGTTT 2483
             | | |||             | |  || | |  |   ||| |  | |   |||
Db        2146 --GTAGTTTTT-------------GTAGTTTTATATTGGATACTGAG-
GCATTAGGG--A 2187


Qy        2484 GGCTAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAG-
GGTGTCATT 2542
             |||  || ||          |||||| || |||     | || | |  |
||||
Db        2188 GGCATGAAAGG-----------AAGAGGAATGAGGATTGA----
GACATGTGAAGACATT 2232


Qy        2543
TTCTCGCACAATACAACTCACTGAGGATGCTTCTGTAGAAGTGAGAAACACGATGAGTAC 2602
             |   ||| |||   ||| ||| | |  |||||||   | ||  || | ||
||||
Db        2233 GT---GCATTATA----TCAATGTGCATTC--CTGTAGT--TCATTAACAAG----
GTAC 2277


Qy        2603
ATTCAGAATTACAATAACTCACTCTCACTGGGTAACTTCTCATGATAGATTTGTATGATC 2662
              || || | ||| | | | | |    | | ||| || || |  | | | ||     ||
|
Db        2278 ATGCAATAGT-CTAAAGAAC-------CAGAGTCACTACT-ATAGTGGCTTAACAT--
TT 2326


Qy        2663
AATACGGGTCTATTTTTATGTCAACTGAACACTGTAGGGTACCTTCCAGTCTTTTTCAAG 2722
             |||  | |  | | | | | | |   |||| | ||||  | |     |||||
Db        2327 AATCTGTCTCCAATATTTTAACCAAGTGACACCG--
```

```
GGGTTTTTATCGAAGCATTTCAC- 2383


Qy      2723
ATTGTTAAATTGAGACAAGTAATTGAATAATTTGTCCTATTTTTATTTTAAAAAAAGTGA 2782
                  | || ||| |||| | ||| |        ||| ||| || | || ||| ||| |
Db      2384 -----TTAAATGA-ACAAATCATGGC------TGT--
TATATTAACTTGAAATAAAATAT 2429


Qy      2783 ATGGACTGAAATGTTAAATGTGAATGTACATTTCTTAAT-
TGCAATTTTTCTACTGAGTG 2841
              || |  |  | |||| |||    || | |   |  || |||  |    || | |
|
Db      2430 ATTTA--AACATGTAAAAAAAAAAAAAAAAAAGGCCACATGTGC--
TCGAGCTGCAGGTCG 2485


Qy      2842 TTTGCACTA 2850
                  | |||
Db      2486 CGGCCGCTA 2494



RESULT 8
US-10-478-914-57/c
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match            31.2%;  Score 5366.5;  DB 1;  Length 2336;
  Best Local Similarity  44.0%;  Pred. No. 0;
  Matches 1320;  Conservative   0;  Mismatches  904;  Indels  773;
Gaps  170;

Qy       16 CAGGCCGGGCGCA-GTGGC--------------
TCATGCCTGTAAGCCCAGCACTTTGGG 60
                 ||| || || || |||||               |  |   |||| | ||| ||
Db      2336
CAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTGTATTCTCAGAGCT----- 2282

Qy       61
AGGCGGAGGCGGGTGGATCCATTGAGGTCAGGAGCTCAAGACCAGCCTGGTCAACATGGT 120
                | | |    | ||| |||              |||| |  |    |||| ||
|
Db      2281 -GCCAG----GAGTGCATC------------GAGC-
```

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CTGTAATTTCCTGTTCTC-----T 2245

Qy         121 GAA-
ACCCCGTCTCTACTAAAAATACAAAAAAAAAATTAGCTGGGCGTGTTGGCGGGAGC 179
               ||| |||| ||| || | ||  | |||           |||| | ||       |
|||
Db        2244 GAATCCCCCATCT-TTCTGCAGCTCCA-----------AGCTTTGTGT----
CCCCACAGC 2201

Qy         180 CTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAGAATTGCT-
TGAACCCGGGAGGCGG 238
               |||| | | |       ||||||      ||| ||| |   || ||  |
||||
Db        2200 CTGT-GACTCTGT----------GCTAA------
CAAATCGCTATTGTCCAGTGGGGCGA 2158

Qy         239 A-GGTTGCAGTGAGCTGA--GATTGC---------
ACCATTGCACTCCAGCCTGGGCGAC 286
               | ||| ||| |||  | |   |||||        | ||| | ||||| | ||
||
Db        2157 ATGGTGGCTG-
GAACTAAAGAATTGCTGTCTGGTTTCTATTCAAATCCAGGTAGCGAGAT 2099

Qy         287 AGAGCAA--
GACTCTCTCAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGAC-- 342
               | | | || |||| | |     |  |     | | || ||| | | |
Db        2098 ATATGAATGGACT-TTTCGA------------------
ATCGTCATGTGAATAACGTCTG 2058

Qy         343 CACAGTG-
GTAGCCACCTGGCCTAATGCTGTGTTTTTGTACCTGACAGGGGTCACTCATT 401
               | | |   | ||| |   ||| |||||         |  ||| | ||||
Db        2057 CTCGGCATGAAGGCTCAGAGCC--ATGCT-------------
AGGAAGGATTAACTCG-- 2015

Qy         402 TTAGGCACAACTCCTTCATTCTTTGTGAAATTAGTGAGTTTCCTTCTACCCGTCACCAGA 461
               ||||| | |    ||| ||||| |  || |||| |  | ||      | |
||
Db        2014 -TAGGCTGACCACTAACATCCTTTGTGGTACGAGGGGAGAAACAT--------
TCCCAAGT 1964

Qy         462 TTCAATATGTTCTATTAATACACCGATAACCACAGGGGAAGGGCACTTG--
TCGCTCTCC 519
               ||| | |                           ||||| |  | ||
|||
Db        1963 ATCATTTTATTC-----------------------------
ACACTTAATTTTCTATCC 1934

Qy         520 CACCTGGTTACCACAGTCTCCATGGGTCTTTTGCCGTGACCACAAATAAAGGAAACACTC 579
               || |     ||| |  |                            || |||| ||||
Db        1933 CA------TAC----------------------------
CCCCAAAATAAGG-------- 1916

Qy         580 ATCACTAGTATCTAAGTCGGGCTTTACAGTAACTATGCACCTTCTGTGTGCTTCACCTCA 639
               | | ||| | ||| | ||| ||             || | ||||
Db        1915 CTAGCTATTTAATTAGTTGG-------------------CC--------
GCTT------- 1890
```

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Qy         640
CTCTCTACTTCAAACAGCCCATGGAGGGAGGTATTATTATACTCCTTATGTTGACAGTGA 699
            |||||   |                          || ||   |   || |||||| |
                                                                    ||
Db      1889 TTCTCTTAAT------------------------
TTTTAGTGTTTCTGTTGATAATG- 1857


Qy         700
AGAATCTGAGGCCCAGAGAGAGGTTGGGGACTTGAGTAAAGTCACACAGCCCTGAGAGGCAG 759
                            | ||| ||||| |  ||    |||| |    |  || |
Db      1856 --------------TGTGAGTTTGGGAAAATGC--
TAAGTAGCTTTTCACTTA------- 1820


Qy          760 GACCAGGGTTCCATTCCTGCTCTATCCAG--TTCCAAGCCCTTGTGTTTTCCATTAT-
GTT 817
            || ||  |||   ||     |||| |  || || | |   |||| |   |||   |||||| |
Db      1819 GAACACTGTTATTTT----CTCTTTAAAGTTTTCTA--CCTTACATTT---
ATTATAGCA 1769


Qy         818
TAGTGCCTCTTTGCTAACAGCAACATCTGCAAGATTTGTGTTGGTTTTGATGGAGAACTC 877
            ||||  |||||   | |||| |  |||| |                    |    ||||
                                                                            |
Db      1768 TAGT-TATCTTT----ATAGCAT-AGATGCAGAA-------------
AGTAAGAGAGC 1728


Qy         878
TAGCTCATCCACATGCTAGTGCCCAAGTGGTGGAGGGGCCACCTCAGCAGGTGGGTTCTG 937
            | | | | ||                     ||   || |              ||
Db      1727 TTGTTTTTTCA--------------------AGAAAACAACCC----------
TTTAA 1700


Qy         938 AATGC-
AGCCAAGGCTGTCCCCGCAATGGGTGAGACTCGCTCCAACTGCCCGCCCTCAGA 996
            ||| |  ||||        ||| | ||| | |||    |  |   ||| 
CCC----- 1656
Db      1699 AATACTTTCCAA-------CCCATGAAGGG-AAAAATC-CTCCTTTTTTC--


Qy          997 GCAGGTGCCTAAGTCCTCCCTGGCAC-TGGCAGGCCTTACCTCACATTG-
CTAAATTAAA 1054
            || |||| |    || | |   || | |||    || ||| |  | | |||||
                                                                               |
Db      1655 -CAAGTGCATT----CTACTTATTACTTTGCA---
TTTTTCTCCCAAAGTCCAAATTTAT 1604


Qy         1055 GCAATGCAATT--
CCTCTTGGGTAAGAGGAATTCCTCCTTCTTTACTAACTGATCCCCAG 1112
            |||| | || |   |  |   |||| |  |          |||   || ||
Db      1603 GCAAAGAAAATAGAAACAAGTTCAAATGCAATGCATTAACCAAATAAAACAAGTCTCCTT 1544


Qy         1113 CA----AGGAAATAAAATGTTAGGCTTTAAAAATCCCTACTTTGTCA-
TATCAGACTATA 1167
            ||    |||||  |     || | || || |    | | ||  |||||| |
Db      1543 CAAATTAGGAACCAACC---TAAGCATTTGTAA-----
AGTGTAGCAGAATCAGAATTCT 1492


Qy         1168
TTCTAAAACTATATTTGAGCGAAACCTGTCATTGCGTCTAATTTCAAATATACAGAATCT 1227
```

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                      ||  |||| || ||||    | |||||| |    |  ||||| |||
||||
Db      1491 TTTAAAAATTAGATTT----GGAACCTGAACT---ATATAATTCATAAT--------
TCT 1447

Qy      1228 CCTTAAGAGCTGTTG--
CCTTATTTTTTGTAAAGCCTCTCTGACATCAAATGGGGAGAA 1285
              | |     |||| |   ||||||| |  |  ||| ||| |        | |
||
Db      1446 CATTT--TTCTGTGGAAAATTATTTTATCTTT----CTC-CTGTATACCT----
GAAAAA 1398

Qy      1286
ATGGTGGCACCTCCAGACACCCTGAAACTACACACCATTTCTTCCCTGCTCAGCTTCTGC 1345
              |||        |||| | | ||    || |  || | |||  | |  | | |
|
Db      1397 ATG--------TCCATA-GGCTTAAAGGGTCATGCTTTTACATTCCTTC----
CATAT-C 1352

Qy      1346 TCAGGAGTTCTGTGAGCTATGGGAAGGCCATTGGTTGTATTTGCTACTTTTACTT--
TCA 1403
              |||  || || ||| || | ||| | || |  || | | | |||   ||| |||
||
Db      1351 ACAG--GTACTATGAAGTAAGG--
AGACTTTTAGGTTTCTTTTTGTCTTAAACTCAGACA 1296

Qy      1404 TCTTCCTCTGCTGTAGAG---
CCATTTAATGTTATTGTCATATGCTGCTGGTGAGGTAAA 1460
              ||| | || |||| |  || | |  |  | | ||     || || |
|
Db      1295 GCTTTGTAAGCAGTAGTGTGTAGATTACAAGAGTTAGACAAA---
AGCAGGCGCGACTGA 1239

Qy      1461 GGTGGGTCCGGGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGGGCCGATTTCAGCAGGA 1520
              | | || |||        |||| ||| |      | |||| | ||| | |
Db      1238 GAAGAGTT--GGTG--------GGGG--AGAAG-----CTTGGGGC--ACTTC--
CTGTC 1200

Qy      1521 GTTCAGAGGGCTTATGATGGATGGTGAGAGATTTGACA-
ACCACCAGAGCACATGTGCTC 1579
              |||       |  || |    |||   | | | || || || ||| | |   ||| |
|
Db      1199 ACTCA----ACACATTCCAGATCACTAAAAAATTTCCACACCCTCTG----
CATTCCCCC 1148

Qy      1580 TGACCCTCTCCTGGGCATTGGTTCCTGCTGGTACCGGGCGGTTCAGA--
CCTTCAAATAG 1637
              | | ||| ||||        ||||     |||    ||| || || |     |
Db      1147 TTGCCCACTCC--------AGTTC---------
CCGGTATTTCTGATTCCATATGTTGT 1105

Qy      1638 GTTGCTTTCAAAAGAGCTTTCAGGCACTT--
ATTGAGAATTAATGTTTAAACAGACATAA 1695
              | |  || || | |   || || |||| |    |   | | ||||  | |   | ||
Db      1104 GGTATTTACCATACTTCTCTCCCTCACTAGGCTCTGGCAAGACTGCTTCAGAGGGGATGC 1045

Qy      1696 TAGCC--
TAGATGAACTCCCAAGAGATCTATTAAATCTTGTGGGCTGAATAAATATCTCG 1753
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                 ||  ||||| | | |  |||| |||  |  |  ||| | | | ||||
|
Db      1044 ATTCCTTTAGAT-TGCACAAAGCGGAGCTGGGAAA-
ATGGCTGGCAGTTTCAGAATCTAG 987

Qy      1754 T-------GCAGGACTGTGCAACAGTAGCCCAGAGCATCC---
TGCCTGTGGGCATCCAC 1803
             |        ||| | || |||| |  | || |||||  | ||| |      | ||
|
Db       986 TCACGATCGCACGCATGAGCACCT----CACA---CATCCATGTCCCT------
ACCCGC 940

Qy      1804
CTCCCAGGTGAGGGCAGTGGGAAGCTGGCCCGACGGCAGCCAGAACTTGTTTCTCACCTC 1863
             | ||| | |          |       | | |||| | | | || |  | ||||||||
Db       939 CCCCCCGCT-----C---------CCGCCCCTGCAGCTGGCTGACC---
TGTCTCACCCA 897

Qy      1864 CCACCAG-CAACCCCCCACCCA---AC--TCTGG----
GCCCCAGGCACACGAAGCACAAG 1914
             |  | | | | |      | |||  ||  |        | | ||    |   | ||
|
Db       896 CTGCTGGCCTATCGAACGGCCAGGACTGTCTGGTTTTGGCTCGTGC---
CTTTGTCCATG 840

Qy      1915 TCT--
CAGGGGACCATTCCCACATTGGGGGATCCTGAGGGAGCCCATCACCGCCTCTTGC 1972
             |||  |   | || || |   | ||   |   ||      | ||| ||||||| |
Db       839 TCTGGCTTAGTTCCTCTCTGTCTATGCTTGCCTCT-----ACCCC--
CACCGCCCCAGGC 787

Qy      1973 -
ATACAACTGTCCACTAGGAGGCACGCCCAGTGTGGGAGAGATGTATGGTCTTGCCTTCC 2031
             |||| ||| |  |  ||         |              ||
||||
Db       786 GGCACAAGTGT----TTGGCCACACAAAACTAGAGATAGAAAAG-
GTGGTAAAAACTTCA 732

Qy      2032 ACCTGTAAAAACTGCACATATGCAAGCCATTTGCACTCTGG-----
AACTGCATGCCGTG 2086
             | | | || | |   ||| || || ||| |         || | | |
|
Db       731 AACTTTTCTAAATTCTC-----CAA--
CAGTTTATTTCTTGTGAATTTCTTCCTTCTTTA 679

Qy      2087
AAAACTCCTAATGGTGTGGAACTTAGTTTGAATTTGAAATCACGCCGCATGCACAAAGGG 2146
             || ||||| | |   ||| |     ||||| |||   ||| |   | ||
||
Db       678 AATACTCCATTTTAAG-AAAACAAA---AAAATTAATTATCTAAAGGCA---
AAGAATGG 626

Qy      2147 ACAGGCCCAGGCCCGACCTCAG--GT--
CATCCGCCCGCTGGCTGCAGAGCATCCCTGGGA 2203
             | ||          | |||| | |  | |         ||| || || | || ||
Db       625 AAAG---------CAACCTTTGTGTTCCTTATAATAACTGACTTCATAAC-
TCTCT---- 580

Qy      2204 GCCA-AGGCG---
```

```
AGGCCCGTGGAGCCTGAGCTTTGTGTAGCTCGAGCTTTGTGTAGCTC 2259
          |||     |||     ||    || || |||     |  | |||
|
Db       579 -CCAGCTGCGTTATGGGATGTGTATAAAAAGCTTC-TGTT-CT-
GAGAACAAAGGAGCAC 524


Qy      2260
GTGCACTTATTATGCACCACCTCCCTTCAGTCACCACTCCTCTTCCTCCGCCATCCTCAT 2319
              |||||   || | |  || |  || | ||| ||  ||| |    | |
|
Db       523 GTGCAGAAATGAGACGAAAAAATCC-ACTGACAGTATTCC-
ATTACACAAATTACTTAAA 466


Qy      2320
TTATACTGATTGCACACCCCCCGCTCAAACAACAATGTCCTTATTATGATGACCATCTCG 2379
            || |  || | || ||||        |||||    || | ||| ||| | |
Db       465 AGATTTTAGT--CAAGCCCC--------
TCAACAGATTCAATTTTAAAATGGCTTT---- 420


Qy      2380
TAGTGGTACATTCCATTCCTATTTAAGGTAAGCCCAAAGCCCACTTTTGGATTTTCTCGA 2439
             |||| | |  |    ||| || || ||  |  |||| |     ||
|||
Db       419 TAGTTAAAAA----AAAAAAATTGAAAGT--GCTTA---CCCAGTAAAAGA----
ACCGA 373


Qy      2440 C--
TGTCCGAGAAAAGTTGTGTAAGCGCCTGCGTTCTTCTGGGTTTGGCTAGATAGGGTT 2497
             |||| ||| ||| |||||    | || | ||||  | |||| |
|
Db       372 AGTAGTCC-TGAACTGTTACGTAAG-----ACTTTTTACAG---
TTGGATC--------T 330


Qy      2498
GTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAGGGTGTCATTTTCTCGCACAATACA 2557
             |||  |   | || |||| ||||| | |||  | |  ||       ||
||     |||
||
Db       329 TTGT--CAAAAGGGGATGG-GGGTGATGGGAGAAAG-----CA-------GCA----
ACG 289


Qy      2558 AC--TCACTGAGGAT---
GCTTCTGTAGAAGTGAGAAACACGATGAGTACATTCAGAATT 2612
             || ||| | | ||| ||| |           |  || || ||| |
||
Db       288 ACAATCAAAAAAGTTCGAGCTGCTGTGG----------CTAGAGGACAAC-
TTCGTGTT 240


Qy      2613
ACAATAACTCACTCTCACTGGGTAACTTCTCATGATAGATTTGTATGATCAATACGGGTC 2672
             | |    | ||| |||   |          |||| ||| | ||  | |
|
Db       239 TCCAGATAGGATTCTTGCTG---------------
TAGAAATGGAACTTCCAGCCAGCAC 195


Qy      2673
TATTTTTATGTCAACTGAACACTGTAGGGTACCTTCCAGTCTTTTTCAAGATTGTTAAAT 2732
             || |     | | |||| | |         | ||| |||
||||||
Db       194 AG---------CATCCTGTCCCAGTAGAGAA-----ATGAGTTTGTCA-----
GTTAAAA 154
```

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Qy        2733
TGAGACAAGTAATTGAATAATTTGTCCTATTTTTATTTTAAAAAAAGTGAATGGACTG-- 2790
               |  | || |||| |||  ||| |   ||  |    |   | |  || | ||  || |
Db         153 C-AAAAAAAAAATTAGATACTGGAACCCAGGCT-------
AGACGAGGTATTGAACCGCG 102


Qy        2791 -AAATGTTAAATG------
TGAATGTACATTTCTTAATTGCAATTTTTCTACTGAGTGTT 2843
               |   ||  ||    ||     ||  | ||  ||   ||| || |    | ||  |
Db         101 CCAGATTTCCTTGCAGCCCTGTCTGCTCAGCTC-
GCATTCCAGTAGGCCAACAG------ 49


Qy        2844 TGCACTATACTTTCTGGAATCTTATTTAACAAAAATAAAGGGAAAAAATTGCTTGAC
2900
                ||| | |    ||| | |||| |  | ||| ||       | | | || | | ||
Db          48 TGCTCGAGGAATTCC-GCAGCTTTTAGAGCAGAA-------GTAACACTTCCGT-AC
1



RESULT 9
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match             31.1%;  Score 5351;  DB 1;  Length 2495;
  Best Local Similarity   44.0%;  Pred. No. 0;
  Matches 1350;  Conservative    0;  Mismatches  962;  Indels  758;
Gaps  182;

Qy           8
CAGGAAATCAGGCCGGGCGCAGTGGCTCATGCCTGTAAGCCCAGCACTTTGGGAGGCGGA 67
               |  |      ||||| |  | |  |||| ||  |  | ||     |||
Db        2495 CTAG-----
CGGCCGCGACCTGCAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTA 2441


Qy          68 GGCGGGTGGATCCA-TTGAGGTCAGGAGCTCA-AGACCAGCC------
TGGTCAACATGG 119
               |  |  ||  | || | |||  ||| || | | | | | |||||    || |||
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```
Db       2440 CATGTTTAAATATATTTTATTTCA--
AGTTAATATAACAGCCATGATTTGTTCATTTAAG 2383

Qy        120
TGAAACCCCGTCTCTACTAAAAATACAAAAAAAAAATTAGCTGGGCGTGTTGGCGGGAG- 178
              |||||        ||  |  ||| ||        |  |  |    | |||| |
||
Db       2382 TGAAA------
TGCTTCGATAAAAACCCCGGTGTCACTTGGTTAAAATATTGGAGACAGA 2329

Qy        179 ---CCTGTAGTCCCAGCTACACGGGAGGCTAAGG----
TGGGAGAATTGCTTGAACCCGG 231
                 |||   ||| ||| |   | | ||  |    |  ||  ||||| || |||
Db       2328 TTAAATGTTAAGCCA-
CTATAGTAGTGACTCTGGTTCTTTAGACTATTGCATGTACC--- 2273

Qy        232 GAGGCGGAGGTTG-CAGTGAGCT--
GAGATTGCACCATTGCACTCCAGCCTGGGCGACAG 288
                 ||| | |||| ||   || |||| |||||    | ||        | |
Db       2272 ----------TTGTTAATGAACTACAGGAATGCA-CATTGATATAATGCAC-
AATGTCTT 2225

Qy        289
AGCAAGACTCTCTCAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGACCACAGT 348
                  || |  ||| ||                     ||   | ||   |
|
Db       2224 CACATGTCTCAATC--------------------------CTC----
ATTCCTCTTCCTT 2195

Qy        349
GGTAGCCACCTGGCCTAATGCTGTGTTTTTGTACCTGACAGGGGTCACTCATTTTAGGC- 407
                   ||| |  ||||||         ||| ||   || |  || | |
|
Db       2194 TCATGCCTC----CCTAATG-------------CCT--CA---
GTATCCAATATAAAACT 2157

Qy        408 ACAACTCCTTC-
ATTCTTTGTGAAATTAGTGAGTTTCCTTCTACCCGTCACCAGATTCAA 466
                ||||  || |  |||||| |  || |    |  |  | | ||| |||| 
Db       2156 ACAAAAACTACTGTTCTTTTCG-TTTGAGTGGTATTTAATTAAAACTTCA----
ATTC-- 2104

Qy        467
TATGTTCTATTAATACACCGATAACCACAGGGGAAGGGCACTTGTCGCTCTCCCACCTGG 526
                |||||| | |                |||||                        ||
|
Db       2103 TATGTTATTT--------------CCACAG-------------------------
TCCAGT 2082

Qy        527
TTACCACAGTCTCCATGGGTCTTTTGCCGTGACCACAAATAAAGGAAACACTCATCACTA 586
                   |  |     || || ||| |    |||||||| ||      |   || ||
||
Db       2081 AATTTATTTTAAATTTGAGTAATTT-
CAAATTCCACAAACAAAACTGAAGAACAGCAATA 2023

Qy        587 GTATCTAAGTCGGGCTTTACAGTAACTATGCACCTTCTGTGTGCT---
TCACCTCACTCT 643
                || |    || | |||    || | ||| ||  ||| ||  |||| || |
|
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Db        2022 TTTT----GTTTGAATTTCTCTCTTCTGTACAC--
TCAGTGATCTAAAACACCACAATAT 1969

Qy         644 CTACTTCAAACAGCCCATGGAGGGAGGTATTATTATACTC-
CTTATGTTGACAGTGAAGA 702
               | |     |  | ||| ||    ||||| |  ||| |||||  || |       ||
|| 
Db        1968 CCAACATACACAAACCTC--AGGGAAGGGTTAGTAAACACACACAAGAT-----TG--
GA 1918

Qy         703 ATC-TGAGGCCCAGAGAGGTTGGGGACTTGA---
GTAAAGTCACACAGCCCTGAGAGGCA 758
               ||| ||  || |        |  | ||| ||  | |  ||| |||||     | |
|||
Db        1917 ATCATGGTGCTC--------TTTGCTCCTGAATGGAATGGTCCCACAG----
AAAAAGCA 1870

Qy         759
GGACCAGGGTTCCATTCCTGCTCTATCCAGTTCCAAGCCCTTGTGTTTTCCATTATGTTT 818
               ||||    | | | ||  |  |    ||  | | |    || || ||||
Db        1869 ----CAGG------ATACAGCACAA--CA--TAAGGGCACCTG----TTACA-
TATGAAG 1829

Qy         819 AGTGCCTCT-TTGCTAACAGCAAC-
ATCTGCAAGATTTGTGTTGGTTTTGATGGAGAACT 876
               | ||     | ||| ||    | || ||||               | |||| |||
Db        1828 TGAGCAAAACATACTAGCATTTTCTATATGCA----------------
TAATGGGGAA-- 1787

Qy         877
CTAGCTCATCCACATGCTAGTGCCCAAGTGGTGGAGGGGCCACCTCAGCAGGTGGGTTCT 936
               || ||| |        | |||     |  ||| |||||| |  || |     ||
Db        1786 -----------ACCTGC---------ATAGGTTAGAGGGCCTTTTACGCTCAT---
TTAA 1750

Qy         937 GAATGCAGCCAA---GGCTGTCCCC----GCAATGGG-
TGAGACTCGCTCCAACTGCCC- 987
               ||| ||| ||| | |||| |        |||| || || | || |||  ||
Db        1749 AAAT-CAGGCAAGTTGTCTGTAACATTTTTCAATAATCTGGGAAGCACTGCAAT--
CCAG 1693

Qy         988 -GCCCTCAGAGCAGGTGCCT-AAGTCCTCCCTGGCACTGGCAGGCCTTACCT-
CACAT-T 1043
               | |  | | || | |    | |||  | ||||||||| || | ||| | |   |||
|
Db        1692 TGTACGATGTGCTGATTAGTGTTGTCTTTGTTGGCACTGACA-
GTCTTGCATGGTCATAT 1634

Qy        1044
GCTAAATTAAAGCAATGCAATTCCTCTTGGGTAAGAGGAATTCCTCCTTCTTTACTAACT 1103
               ||      || ||  || |    |                    |||| ||
Db        1633 GC----------CAGTGTTTTTGCTTTAG--------------------
CTTTTCTTTGA 1604

Qy        1104 GATCCCCAGCAAGGAAATAAAATG---
TTAGGCTTTAAAAATCCCTACTTTGTCATATCA 1160
                   |||     | | |||||  |||| |       ||| | || |||||
                |
Db        1603 ATAAAACAG------ATTTAAATGCATTTAGAC------AATACGTA-
TTTGT------A 1563
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Qy        1161 GACTATATTCTAAAACTATATTTGAGCGAAACC---------
TGTCATTGCGTCTAATTT 1211
               || | |  | |||| |||| || ||  |      | || ||| ||
|||
Db        1562 AGCTGTTTACATACACTAAATTTAAGAGATTCAATATTAGAGTTTCTTTGTTTC---
TTT 1506

Qy        1212 CAAATATACAGAAT-CTCCTTAAGAGCTGTTGC--CTTATT--
TTTTTGTAAAGCCTCTC 1266
               ||  |||||| | |   | | |||| || |  || |  | ||| || | |||  ||
|||
Db        1505 AAACACTACAGAGTGCAAATCAGGTTCT-TCACAACAGATTGAATATTGAGCAG-
TTCTT 1448

Qy        1267 TGACATCAAATGGGGAGAAATGGTGGCACCTCCAG----
ACACCCTGAAACTACACACCA 1322
               |  |   | ||||| | | || |  || |    | || |||||||| |
||
Db        1447 TAAAGAAAGAGGGGGAAGAAAAAAAGC-
CCAAGTGAATAAAACATTGAAACTATTCCCC- 1390

Qy        1323 TTTCTTCCCTGCTCAGCTTCTGCTCAGGAGT--
TCTGTGAGCTATGGGAAGGCCATTGGT 1380
               ||| |||| |  | ||   | ||   ||||| || ||       |||
|||
Db        1389 -TTCGAAAAT----
AAATTCTAAAATGATGTGGAATGTGAAATAAGGTTTTAACATAGGT 1335

Qy        1381 TGTATTTGCTACTT-TTACTTTCAT---------CTTCCTCTGCT----GT----
AGAGC 1422
               |   | | |  ||| ||     |||| |    |     || |||
|
Db        1334 GATCCAAGTTTATAGTTAGAAACAAAAAGAAGTCCTTCATGAAATAAAGGTTACAAGAAC 1275

Qy        1423 -CATTTAATGTTATTGTC----ATATGCTGC-TGGTGAGGTAAAGGTG-------
GGTCC 1469
               | ||  |||| |  |    ||| |||   ||| ||||||| |          ||
|
Db        1274 ACGTTGCCTGTTTTCCCCCATTATAAACTGAGAAGTG-
GGTAAAGACGATGTTTCAGTAC 1216

Qy        1470 G------GGTGCCTTCC----CAGGGGTT------AGAGGATGTTCAAAGGGCC-
GATTT 1512
               |      |||| || |     ||| | ||      | | ||| |  |  ||| |
|
Db        1215 GAAAATAGGTGACTACAGGATCAGCGCTTCATCTCACATGCTGTACCCAAAGCCAGGCTG 1156

Qy        1513 CAGCAGGAGTTCAGAGGGCTTATGATGGATGGTGAGAGATTTGACAACCACCAGA--
GCA 1570
               || |   || |    || | | | |    | | | || | | |||| |  |
Db        1155 TGGCTG----TC------CATACGGTG------
GTGCGGTATAACCATAACCAAAAGGTG 1112

Qy        1571 CATGTGCTCTGAC--CCTCTCCTGGGCATTGGTTCCTGCTG---
GTACCGGGCGGTTCAG 1625
               | ||  |   ||| | | |        ||| |||||||||  | |   ||  |
|
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Db      1111 CCTGGGGAGGGACGGCAACAC--------
TGGGTCCTGCTGTCAGCATCAACTGGGGCTG 1060

Qy      1626 ACCTTCA--AATAGGTTGCTTTCAAAAGAGCT--TTCAGGCACTTAT-
TGAGAATTAATG 1680
             ||| | |  ||| ||||| | |||      |||| |||   ||| | | ||    |
||
Db      1059 ACCATAAACAATGGGTTG-
TGTCTCTGTAGCTTGTTCTTCTTCTTTTCTCAGTGATTCTG 1001

Qy      1681 TTTAAACAGACATAATAGCCTAGAT---
GAACTCCCAAGAGATCTATTAAATCTTGTG-- 1735
               | | ||| |   || ||   |     | ||||| || ||     | | | |
Db      1000
AAGCATCTAATTTATCCACCTTTGTCAAGTACTCCTTCATGACCTGGATGAAATAGGGCA 941

Qy      1736 -GGCTGAATAAAT-ATCTCGTGCAGGACTGTGCAACAGTAGCCCAGA--
GCATCCTGCCT 1791
              |||   |||  || ||| ||||     |  || ||||  |   ||   ||||
||||
Db       940 TGGCAAAATCCATGATATTGTGCC--TCCATG---
CAGTTTCTAGGACGACATCTGGCCT 886

Qy      1792
GTGGGCATCCACCTCCCAGGTGAGGGCAGTGGGAAGCTGGCCCGACGGCAGCCAGAACTT 1851
                        ||   | |  ||||| |   |||        |  || | | ||| |
|||
Db       885 TAAAAGAT---CGTAACAGGTAA--ACAG------ACAAGCTCCAAAGCACTC---
TCTT 840

Qy      1852 GTTTCTCACCTC-----CCAC--
CAGCAACCCCCCCACCCAACTCTGGGCCCCAGGCACAC 1904
              |||||  |  |    | |||| ||| |   |  || |||| ||
Db       839
TTTTCTTCCTGCAAAAACCACTGCAGGAGTTCTTCAGCCAATTC--------------A 795

Qy      1905
GAAGCACAAGTCTCAGGGGACCATTCCCACATTGGGGGATCCTGAGGGAGCCCATCACCG 1964
              | | | ||| ||| ||||| | |  | |  | |||||     || |   ||
Db       794 GTATCTTTAGATTCAGAAG--CA-TACTGCATT---
GCATCCTTGTAAAGGCTGTCT--- 744

Qy      1965 CCTCTTGCATACAACTGTCCACTAGGAGGCACGC--------
CCAGTGTGGGAGAGATGT 2016
              ||||||  ||| ||| |||| |        || ||   |||| |
|
Db       743 -TTCTTGC--ACAGCTCTACACTCTGTTTCCAGCGATTGTTGCCTTTG-
AAGAGATAAGC 688

Qy      2017 ATGGTCTTGCCTTCCACCTGTAAAAACTGCACATATG------
CAAGCCATTTGCACTCT 2070
              |        ||  | | ||||  |  | ||     |||    ||| | | |||
|
Db       687 A-------
GCAATTCTCCTGAACTCAATGAGTTCATGTTTTTCCAAACGCTGAGCAAGCG 635

Qy      2071 GGA--ACTG-CA----TGCCGTGAAAACTCCTAATGGTGT-----GGAACT--
TAGTTTGA 2117
              || | || ||     ||| ||||  ||  | ||| || ||||    |   || || |
Db       634 AGATATTGTCAAAGTTGTCAT--
```

```
AAGCATCTATTGATGTTCGCAGAGCCTGATAATCTTC  577

Qy      2118 ATTTGAAATCACGCCGCATGCACAAAGGGACAGGCCCAGGCCCGACCTCA-
GGTCATCCG 2176
                | || ||| |    |  || ||| |   || | ||| |    |  | | ||| ||
|
Db       576 TTCTGTAAT-AAAAAGATTGTTCAATGATTCATTCACAGATTTGTTGTTATGGT--
TCTG 520

Qy      2177
CCCGCTGGCTGCAGAGCATCCCTGGGAGCCAAGGCGAGGCCCGTGGAGCCTGAGCTTTGT 2236
                  ||| ||| |||  || |  ||        | ||  ||
Db       519 --AACTGAACGCA---AATAC---GGTTTCA--------CCAGTGGTAGCTGT--
TTAAC 478

Qy      2237 GTAGCTCGAGCTTTGTGT-
AGCTCGTGCACTTATTATGCACCACCTCCCTTCAGTCACCA 2295
                | |||| || |   ||   || || |      | ||  ||| ||| || |  || ||
||
Db       477 CTTGCT-GAAATAATTGACTGCACGAG-------TGTGATCCA--
ACCGTGGAGACAGCA 428

Qy      2296
CTCCTCTTCCTCCGCCATCCTCATTTATACTGATTGCACACCCCCCGCTCAAACAACAAT 2355
                |      |  | || || |  |||||||                           |||||||
Db       427 C-------CATCAGCAA--ATCATTT-------------------------
AACAACAGA 402

Qy      2356
GTCCTTATTATGATGACCATCTCGTAGTGGTACATTCCATTCCTATTTAAGGTAAGCCCA 2415
                | | | |                 || ||| |  || || ||  ||
|||
Db       401 GGCTTGAAT------------TCTAAGTAGAACTGT--
ATTGCTCTGTAGTATAGTTCCA 356

Qy      2416 AA--
GCCCACTTTTGGATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGCGCCTGCGTTC 2473
                | | | || || |  | |      | || |||            || ||| |
|||
Db       355 CATTGGCAACCTTGGTAAT------GATATCTTTGAA---------TTGC-
CCTTCTTTC 312

Qy      2474
TTCTGGGTTTGGCTAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAG 2533
                 | || |  | || | | |    || |||      ||| || | ||   ||||
Db       311 --CAGGCATCAGTTGGAT--GATT-----CATC------ATG----
GTAATTATGGCAT- 272

Qy      2534
GGTGTCATTTTCTCGCACAATACAACTCACTGAGGATGCTTCTGTAGAAGTGAGAAACAC 2593
                | |||| |||    ||| | ||| |       | |               | |
Db       271 --TATCATATTCT----TCATACTTGTCA-TACAAAAACACCAGT-----
TCTGCCCAAA 224

Qy      2594 GATGAGTACATTCAGAATTACAATAACTCACT-
CTCACTGGGTAACTTCTCATGATAGAT 2652
                ||||||   ||| |         | |||    | | |||| |  ||| |
Db       223 GATGAGCTTGTTCTGC--------
AGCTCTTAGCACCTTGGGAATATTCAC--------- 181
```

```
Qy      2653 TTGTATGATCAATACGGGTCTATTTTTATGTCAACTGAACA-
CTGTAGGGTACCTTCCAG 2711
             || | ||                   | ||||| || |||    || ||
Db       180 --------TCTAGAC-------------------CAGAACAGCTCCAGG--
TGCTCCC-- 152

Qy      2712 TCTTTTTCAAGATTGTTAAATTGAGACAAGTAATTGAATAATTTGTCCTATTTTTATTTT 2771
             || ||||| ||  |||||| ||  ||| |||| |||  ||| ||
Db       151 TCATTTTC-TGAGGCTTAAATTTAG---AGT-ATAGAATAG------
CTAATT------- 110

Qy      2772 AAAAAAAGTGAATGGACTGAAATGTTAAATGTGAATGTACATTTCTTAAT--
TGCAATTT 2829
                   ||| ||   | |||     || |  |  || || || | | |||
|
Db       109 -----CAGTAAACATTC--CCATG-----
TGAGCTCGCTCAAGTCCCAGTGCTGC----T 66

Qy      2830 TTCTACTGAGTGTT-TGCACTATACTTT---CTGGAATCTTATT-
TAACAAAAATAAAGG 2884
             | | ||   ||| |  || || |    |   | || |||  || | |
|
Db        65 TCCAACATGGTGATCAGCTCTTCAAAATAGCCACGATCCTGATAGTAGCCAGTA-----G 11

Qy      2885 GAAAAAATTG 2894
             |  || || ||
Db        10 GCCAACAGTG 1


RESULT 10
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match            30.6%;  Score 5267;  DB 1;  Length 2120;
  Best Local Similarity   42.0%;  Pred. No. 0;
  Matches 1253;  Conservative   0;  Mismatches  721;  Indels 1008;
Gaps  181;
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```
Qy          17
AGGCCGGGCGCAGTGGCTCATGCCTGTAAGCCCAGCACTTTGGGAGGCGGAGGCGGGTGG 76
             |||||  |  | ||        ||| |  | || ||      |  |||||
Db           2 AGGCC-TGTACGGAAG--------
TGTTACTTCTGCTCTAAAAGCTGCGGA--------A 44

Qy          77
ATCCATTGAGGTCAGGAGCTCAAGACCAGCCTGGTCAACATGGTGAAACCCCGTCTCTAC 136
            |||         || | ||  |  |  ||       | ||  | | |  |   |
|
Db          45 TTCC-------TCGAGCACTGTTGGCCT-ACTGGAGTGC-
TGAAGTAGGCGCGGACGTGC 95

Qy          137 TAAAAATACAAAAAAAAAAATTAGCTGG-
GCGTGTTGGCGGGAGCCTGTAGTCCCAGCTAC 195
                 | |             |||| ||||| | || ||| |  | ||| ||
|
Db          96 --CCGGTGC--------------
CTGGCGCGTGGTAGCAGGCGCCCGGTGCCCCGGC--C 137

Qy          196 ACGGGAGGCTAAGGTG----
GGAGAATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGA 250
                 | || | || |    || |||     ||| || ||       || |
|
Db          138 GGCGAAGACCATGGCGTTCATGGTGAA-------GACCATGGTGG--------
GCGGCCA 182

Qy          251 GCTGAGATTGCACCATTGCACT-
CCAGCCTGGGCGACAGAGCAAGACTCTCTCAAAAAAA 309
                 |||||  | |||    ||||  |||||||| | | |
Db          183 GCTGA---AGAACCT---
CACTGGGAGCCTGGGAGGCGGCG-------------------- 217

Qy          310
AAAAAAAAGAAAGAAAGAAATCAGAAAATCGACCACAGTGGTAGCCACCTGGCCTAATGC 369
              |  | ||| ||| | | ||    ||| | | |  |  | | ||| | |
||
Db          218 -AGGATAAGGGAGATGGGGACAAG----TCGGCAGCCGAAG----CTCAGGGCATGA-
GC 267

Qy          370
TGTGTTTTTGTACCTGACAGGGGTCACTCATTTTAGGCACAACTCCTTCATTCTTTGTGA 429
                 | |   |||    ||| ||  |     ||| || |      |
||
Db          268 CG-GGAGGAGTAC----GAGGAGTATC-------AGAAGCAACTCGTGGA-----
AGAGA 310

Qy          430
AATTAGTGAGTTTCCTTCTACCCGTCACCAGATTCAATATGTTCTATTAATACACCGATA 489
              |  | | |                     | |              || ||| |
|
Db          311 AGATGGAG--------------------CGG------------------
GATGCACAGTTC 333

Qy          490
ACCACAGGGGAAGGGCACTTGTCGCTCTCCCACCTGGTTACCACAGTCTCCATGGGTCTT 549
              |  ||||| ||||||       |  | | | |||||| || | ||  |
Db          334 A-CACAGAGGAAGG--------------CAGAGCGGG---CCACA--CTGC--
GGAGCCA 371
```

```
Qy          550
TTGCCGTGACCACAAATAAAGGAAACACTCATCACTAGTATCTAAGTCGGGCTTTACAGT 609
                 |  |||  |  |||||||  ||      |   |  |||      ||  |
                 ||||
Db          372 CTTCCGAG---ACAAATACCGG-------CTACCCAAGAA-------CGAG----
ACAG- 409


Qy          610
AACTATGCACCTTCTGTGTGCTTCACCTCACTCTCTACTTCAAACAGCCCATGGAG---- 665
                             || | ||  || ||        || | ||  |||||
Db          410 -------------ATGAGAGC--CAGATC-----------
CAGATGGCAGGTGGAGACGT 443


Qy          666 GGAGGTATTATTATACTCCTTATGTTGACAGTGAAGAATCTGAGG----
CCCAGAGAGGT 721
                 ||||         | | |   | | |   || ||| ||||    | |||||
                 |
Db          444 GGAG--------CTGCCCCGGGAGCTGGCCAAGATG-ATC-
GAGGAGGACACAGAGGAGG 493


Qy          722 TGGGGACTTGAGTAAAGTCACACAG-CCCTGAGAGGCAGGACCAGGGTTCC------
ATT 774
                 || |        |  ||| | ||| | |    | |  || |||| ||||
Db          494 AGGAG------GAGAAGGC-CTCAGTCCTTGGGCAGCTGG-
CCAGCCTTCCTGGCTTGAA 545


Qy          775 CCT--
GCTCTATCCAGTTCCAAGCCCTTGTGTTTTCCATTATGTTTAGTGCCTCTTTGCT 832
                 ||| |||| || || | | |||| |   ||| ||   | | |||
Db          546 CCTGGGCTCACTCAAGGACAAGGCCCAGG------CCACACTG----GGGGATCT---
CA 592


Qy          833
AACAGCAACATCTGCAAGATTTGTGTTGGTTTTGATGGAGAACTCTAGCTCATCCACATG 892
                 | || | || ||| ||| || | |   |     |||       ||| |
                 |
Db          593 AGCA--ATCAGCTG--AGAAGTGTCACGTCAT-----GTGACCACT------
TCCCCGGG 637


Qy          893 CTAGTGCCCAAGTGGTGGAGGGGCCACCTCAGCAGGTGGGTTCTGAATG---CAGC--
CA 947
                   ||   || | ||  || |||||  |    || | ||| |  || ||    || |
                 |
Db          638 ---GTTACCCACTG--GGCTGGGCCCC-----
CATGAGGGCTAAGAGTGTGTCAACTTCC 687


Qy          948 AGGCTGTCCC---
CGCAATGGGTGAGACTCGCTCCAACTGCCCGCCCTCAGAGCAGGTGC 1004
                 ||| | ||| ||||      ||| | || ||||  || ||     |  ||
                 |
Db          688 AGG--GACCCATACTCCATTTG-GGGCTTTGTTTCCCTTGCC--CCATC----
CTAGTTC 738


Qy          1005 CTAAGTCCT------
CCCTGGCACTGGCAGGCCTTACCTCACATTGCTAAATTAAAGCAA 1058
                 | |||| |||       ||  || |||   || |||| | || |||   | |
Db          739 C-AAGACCTTTCCCATCCATGCCC---
CAAGCCTATCTTCTGGTTTC------------- 781
```

```
Qy         1059
TGCAATTCCTCTTGGGTAAGAGGAATTCCTCCTTCTTTACTAACTGATCCCCAGCAAGGA 1118
           |||||||  | |  ||| ||   | ||  |||| |||    | |||  || |
Db          782 -----TTCCTCTCCGCTGGGAGTAAAGTCCCCATCTTCACT-----
CTACCCTTCAGG-- 829


Qy         1119 AATAAAATGTTAGGCTTTAAAAATCCCTACTTTGTCATATCAGACTAT------
ATTCTA 1172
                              |  |||| ||   ||  |||| || |       | |
|
Db          830 ------------------ACCCTCCCCAC-----
CAGCTCAGCCTGTGGAGGCCTCCCA 865


Qy         1173 AAACTAT---ATTTGAGCGAAACCT-----
GTCATTGCGTCTAATTTCAAATATACAGAA 1224
                 | | |   | |  ||| |||     | ||| ||  | || |||    | ||||
|
Db          866 AGATTGTAGGAATAGGCCCATCCCTCTCTGGCCATGGC-
CCCAAGTTCCTGCACACAGGA 924


Qy         1225
TCTCCTTAAGAGCTGTTGCCTTATTTTTTTGTAAAGCCTCTCTGACATCAAATGGGGAGA 1284
                | ||  ||||           | |  | | |     |||
|
Db          925 GCACCCACAGAG-------------------
AGACACACACAGGACACAA--------A 956


Qy         1285 AATGGTGGCACCTCCAGACACCCTGAAACTACACACCATTTCTTCCCTGCTCAG-
CTTCT 1343
                |   |||||| | |||| |  | ||| ||| ||      | |||| || ||| |
Db          957 ACCCCTGGCACGTTCAGAGA--CAGAAGCCACAGAC----
ACATCCCGGCACAGACAGAC 1010


Qy         1344
GCTCAGGAGTTCTGTGAGCTATGGGAAGGCCATTGGTTGTATTTGCTACTTTTACTTTCA 1403
                 | || |                ||||||           ||| | ||    |
||
Db          1011 ACACACG-------------------AGGCCA------------
GCTCCCTTGCGTGTC- 1038


Qy         1404
TCTTCCTCTGCTGTAGAGCCATTTAATGTTATTGTCATATGCTGCTGGTGAGGTAAAGGT 1463
                | || || | |     |||                       |  ||
Db          1039 -CAGCCCCTCCAG--ACACCA--------------------
CCACT-------------- 1061


Qy         1464
GGGTCCGGGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGGGCCGATTTCAGCAGGAGTT 1523
                 | |   | || || | |    |||| |||  || |    || |||||||
Db          1062 -----CAGAAAC--TCTGAGAG---AGAGCATGGGCAGACACCC----
TCAGCAG----A 1103


Qy         1524 CAGAGGGCTTATGATGGATGGTGAGAGATTTGACAACCACC---AGAGCACATG--
TGCT 1578
                 |||  ||| |                 ||| |     ||||| |   | ||
||
Db          1104 CAGGAGGCCT--------------
GAGTTCCAGTCTCCACCTTTATTGTTCTTGAAAGCC 1149
```

```
Qy        1579 CTGACCCTCTCCTGGGCATTGGTTC--
CTGCTGGTACCGGGCGGTTCAGACCTTCAAATA 1636
               |   |  |||| ||| ||  || || |  |||   |  ||| |   || |   | |||
Db        1150 CCTGCTCTCT-CTGAGCCTTATTTCATCATCTGTAAAATGGGAAT---
GTCCT------- 1198


Qy        1637 GGTTGCTTTCAAAAGAGCTTTCAGGCACTTATTGAGAATTAATGTTTAAACAGACATAAT 1696
               |  ||  ||| ||| | |  ||||| |||                        || ||| | |
|
Db        1199 GAATGACTTCTAAGGCTCTTTCTGGC-------------------TTGAACTGTC---
AG 1236


Qy        1697
AGCCTAGATGAACTCCCAAGAGATCTATTAAATCTTGTGGGCTGAATAAATATCTCGTGC 1756
               |||| ||   |   ||||              ||                    || |||   |
||
Db        1237 AGCCAAGCCCACATCCC---------------TC--------------------
CTTGGGC 1262


Qy        1757 AGGACTGTGCAACAGTAGC--
CCAGAGCATCCTGCCTGTGGGCATCCACCTCCCAGGTGA 1814
               |||    ||| ||  || ||| ||| ||| || |     ||| ||||
||
Db        1263 AGG-----GCAGCAGCTGCTGCCACAGCCTCCAGC-----GGCTGCCAC--------
TGT 1304


Qy        1815 GGGCAGTGGGAAGCTGGCCCGA-----------CGGCA----
GCCAGAACTTGTTTCTCA 1859
               ||||  |||| ||| ||  |||              ||||   |||| |   ||   ||
Db        1305 GGGCTCTGGG-AGCCGGGAGCGATGCTGTGTGAGAGGCAGAGTGCCA-
AGGATGAAGCT-G 1361


Qy        1860 CCTCCCACCAGCAACC--CCCCA-
CCCAACTCTGGGCCCCAGGCACACGAAGCACAAGTC 1916
               | | | ||| || | ||| |  | |||||||||  ||| |    ||| |
||
Db        1362 GCACTGAACAGTAAGCGGCTCCAGGCCTCCTCTGGGCCCAGGGCCC----
AGCCAATTTC 1417


Qy        1917 TCAGGGGACCATTCCCACATTGGGGGATC-CTGAGGGAGCCCATCAC------
CGCCTCT 1969
               |   | |  |||| |  | | |  || |||| ||||  |         |
|||||
Db        1418 T----GTTCTGTTCC--TGTAGAACGCTCTCT---
GGATTCCATAGCTGGAATCTCCTCT 1468


Qy        1970
TGCATACAACTGTCCACTAGGAGGCACGCCCAGTGTGGGAGAGATGTATGGTCTTGCCTT 2029
                |  || | || | ||  || ||   | | || |           || ||  | |
||||
Db        1469 --CTTAGCTCAGTGAAAAATAAAAATC-CCAAATG----------GTGTG--
CCTACCTT 1513


Qy        2030 CCACCTGTAAAAACTGCACATATGCAAGCCATTTGCACTCTGGAACTGCATG-----
CCG 2084
               || | |   ||||       ||  |||  | | ||| |  | |  |
|||
Db        1514 CCCAC--TTCTTACTG-------GCTT-CCA---
GGAGTCTTGGAGTTCATAGCCCCCCG 1560
```

```
Qy        2085 TGAAAACTCCTAATGGTGTGGAACTTAGTTTGAATTTGAAATCACGCC----
GCATGCAC 2140
                |     |  | |III |II | II              |     | III       || |
|||
Db        1561 AGCCTGC-CTTAAAGGGGT-GTCCTCC-----------ACCCCCCACCTACAGCTT-
CAC 1606

Qy        2141 A--AAGGGACAGGCCCAGGCCCGACCTCAG-GTCATC----
CGCCCGCTGGCTGCAGAGC 2193
                | |  |||| ||| |     || |  || | ||        | || ||| |||
Db        1607 AGGAGGGGAGAGGGCAT--CCAGTGCTAGGAGTAGAAGTGTCTCCAGCT--
CTG------ 1656

Qy        2194 ATCCCTGGGAG-CCAAGGCGAGGCCCGTGGAGCCTGAGCTTTGTG---TAGCTC-
GAGCT 2248
                    || || ||  || |   || |||   |||| |||| || || |   ||| ||| |
|||
Db        1657 TTCTCTTGGGGCCCTGGGTGAAG---
GTGGGGTCTGGGGCTTATGAAATAGGTCTGGGCT 1713

Qy        2249 TTGTGTA-GCTCGTGCA--CTTATTATGC----ACCA-----CCTCC----CTTCA--
GT 2290
                ||| | | | | ||| || |||||        |   |        |||| | |||
|
Db        1714 TTGAGGAGGATGGGAGCAGCCTCATTATGTGGGGAAGATGGGGCCTCTGGGGCGTCACTGA 1773

Qy        2291 CACCACT-------CC---TCT--
TCCTCCGCCATCCTCATTTATACTGATTGCACACC- 2337
                    |||||          ||    ||   || | || || |        || |||||
||
Db        1774 GACCACAGGTGGGGCCGGGGCTGGACCGCAGCTGTCTTGGGTGCCTGTGCCTGCACCCCT 1833

Qy        2338 CCCCGCTCAAACAAC----AATGTCCTTAT--
TATGATGACCATCTCGTAGTGGTACATT 2391
                    || | ||| || ||    |||| |   | | | |        | || |  ||
|
Db        1834 CCTCACCCTAGAGACGGAAGATGTGCAAAAAGAAAGAAG--------
GAAGGGCAAC--T 1883

Qy        2392
CCATTCCTATTTAAGGTAAGCCCAAAGCCCACTTTTGGATTTTCTCGACTGTCCGAGAAA 2451
               ||||||             || |   | ||| | |||       |||| |
Db        1884 GCATTCC-----------AGCCC----CACACTGT--GAT------
GACTTT-------- 1912

Qy        2452
AGTTGTGTAAGCGCCTGCGTTCTTCTGGGTTTGGCTAGATAGGGTTGTGTCCCTCTATGG 2511
                          | |||| ||| ||||                       ||||||
Db        1913 ----------GAGCCT--GTCCTT------------------------
TCCCTCCT--- 1932

Qy        2512
AATGGAGAGTGATGTGGGCAAGGGTGTCATTTTCTCGCACAATACAACTCACTGAGGATG 2571
                          || ||  |||| |||| || |         || |
Db        1933 --------------TGAGCC----TGTC--TTGCTTG-----------
TCCC-------- 1953
```

```
Qy       2572
CTTCTGTAGAAGTGAGAAACACGATGAGTACATTCAGAATTACAATAACTCACTCTCACT 2631
               ||||| ||                 | ||| ||            ||| | | ||
Db       1954 ---CTGTAAAA---------------TGAACAGTCC----------
CCCTCTCCCCCAAA 1985

Qy       2632
GGGTAACTTCTCATGATAGATTTGTATGATCAATACGGGTCTATTTTTATGTCAACTGAA 2691
               ||||     |||| |           ||||   | | |||| ||   ||
|||
Db       1986 TAGTAATAATACATGTT------------
TCAAAGGGTGACCATTTATAAAGCATATGA- 2032

Qy       2692
CACTGTAGGGTACCTTCCAGTCTTTTTCAAGATTGTTAAATTGAGACAAGTAATTGAATA 2751
                          || | | |||| |||||      |||| |
Db       2033 -----------------CAAACCATATCAA------TAAAT--------
GTAA------- 2054

Qy       2752
ATTTGTCCTATTTTTATTTTAAAAAAAGTGAATGGACTGAAATGTTAAATGTGAATGTAC 2811
                 |  ||| || |  ||||||||   || || |        | ||||||   |
|
Db       2055 ------CTCATTCTTTTAAAAAAAAAAAAAAAAAGGCC---------
ACATGTGCTCGAGC 2099

Qy       2812 ATTTCTTAATTGCAATTTTTCTACTGAGTGTTTGCACTATAC 2853
                  ||||   | | |              | ||| ||
Db       2100 ----------TGCAG-GTCGCGGC----------CGCTAGAC 2120


RESULT 11
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match          30.2%;  Score 5196.5;  DB 1;  Length 2120;
  Best Local Similarity   43.3%;  Pred. No. 0;
  Matches 1207;  Conservative    0;  Mismatches  792;  Indels  789;
Gaps  169;
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Qy          7 TCAGGAAATCAGGCCGGGCGCAGTGGCTCATGCCTGTAAGCCC--------
AGCACTTTG 58
              ||   |      ||||| |  | |  |||| ||   | | ||
|||
Db       2119 TCTAG-----
CGGCCGCGACCTGCAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTA 2065

Qy         59 GGAGGCGGAGGCGGGTGGATCCATTGA-------
GGTCAGGAGCTCAAGACCAGCCTGGT 111
              ||  ||   || | | |||||     |||| ||| | |
||||
Db       2064 AAAGAATGA----GTTACATTTATTGATATGGTTTGTCATATGCTTTATA----
AATGGT 2013

Qy        112
CAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAAAAAATTAGCTGGGCGTGTTG 171
              ||| |  ||||| | | |  |  | |        | |   ||| | |
||
Db       2012 CACCCT-TTGAAA---
CATGTATTATTACTATTTGGGGGAGAGGGGGACTGTTCATTTTA 1957

Qy        172
GCGGGAGCCTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAGAATTGCTTGAACCCGG 231
              |||  |  | |    | ||| || || || | |   ||   | | | | | |
|
Db       1956 CAGGGGACAAGCAAGACAGGCT-CAAGGAGGGAAAGGACAGGCTCAAAG--
TCATCACAG 1900

Qy        232 ---GAGGCGGAGGTTGCAGTGAGCTGAGATTGCACC------
ATTGCACTCCAGCCTGGG 282
              | |||| | |  ||||||     ||   ||| |     ||||||  | ||
Db       1899 TGTGGGGCTG-GAATGCAGT----
TGCCCTTCCTTCTTTCTTTTTGCACATCTTCC---- 1849

Qy        283
CGACAGAGCAAGACTCTCTCAAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGAC 342
                 | ||||              | |  || | |    |||
Db       1848 -----------GTCTCT---------------
AGGGTGAGGAGGGGTGCAGG-------- 1823

Qy        343
CACAGTGGTAGCCACCTGGCCTAATGCTGTGTTTTTGTACCTGACAGGGGTCACTCATTT 402
              |||||    || ||  |     ||| ||         || |
Db       1822 CACAG-----GCACCCAAGACAGCTGCGGT---------
CCAGCCC-------------- 1791

Qy        403
TAGGCACAACTCCTTCATTCTTTGTGAAATTAGTGAGTTTCCTTCTACCCGTCACCAGAT 462
              ||| |||  |||   |||| |  |||    ||   ||  || | | || |||
|
Db       1790 -CGGCCC--CACCTGTGGTCTCAGTGACGCCCCAGAGGCCCCATCTTCCC--CA-
CATAA 1737

Qy        463
TCAATATGTTCTATTAATACACCGATAACCACAGGGGAAGGGCACTTGTCGCTCTCCC-- 520
              | |  || || |   || | ||  || | ||   | |  | | ||     |||
Db       1736 TGAGGCTGCTC----CATCCTCCTCAAAGCCCA-------
GACCTATTTCATAAGCCCCA 1688

Qy        521 -
```

```
ACCTGGTTACCACAGTCTCCATGGGTCTTTTGCCGTGACCACAAATAAAGGAAACACTC 579
               |||     ||||  || ||  ||| |    || ||  ||| |     |||
|||||
Db      1687 GACC------CCACCTTCACCCAGGGCC-----CCAAGAGAACAGA-
GCTGGAGACACT- 1641


Qy       580 ATCACTAGTATCTAAGTCGGGCTTTACAGTAACTATGCACCTTCTGTGTGCTTCACCTCA 639
                           ||||        ||        |   |||     ||| |||
||||
Db      1640 ----------TCTA-------CT---------CCTAGCA----CTGGATGC----
CCTCT 1615


Qy       640 CTCTCTACT-
TCAAACAGCCCATGGAGGGAGGTATTATTATACTCCTTATGTTGACAGTG 698
             | | ||| || | ||| |       ||| ||| ||   |  | || ||||        |
|
Db      1614 C-CCCTCCTGTGAAGCTGTAGGTGGGGGGTGG----AGGACACCCCTTT-------
AAGG 1567


Qy       699 AAGAATCTGAGGCCCAGAGAGGTTGGGGACTTGAGTAAAGTCACACAGCCCTGAG-
AGGC 757
               ||  || | ||| |  | | || ||     ||||   |  ||| ||   || || |
|||
Db      1566 CAGGCTCGGGGGGCTA-TGAACTCCAAGACTCCTG-
GAAGCCAGTAAGAAGTGGGAAGGT 1509


Qy       758 AGGACCAGGGTTCCATTCCTGCTCTATCCAGTTCCAAGCCCTT------
GTGTTTTCCAT 811
               ||| ||   ||||| | | |  ||| |  ||       | | || |
||
Db      1508 AGGCACA-----
CCATTTGGGATTTTTATTTTTCACTGAGCTAAGAGAGGAGATTCCAGC 1454


Qy       812 TATGTTTAGTGCCTCTTTGCTAACAGCAACATCTGCAAGATTTGTGTTGGTTTTGATGGA 871
             ||||      |  ||     | ||||   ||| ||| |   | ||  | |      |||
Db      1453 TATG------GAATC----CAGAGAGCG--
TTCTACAGGAACAGAACAGAAATTG----- 1411


Qy       872 GAACTCTAGCTCATCCACATGCTAGTGCCCAAGTGGTGG--
AGGGGCCACCTCAGCAGGT 929
                           |||   ||      || | |||| || || ||    || ||| | |
| |
|
Db      1410 -------GCTGGGCC-----CTGG-GCCC-AGAGGAGGCCTGGAGCCGCTT--
ACTGTT 1368


Qy       930 GGGTTCTGAATGCAGCCAAGGCTGTC-----
CCCGCAATGGGTGAGACTCGCTCCAACTG 984
               ||  |   | || || ||||  |   | | ||          ||  ||||||||
||
Db      1367 CAGTGCCAGCTTCATCCTTGGCACTCTGCCTCTCACAC------
AGCATCGCTCCGGCT- 1315


Qy       985 CCC---GCCCTCAG-
AGCAGGTGCCTAAGTCCTCCCTGGCACTGGCAGGCCTTACCTCAC 1040
               |||   |||| ||| |||  |||| |   |       ||| ||||||     |  |
Db      1314 CCCAGAGCCCACAGTGGCAGCCGCTGGA---------GGCTGTGGCAG------
CAGC-- 1272


Qy      1041 ATTGCTAAATTAAAGCAATGCAATTCCTCTTGGGTAAGAGGAATTCCTCCTT--
```

```
CTTTAC 1098
            ||||        ||  |||      ||    || | | ||        ||| ||
            |
Db     1271 --TGCT-------GCCCTGC----CCAAGGAGGGATGTGGG-------
CTTGGCT---C 1236

Qy     1099 TAACTGATCC--
CCAGCAAGGAAATAAAATGTTAGGCTTTAAAAATCCCTACTTTGTCAT 1156
            | || | ||    |||| |||              || ||| ||
||||||
Db     1235 TGACAGTTCAAGCCAGAAAG-------------AGCCTTAGAA-----------
GTCAT 1201

Qy     1157
ATCAGACTATATTCTAAAACTATATTTGAGCGAAACCTGTCATTGCGTCTAATTTCAAAT 1216
            |||  ||||     | || ||          | |    ||
||||
Db     1200 TCAGGAC---ATTC-----CCATTTT---------ACAGATGATG-----------
AAAT 1169

Qy     1217
ATACAGAATCTCCTTAAGAGCTGTTGCCTTATTTTTTTGTAAAGCCTCTCTGACATCAAA 1276
            |    |   |||   ||||| | || |          ||    |||
|||
Db     1168 A-----AGGCTCAGAGAGAGCAGGGGCTT-----------------
TCAAGAACAATAAA 1131

Qy     1277 TGGGGAGAAATGGTGGCACCTCCAGCACCCTGAAACTACACACCATTTCTTCCC-
TGCT 1335
            | |||||      ||| ||    ||| |  ||||    || |   |  | ||| |||
||||
Db     1130 GGTGGAGAC----TGGAAC--TCAGGCCTCCTG--
TCTGCTGAGGGTGTCTGCCCATGCT 1079

Qy     1336
CAGCTTCTGCTCAGGAGTTCTGTGAGCTATGGGAAGGCCATTGGTTGTATTTGCTACTTT 1395
            |    ||| ||||| ||||| | |  | |  ||| | ||||      ||  | | || |
Db     1078 C----TCT-CTCAGAGTTTCTGAGTGGTGGTGTCTGG--AGGGGCTGGACACGC-
AAGGG 1027

Qy     1396 TACTTTCATC---TTCCTCTG-
CTGTAGAGCCATTTAATGTTATTGTCATATGCTGCTGG 1451
            || | || |  | |||| ||||  |||      |||    || | | ||
|||
Db     1026 AGCTGGCCTCGTGTGTGTGTCTGTCTGT---
GCCGGGATGTGTCTGTGGCTTCTGTCTCTGA 970

Qy     1452 TGAGGTAAAGG----TGGGTCC---
GGGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGG 1504
            |  | ||   ||  ||||   | |||  | | |        | || ||| ||
Db      969 ACGTGCCAGGGGTTTTGTGTCCTGTGTGTGTGTC-TCTC-------
TGTGGGTGCTC----- 923

Qy     1505 GCCGATTTCAGCAGGAGTTCAGAGGGCTTATGATGGATGGTGAGAGATTTGACAA--
CCA 1562
            | | |   |||||||    ||||      ||||  | ||| |||   | |
||
Db      922 -CTGTGT---GCAGGA--ACTTGGGGCC----
ATGGCCAGAGAGGGATGGGCCTATTCCT 873
```

```
Qy      1563
CCAGAGCACATGTGCTCTGACCCTCTCCTGGGCATTGGTTCCTGCTGGTACCGGGCGGTT 1622
              ||     | || |    | || | |   ||| ||       ||||||   ||| ||
|
Db       872 ACA---ATCTTGGG---AGGCCTCCAC--AGGC--TG-----AGCTGGTG--
GGGAGGGT 830

Qy      1623 CAGACCTTCAAATAGGTTGCTTTCAAAAGAG--
CTTTCAGGCACTTATTGAGAATTAATG 1680
             |      | |  ||| |  | | | |  ||||     ||| |  | | |    |
|
Db       829 C-------CTGAAGGGTAGAGTGAAGATGGGGACTTT-----ACTCCCAGCGGA--
GAGG 784

Qy      1681
TTTAAACAGACATAATAGCCTAGATGAACTCCCAAGAGATCTATTAAATCTTGTGGGCTG 1740
                ||||  | | |||| || |    || ||| |     |   |  |||||
|
Db       783 AAGAAACC-AGAAGATAGGCTTGGGG------CATG-
GATGGGAAAGGTCTTG------G 738

Qy      1741 AATAAATATCTCGTGCAGGAC-TGTGCAACAGTAGCCCA----GAGCAT-----
CCTGCC 1790
                ||      ||  |   || |  | | |||||   ||||    ||| ||     ||||
Db       737 AA-------
CTAGGATGGGGCAAGGGAAACAAAGCCCCAAATGGAGTATGGGTCCCTGGA 685

Qy      1791 TGTGGGCATCCACCT--CCCAGGTGAGGG-------
CAGTGGGAAGCTGGCCCGACGGCA 1841
                 || || |  | |  |||    || |||       |||||||| | |   |||| ||
|
Db       684 AGTTGACACACTCTTAGCCCTCATGGGGGCCCAGCCCAGTGGGTAAC---CCCGG-
GGAA 629

Qy      1842 G-----CCAGAACTTGT---TTCTCACCT-
CCCACCAGCAACCCCCCACCCAACTCTGGG 1892
             |      ||  || ||    ||||||| ||     | | | ||||||
|||||
Db       628
GTGGTCACATGACGTGACACTTCTCAGCTGATTGCTTGAGATCCCCCAGTGTGGCCTGGG 569

Qy      1893 CCCCAGGCACACGA---AGCACAAG-TCT---CAGGG-----GACCA--
TTCCCACATTG 1938
                || |  | ||    ||| || ||  |   ||||      | ||| | ||||
Db       568 --
CCTTGTCCTTGAGTGAGCCCAGGTTCAAGCCAGGAAGGCTGGCCAGCTGCCCA----- 516

Qy      1939 GGGGATCCTGAGGGGAGCCCATCACCGCCTCTTGCATACAAC--
TGTCCACTAGGAGGCAC 1996
                |||  ||||||    || || || |||| |     |  |  | |||| |
|
Db       515 -AGGA--CTGAGG----CCTTCTCCTCCTCCT-----CCTCTGTGTCCTC-------
CTC 475

Qy      1997
GCCCAGTGTGGGAGAGATGTATGGTCTTGCCTTCCACCTGTAAAAACTGCACATATGCAG 2056
             |  ||        |||||   | ||| |   | || |     | || ||| | |
|
Db       474 GATCA--------------------
TCTTGGCCAGCTCCCGGGGCAGCTCCACGTCT---- 438
```

```
Qy        2057
GCCATTGCACTCTGGAACTGCATGCCGTGAAAACTCCTAATGGTGTGGAACTTAGTTTG 2116
                |||  |||  ||||||| |||  |   |      ||| |  | ||| | |
||||
Db         437 -CCACCTGCCATCTGGATCTGGCTCTCAT-CTGTCTCGTTCTTGGGTAG-
CCGGTATTTG 381


Qy        2117
AATTTGAAATCACGCCGCATGCACAAAGGGACAGGCCCAGGCCCGACCTCAGGTCATCCG 2176
                 |  ||| |  ||||      || |            ||||||| ||| |
||
Db         380 TCTCGGAAGTGGCTCCGC--------AGTG--------TGGCCCG--CTCTG-----
CCT 344


Qy        2177 CCCGCTGGCTG--CAGAGCATCCCTGGGAGCCA-AGGCGAGGCC-CGTGGAGC--
CTGA- 2229
                  || |||  || | | |||||||   |  |||     ||  || | |
||||
Db         343 TCCTCTGTGTGAACTGTGCATCCC---
GCTCCATCTTCTCTTCCACGAGTTGCTTCTGAT 287


Qy        2230
GCTTTGTGTAGCTCGAGCTTTGTGTAGCTCGTGCACTTATTATGCACCACCTCCCTTC-A 2288
                  ||        |||| ||     |||| |||| | ||  | |    ||  |  || ||   |
Db         286 ACTC-------CTCGTACTCCTCCCGGCTCATGCCCTGA----
GCTTCGGCTGCCGACTT 238


Qy        2289 GTCACCACTCCTCTTCCTCCGCCATCCTCATTTATACTGATTGCACACCCCCC--
GCTCA 2346
                ||| |||   ||| |||     ||||||              || | || |||
||||
Db         237 GTCCCCA----TCTCCCT----TATCCTC-------------GC-
CGCCTCCCAGGCTC- 201


Qy        2347
AACAACAATGTCCTTATTATGATGACCATCTCGTAGTGGTACATTCCATTCCTATTTAAG 2406
                   || ||  || || |  || | | |          ||  |||| 
|
Db         200 ----CCAGTGAGGTTCTTCAGCTGGCCGCC-----------CA--
CCAT----------G 168


Qy        2407
GTAAGCCCAAAGCCCACTTTTGGATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGCGCC 2466
                  ||  | || | ||  ||         |  || ||||||| |
|||||
Db         167 GTCTTCACCATGAACGCCATGG----TCTTCGCCGGCCGGGGCACCG-------
GGCGCC 119


Qy        2467
TGCCGTTCTTCTGGGTTTGGCTAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGT 2526
                ||| | |  | | |  |||                    ||
Db         118 TGC-TACCAC-GCGCCAGGC---------------
ACC---------------------- 98


Qy        2527
GGGCAAGGGTGTCATTTTCTCGCACAATACAACTCACTGAGGATGCTTCTGTAGAAGTGA 2586
                ||||| |          | | |||| | | || | |  || | ||           |
||||
Db          97 GGGCACG---------TCCGCGCCTACTTCAGCACTCC-AGTAGGC-----
CAACAGTG- 54
```

```
Qy      2587
GAAACACGATGAGTACATTCAGAATTACAATAACTCACTCTCACTGGGTAACTTCTCATG 2646
                  | ||| || | |                            | | |     ||| |
|
Db        53 ----CTCGAGGAATTC-----------------------CGCAG-----
CTTTTAGAG 28

Qy      2647 ATAGATTTGTATGATCAATACGGGTCTA 2674
                 ||| |      || ||| || |||
Db        27 C-AGAAGTAACACTTCCGTACAGGCCTA 1


RESULT 12
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match            29.7%;  Score 5120;  DB 1;  Length 2198;
  Best Local Similarity  42.8%;  Pred. No. 0;
  Matches 1258;  Conservative    0;  Mismatches  805;  Indels  874;
Gaps  174;

Qy        84
GAGGTCAGGAGCTCAAGACCAGCCTGGTCAACATGGTGAAACCCCGTCTCTACTAAAAAT 143
               | | | | ||||| || ||                  || ||   | | | |
|
Db      2198 GCGACCTGCAGCTCGAGCACA---------------
TGTGGCCTTTTTTTTTTTTTTTTTT 2154

Qy       144 ACAAAAAAAAAATTAGCTGGGCGTGTTGGCGGGAGCCTGTAGTCCC-
AGCTACACGGGAG 202
                            ||       | ||   || |||  | |     || |  |
||
Db      2153 ------------TT---------
TTTTTTATGGTGCCAATTTTAAATAGTTTTATTTAAG 2115

Qy       203
GCTAAGGTGGGAGAATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATTGCA 262
               |             ||||| |  ||        |  |   | |||||     | |
||||
```

```
Db       2114 AC------------ATTGCATTTTCC------
ACTTACAATACAGTGTTTATAAAGTGCA 2073

Qy        263 C---
CATTGCACTCCAGCCTGGGCGACAGAGCAAGACTCTCTCAAAAAAAAAAAAAAGA 319
              ||| |  ||| ||||| ||  | | ||| ||           || |
|||
Db       2072 ATGTTATTTCCTTCC--CCTGTGCATATGTTCCATATTC----------
AAGTATTGAGA 2025

Qy        320
AAGAAAGAAATCAGAAAATCGACCACAGTGGTAGCCACCTGGCCTAATGCTGTGTTTTTG 379
                | |       ||| || | || |    |||| || |
|||||
Db       2024 ATGCC------CAGTAACTT-ACTA------TAGCAGCTTAAC-----------
TTTTTA 1989

Qy        380 TACCTG--ACAGGGGTCACTC--
ATTTTAGGCACAACTCCTTCATTCTTTGTGAAATTAG 435
               | |||  ||||   |  ||   | |||||     |||||||    ||| |
|
Db       1988 AAACTGCCACAGAATTTGCTACGAATTTAGG------TCCTTCA---
AATGTTTTAAATG 1938

Qy        436 TGAGTTTCCTT-
CTACCCGTCACCAGATTCAATATGTTCTATTAATACACCGATAACCAC 494
               || |  || |  |  || | ||     | || | |||   ||||| |||    |
|
Db       1937 TGTGGAACAATGCTA--CATC------TACACTTGGTTGGCTTAATCAACC----
TCTTC 1890

Qy        495 AGGGGAAGGGCACT--
TGTCGCTCTCCCACCTGGTTACCACAGTCTCCATGGGTCTTTTG 552
               | || |||| |||  ||||| ||  | |                 || || ||
Db       1889 AATGG-TGGGCCCTGAGGAAGCACCACCAGAGGG---------------
AGGAGCT---- 1850

Qy        553
CCGTGACCACAAATAAAGGAAACACTCATCACTAGTATCTAAGTCGGGCTTTACAGTAAC 612
               ||   |||||      |||||| | |                  | ||| ||
Db       1849 CC---ACCAC-----CAGGAAATCCCC-----------------
CAGGCATT------- 1823

Qy        613
TATGCACCTTCTGTGTGCTTCACCTCACTCTCTACTTCAAACAGCCCATGGAGGGAGGTA 672
                     |||  ||  ||  | |  ||||                | || |
Db       1822 ------CCTCCTG---GCAT-GCCTC---------------
CTGCAC------------- 1801

Qy        673
TTATTATACTCCTTATGTTGACAGTGAAGAATCTGAGGCCCAGAGAGGTTGGGGACTTGA 732
                | |  ||| |||     |||| ||            | ||||||    ||||
Db       1800 -TCTGGTACAGCTT--------GGTGATGA--------------
TGGGGTTGCAAACTT-- 1765

Qy        733 GTAAAGTCACACAGCCCTG--AGAGGCAGGACCAGGGTTCCATTCCTGCT---
CTATCCA 787
                ||| |||||| ||    |   |  | | |   ||| ||||| ||   |  ||
Db       1764 ------TCTC-CAGCTCTTTCTGTTGATGTTCAA--ATTC--
TTCCTTCTCAGCAGTCTG 1716
```

```
Qy         788 GTTC----CAAGCCC-
TTGTGTTTTCCATTATGTTTAGTGCCTCTTTGCTAACAGCAACA 842
                |||   ||||||  |||    ||  |||||          |  |||   |   |||  |
|
Db        1715 ATTCTTATCAAGCCAGTTGATAATTTCATTA----------CACTTGTC---
CAGAATCT 1669

Qy         843 TCTGCAAGATTTGT-------GTTGGTTTTG--
ATGGAGAACTCTAGCTCATCCACATGC 893
                ||||    |||||     |||  | |||   ||  ||       |  ||||||  ||
|
Db        1668 TCTG-----TTTGTCCTCATCGTTAATCTTGCCTTGAAG-----TTTCTCATCTTCA-
AC 1620

Qy         894 TAGTGCCCAAGTGGTGGAGGGGCCACCTCAG---CAGGTGGGTTC-
TGAATGCAGCCAAG 949
                |||    || ||||   | |||   ||  ||||  ||| || |||    ||
Db        1619 AGTTGCTTTCATGTTGAAGG-----
CATAGGACTCAAGTGAATTCTTGGATGACACCT-- 1567

Qy         950 GCTGTCCCCGCAATGGGTGAGACTCG-CTCCA-------
ACTGCCCGCCCTCAGAGCAGG 1001
                ||||||  |       ||    |||  || ||         ||| |  |  | ||     |
||
Db        1566 --TGTCCCT-C------TGCTTCTCATCTTCAGCTTTGTACTTCTCAGCTTC----
CTGG 1520

Qy         1002 TGCCTAAGT------
CCTCCCTGGCACTGGCAGGCCTTACCTCACATTGCTAAATTAAAG 1055
                 | || ||       || ||||  |  | |||||  |          | | | |
||
Db        1519 ACCATACGTTCAATGTCTTCCTTGCTCAAACGGCCCTTGTC--------
ATTAGTGATAG 1468

Qy         1056
CAATGCAATTCCTCTTGGGTAAGAGGAATTCCTCCTTCTTTACTAACTGATCCCCAGCAA 1115
                  ||| |   | |||||        |||| |  |  |||| ||           || |||
|||||
Db        1467 TAAT-CTTGTTCTCTT------------TTCC-CGTACT-------
CTTGTCCACAGCAG 1429

Qy         1116
GGAAATAAAATGTTAGGCTTTAAAAATCCCTACTTTGTCATATCAGACTATATTCTAA-- 1173
                 || ||  | | |      |       |  |     |  ||||||  |    |||  | ||| |
Db        1428 AGACATTGAGTATAC--CATTGG------
CATCAATGTCAAAAGTGACTTCAATCTGAGG 1377

Qy         1174
AACTATATTTGAGCGAAACCTGTCATTGCGTCTAATTTCAAATATACAGAATCTCCTTAA 1233
                ||| |  | |  | | |    ||  | ||| |||| | |||||||| |              ||
Db        1376 AAC-ACCTCGGGGTGCAGGAGGT--ATGCCTGTGAGTTCAAACTTG--------
CCAAGC 1328

Qy         1234
GAGCTGTTGCCTTATTTTTTTGTAAAGCCTCTCTGACATCAAATGGGGAGAAATGGTGGC 1293
                | |||| |    ||||||| | | | ||
|
Db        1327 AGGTTGTTATC------
CTTTGTCATGGCACGCT------------------------C 1299
```

```
Qy       1294 ACCTCCAGACACCCTGAAACTACACACCATTTCTTCCCTG---
CTCAGCTTCTGCTCAGG 1350
               ||| || | | |||||    |||||||     |||   |||| | |
|
Db       1298 GCCTTCATA-AACCTGAATAAGCACACCAGG------
CTGGTTGTCAGAATAGGTAGTGA 1246

Qy       1351 AGTTCTGTG--AGCTATGGGAAGGCCATTGGTTGTATTT-
GCTACTTTTACTTTCATCTT 1407
               || ||||||  |||   || || ||| | |||| ||||| |||
Db       1245 AGGTCTGTGTCTGCTT--GGTAGG--
AATGGTGGTATTACGCT---------------- 1207

Qy       1408 CCTCTGCTGTAGAGCCATTTAATGTTATTGTCAT-
ATGCTGCTGGTGAGGTAAAGGTGGG 1466
                 || || || ||          ||||| | | | |
Db       1206 ----TGATGAGGA--CA------------
GTCATGACTCCACCAG-------------- 1180

Qy       1467
TCCGGGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGGGCCGATTTCAGCAGGAGTTCAG 1526
                 | | | | ||| ||| |||||| ||         || || || |||
||
Db       1179 --CAGTTTCAATACCAAGGGAAAGAGGA-GT----------GACATC--CAAGAG--
CA- 1138

Qy       1527
AGGGCTTATGATGGATGGTGAGAGATTTGACAACCACCAGAGCACATGTGCTCTGACCCT 1586
                 || || || | |   ||| |||    | |||| ||| |    |||
Db       1137 ---GCAAATCTTGAACATTCTCAGACTTGT----CTCCAG---
ACAAGATGGCTG----- 1093

Qy       1587
CTCCTGGGCATTGGTTCCTGCTGGTACCGGGCGGTTCAGACCTTCAAATAGGTTGCTTTC 1646
                 ||||| ||    |||| ||| | |||| ||| |||||    ||||| |
Db       1092 --CCTGGACAG------CTGC----ACCATAAGCAACAG--
CTTCATCAGGGTTGAT--- 1050

Qy       1647
AAAAGAGCTTTCAGGCACTTATTGAGAATTAATGTTTAAACAGACATAATAGCCTAGATG 1706
                                 || |||||         ||| | | | | ||
|
Db       1049 --------------GCTCTTATT-----------------CAGTTCTTTTC-
CATTGAAG 1022

Qy       1707
AACTCCCAAGAGATCTATTAAATCTTGTGGGCTGAATAAATATCTCGTGCAGGACTGTGC 1766
                 || ||     | || ||||||| ||| |            || | ||| ||
Db       1021 AAGTCTTGGAGAAGCTTCTGAATCTTG-GGGAT-----------
ACGAGTAGAAC----C 978

Qy       1767 AACAGTAGCCCAGAGC---ATCCTGC--
CTGTGGGCATCCACCTCCCAGGTGAGGGCAGT 1821
                 | || |||| | ||| ||| |||||     || | | || ||||
Db       977 ACCA----ACCAGGACAATATCATGAATCTGTG-------ACTTGTCTAGT-
TTGGCATC 930

Qy       1822 GGGAA--
```

```
GCTGGCCCGACGGCAGCCAGAACTTGTTTCTCACCTCCCACCAGCAACCCCCC 1879
          |||  |||  | |||  | ||||         ||  | |     |    ||||| |
Db       929 TCGAAGGGCTTTCTCTACTGGGTCCAGG----
GTGCCACGGAACAGGTCAGCATTCAGTT 874


Qy       1880
ACCCAACTCTGGGCCCCAGGCACACGAAGCACAAGTCTCAGGGGACCATTCCCACATTGG 1939
          |||| || ||||  | ||   |  | ||| |   |  | | ||||| |||
Db       873 CTTCAAATC-GGGCAC--GGGTAATGGAG-----GTAT-
AGAAGTCGATTCCTTCAT--- 826


Qy       1940
GGGATCCTGAGGGAGCCCATCACCGCCTCTTGCATACAACTGTCCACTAGGAGGCACGCC 1999
          ||| ||  | ||| |        | |||| ||    ||   ||
Db       825 -------AGAGAGAATCGATCTC------------AATACTGGCC---
TGGGTGC----- 793


Qy       2000
CAGTGTGGGAGAGATGTATGGTCTTGCCTTCCACCTGTAAAAACTGCACATATGCAAGCC 2059
             ||| |||||     ||    ||  | ||| | | || || || | ||  |
                                                                |
Db       792 -----TGGAAGAGA-----GGGTACGCTTAGCACGTTCACAAGCAGTACGGAGGC--
GTC 745


Qy       2060 ATT-
TGCACTCTGGAACTGCATGCCGTGAAAACTCCTAATGGTGTGGAACTTAGTTTGAA 2118
          |  | || |||| | || | || || | || ||  |                | |||
Db       744 TTACAGCTCTCTTGTTCTCACTGATGT----CCTTCTTAT-------------
GCTTGCG 702


Qy       2119 TTTGAAATCACGCCGCATGCACAAAGGGACAGGCC---
CAGGCCCGACCTCAGGTCATCC 2175
          || || ||| ||| | |||| | ||  | || | |   | | |   | |
|||
Db       701 CTTAAACTCA----GCA---ATAAAATGGTTGACCATTCGG--
TTGTCAAAATCTTCTCC 651


Qy       2176 GCCCGC-TGGCTGCAGAGCATCC--
CTGGGAGCCAAGGCGAGGCCCGTGGAGCCTGAGCT 2232
          |||   |||      | |  ||| || || || | |     | |   || |
Db       650 ACCCAAGTGG-----GTGTCTCCAGCT-GTAGACTTGAC----CTCAAAGATTC----
CA 605


Qy       2233
TTGTGTAGCTCGAGCTTTGTGTAGCTCGTGCACTTATTATGCACCACCTCCCTTCAGTCA 2292
          |         ||| |  | ||| | |  ||| |  | |  |||||||||||
||||
Db       604 TC------CTCAA---TAGTGAGGATTG-ACACATCAAAAGTGCCACCTCCC--
AGGTCA 557


Qy       2293 C-------CACTCCTCTTCCTCCGCCATCCTCATT---TATACTGATTGCA----
CACCC 2338
              |||   ||||| || || ||| ||   || | ||   |||     ||
                                                                |
Db       556
AAGATGAGCACGTTTCTTTCTGCTCCAACCTTTTTGTCTAAGCCGTAAGCAATAGCAGCA 497


Qy       2339 CCC----
GCTCAAACAACAATGTCCTTATTATGATGACCATCTCGTAGTGGTACATTC-- 2392
```

```
                  |    |||||   |   |  |  ||   ||| ||||| |    |  | || |    |
Db        496 GCAGTTGGCTCATTAATAATTCTAAGTACATTGA-GACCAGC----
AATAGTTCCAGCAT 442

Qy       2393 CATT-----CC------------TATTTAAGGTAA----GCCCAAAGCCCACT--
TTTGG 2429
                |  ||      ||          |  |||| ||||   || |    | ||||
||||
Db        441 CTTTGGTAGCCTGACGCTGAGAGTCATTAAAGTAAGCTGGCACTGTGACCACAGCATTGG 382

Qy       2430 ATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGCGCCTGCGTTCTTCTGGGTTTGGCT-A 2488
                  |    | || || ||  | |   |   |  | | | ||| ||    |||| |
Db        381 ---TAACAGTCTTCCCAAGGTAGGCT---TCTGCAATTTCCTTCATC----
TTTGTCAGA 332

Qy       2489 GATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAGGGTGTCATTT--
TCT 2546
                   |  |  |   ||  || |||| | | ||               | |||
|||
Db        331 ACCATAGAAGACACCTCCTCTGGATAGAAG--------------------
CTTTTGGTCT 292

Qy       2547 CGCAC---AATACAACT----
CACTGAGGATGCTTCTGTAGAAGTGAGAAACACGATGAG 2599
               |  |    | ||  |||    |  || |||  | | |     | |||
Db        291 CTCCCTTGTATTCTACTTGGACCTTGGGCCTGC--CAGCATCATT---
CACCAC------ 243

Qy       2600 TACATTCAGAATTACAATAACTCA-CTCTCACTGGGTAACTTC-
TCATGATAGATTTGTA 2657
                  ||| ||    |||| |||  |||  || |||| | ||| | |  |
Db        242 --CATAAAGGG--
CCAATGTTTCATATCAGACTGGACAACAGCATCATCAAATCTGCGTC 187

Qy       2658 TGATCAATACGGGTCTATTTTTATGTCAACTGAACACT------
GTAGGGTACCTTCCAG 2711
               |||| |||        | | || |  || |||| | ||
Db        186 CAATCAG-ACG----------TTTGGCATC-
AAAAACTGTGTTGGTGGGGTTCATTGC-- 141

Qy       2712 TCTTTTTCAAGATTGTTAAATTGAGACAAGTAATTGAATAATTTGTCCTATTTTTATTTT 2771
                           |  ||| | ||| ||| |   |    ||  || |   |
Db        140 ---------AACTTGATTCTTTGCGGCA--TCACCGATCAA-----CC--
GTTCAGTGTC 99

Qy       2772 AAAAAAAGTGA-ATGGACTGAAAT-
GTTAAATGTGAATGTACATTTCTTAATTGCAATTT 2829
               ||| || || || || | |  ||| |  |   ||  |||         |
Db         98 CGTAAAGGCGACATAGCTTGGAGTGGTTCGGTTTCCCTGATCAT-------
TGGCAATTA 46

Qy       2830 T-TCTACTGAGTGTTTGCACTATACTTTCTGGAATCTTATTTAACAAAAATAAAGGG
2885
```

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           | || |||              | | | | |||||||         |||| |  |    ||
Db         45 TCTCGACT------------TTTCCGTGCTGGAAAACACCCACACAAGACCAGTAGG
1
```

RESULT 13
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match   29.4%; Score 5066.5; DB 1; Length 2198;
  Best Local Similarity   43.0%; Pred. No. 0;
  Matches 1271; Conservative   0; Mismatches 845; Indels 843;
Gaps 166;

```
Qy        16
CAGGCCGGGCGCAGTGGCTCATGCCTGTAAGCCCAGCACTTTGGGAGGCGGAGGCGGGTG 75
            |  | ||| | |||    ||| || ||| |||||||         ||   ||  || |
Db         1 CCTACTGGTC-TTGTG-----TGGGTGTTT-TCCAGCAC-------
GGAAAAGTCGAGAT 46

Qy        76 GAT--
CCATTGAGGTCAGGAGCTCAAGACCAGCCTGGTCAACATGGTGAAACCCCGTCTC 133
              || ||| ||| |||||  |  ||||      |  || |      |    |||
|
Db         47 AATTGCCAATGA--TCAGGGAAACCGAACCA-------CTCCAAG------
CTATGTCGC 91

Qy       134 TACTAAAAATACAAAAAAAAAAATTAGCTGGGCGTGTTGG-
CGGGAGCCTGTAGTCCCAGC 192
               || |   |||              ||| || |||| |||     ||  | | ||
Db         92 --CTTTACGGACA-------------CTGAACG-GTTGATCGG-----
TGATGCCGCAAA 130

Qy       193
TACACGGGAGGCTAAGGTGGGAGGAATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGC 252
               |  |   |  || |                |||||||   |  || ||     ||
Db       131 GAATCAAGTTGCAA----------------
TGAACCCCACCAACACAGTTTTTGATG--- 171

Qy       253 TGAGATTGCACCATTGCACTCCAGCCTGGGCGACAGAGC--
```

```
AAGACTCTCTCAAAAAAAA 310
                    |||     ||  |  |  ||| || ||||    | ||  || |
Db      172 ----------CCA---AACGTCTGATTGGACG-
CAGATTTGATGATGCTGTTGT------ 211


Qy      311
AAAAAAAGAAAGAAAGAAATCAGAAAATCGACCCACAGTGGTAGCCACCTGGCCTAATGCT 370
                    ||   || || | | | | |    |||| |   ||   ||||
|
Db      212 --------CCAGTCTGATATGAAACATTGGCCCTTTATGGTGG-----TG----
AATGAT 254


Qy      371
GTGTTTTGTACCTGACAGGGGTCACTCATTTTAGGCACAACTCCTTCATTCTTTGTGAA 430
             |          ||| ||||    | ||    ||| |||            ||
|
Db      255 G-----------CTGGCAGG-----CCCA----AGGTCCAA--------------
GTAGA 280


Qy      431 AT--
TAGTGAGTTTCCTTCTACCCGTCACCAGATTCAATATGTTCTATTAATACACCGAT 488
             ||  || ||| ||     |   |  ||||   | | |||||| | |
Db      281 ATACAAGGGAGAGACCAAAAGCTTCTATCCAGAGGAGGTGTCTTCTATGGTT---
CTGA- 336


Qy      489
AACCACAGGGGAAGGGCACTTGTCGCTCTCCCACCTGGTTACCACAGTCTCCATGGGTCT 548
             || || ||| || | ||| |     || ||||| |  | ||  || |||
Db      337 ---CAAAGATGAA-GGAAATTG-
CAGAAGCCTACCTTGGGAAGACTGTTACCA------- 384


Qy      549
TTTGCCGTGACCACAAATAAAGGAAACACTCATCACTAGTATCTAAGTCGGGCTTTACAG 608
             ||| ||| ||||   ||| |  || ||||  || ||  || ||| ||| |||  |||
Db      385 -ATGCTGTGGTCACAGTGCCAGCTTACTTTAATGAC---TCTCAGCGTCAGGC--
TACC- 437


Qy      609
TAACTATGCACCTTCTGTGTGCTTCACCTCACTCTCTACTTCAAACAGCCCATGGAGGGA 668
             ||  ||||    || |  | |   |  | |||||| ||       |||
Db      438 -AAAGATGCTGGAACTAT-TGCTG---
GTCTCAATGTACTTAGAATTATTAATG------ 486


Qy      669
GGTATTATTATACTCCTTATGTTGACAGTGAAGAATCTGAGGCCCAGAGAGGTTGGGGAC 728
             |   |   || || | |   ||  ||| |||  || ||  | | |||||||| |
Db      487 AGCCAACTGCTGCTGCTATTGCTTACGG--------CTTAG--
ACAAAAAGGTTGGAGCA 536


Qy      729 TTGAGTAAAGTCACACAGC-----
CCTGAGAGGCAGGACCAGGGTTCCATTCCTGCTCTA 783
                    || || ||  |     |||| ||||     || |  || |
Db      537 GAAAGAAACGT-GCTCATCTTTGACCTGGGAGGTGG-----------
CACTTTTGATGTG 584


Qy      784 TCCAGTTCCAAGCCCTTG----
TGTTTTCCATTATGTTTAGTGCCTCTTTGCTAACAGCA 839
             || |  |||    | |||    ||  ||  | | ||  ||| |  |   |||    |
```

```
Db        585 TCAA--TCCTCACTATTGAGGATGGAATCTTTGAGGTCAAGT-CTAC--AGCT---
GGAG 636

Qy        840 ACATCTGCAAGATTTGTGTTGGTTTTGATGGAGAACTCTAGCTCATCCA----
CATGCT- 894
              ||| |  |  | ||| | |||||||   | |    | ||| |||
||||
Db        637 ACACCCACTTGGGTGGAGAAGATTTTGA---
CAACCGAATGGTCAACCATTTTATTGCTG 693

Qy        895 AGT----GCCCAAGTGGTGGAGGGGCCACCTCAGCAGGTGGGTTC-
TGAATGCAGCCAAG 949
              |||   || |||| || |   ||| || |||    ||| |  | ||  || |
|||
Db        694 AGTTTAAGCGCAAGCATAAGAAGG---ACATCA----GTGAGAACAAGAGAGCTG-
TAAG 745

Qy        950
GCTGTCCCCGCAATGGGTGAGACTCGCTCCAACTGCCCGCCCTCAGAGCAGGTGCCTAAG 1009
             | | ||| | || || || ||  || || | || |     ||||||
Db        746 AC-GCCTCCGTACTGCTTGTGA-ACGTGCTAA--
GCGTACCCTC--------------- 785

Qy        1010 TCCTCCCTGGCACTGGCAGGCCTTACCTCACATTGCTAAATTAAAGCAATGCAATTC-
CT 1068
              || |||   |||| | ||||||            | ||  | || | |||
||
Db        786 TCTTCC--AGCACC--CAGGCC-----------------AGTATTGAGAT-
CGATTCTCT 823

Qy        1069
CTTGGGTAAGAGGAATTCCTCCTTCTTTACTAACTGATCCCCAGCAAGGAAATAAAATGT 1128
              || |     ||||| | |||||| ||| |   || |   ||| ||
Db        824 CTATG----AAGGAAT--
CGACTTCTATACCTCCATTACCCGTGCCC------------- 864

Qy        1129
TAGGCTTTAAAAATCCCTACTTTGTCATATCAGACTATATTCTAAAACTATATTTGAGCG 1188
              | ||| ||| |              ||| || ||
Db        865 ---GATTTGAAGA--------------------
ACTGAATGCT----------------- 884

Qy        1189 AAACCTGT--
CATTGCGTCTAATTTCAAATATACAGAATCTCCTTAAGAGCTGTTGCCTT 1246
              ||||||| | | | |    |  | | | | |  |||| |||  | |   | ||||
Db        885 -GACCTGTTCCGTGGCACCCTGGACCCAGTAG--AGAAAGCCCTTCG----
AGATGCCAA 937

Qy        1247
ATTTTTTTGTAAAGCCTCTCTGACATCAAATGGGGAGAAATGGTGGCACCTCCAGACACC 1306
              |        | |  || || |       ||| | | |     |||||| |  | |
||
Db        938 A----
CTAGACAAGTCACAGATTCATGATATTGTCTGGTTGGTGGTTCTACTCGTATCC 993

Qy        1307
CTGAAACTACACACCATTTCTTCCCTGCTCAGCTTCTGCTCAGGAGTTCTGTGAGCTATG 1366
              |         || |    || |||  | |  |||||||  || || ||||       |
|||
Db        994 C----------CAAGATT------CAG--AAGCTTCT--CCAAGACTTCT----
```

```
TCAATG 1029


Qy        1367
GGAAGGCCATTGGTTGTATTTGCTACTTTTACTTTCATCTTCCTCTGCTGTAGAGCCATT 1426
          |  | |         || || |               ||||  || ||| || ||
Db        1030 GAAAAGAAC-----TGAATAAG-----------AGCATCAACC-
CTGATGAAGC------ 1066


Qy        1427 TAATGTTATTGTCATATGCTGCTGGTGAGGTAAAGGTGGGTCCGGG-TGCCTTC---
CCA 1482
                    | ||| | |||| ||| | |              |||| ||  ||| ||
|
Db        1067 ------TGTTG-CTTATGGTGCAGCT-------------
GTCCAGGCAGCCATCTTGTCT 1106


Qy        1483 GG-----
GGTTAGAGGATGTTCAAAGGGCCGATTTCAGCAGGAGTTCAGAGGGCTTATGA 1537
              ||        || | ||| |||||||   ||||               ||| |
Db        1107 GGAGACAAGTCTGAGAATGTTCAA------GATTT------------------
GCTGCTCT 1143


Qy        1538
TGGATGGTGAGAGATTTGACAACCACCAGAGCACATGTGCTCTGACCCTCTCCTGGGCAT 1597
              ||||||                  |||          | |||| ||||        ||
||
Db        1144 TGGATG----------------TCAC-----------TCCTCTTTCCCTT-----
GGTAT 1171


Qy        1598 TGGTTCCTGCTGGTACCGGGCGGTTCA-GAC---
CTTCAAATAGGTTGCTTTCAAAAGAG 1653
                | | |||||||   || | ||| |||   | ||| || | | |  || |
Db        1172 T-GAAACTGCTGGT----GGAG--
TCATGACTGTCCTCATCAAGCGTAATACCACCATTC 1224


Qy        1654
CTTTCAGGCACTTATTGAGAATTAATGTTTAAACAGACATAATAGCCTAGATGAACTCCC 1713
              || || ||| | || | |  |   | | ||| | ||| | |||| | |  ||  ||
Db        1225 CTACCAAGCAGACACAGACCTTCACTACCTATTCTGACA-ACCAGCCT-
GGTGTGCTTAT 1282


Qy        1714 AAGAGATCTATTAAATCTTGTGGGC--
TGAATAAATATCTCGTGCAGGACTGTGCAACAG 1771
               || ||| || |  | | ||  ||| || || ||  | | |  || |||
Db        1283 TC-AGGTTTATGAAGGCGAGCGTGCCATGACAAAGGATAACAACCTG--
CTTGGCAAGTT 1339


Qy        1772 TAG---
CCCAGAGCATCCTGCCTGTGGGCATCCACCTCCCAGGTGAGGGCAGTGGGAAGC 1828
              |         | ||| |||| | ||||        |||| || ||||      |   |
|
Db        1340 TGAACTCACAG-GCATACCTCCTG--------CACC-CCGAGGTGT--
TCCTCAGATTGA 1387


Qy        1829 TGGCCC----GACG--GCAGCCAGAACTTGT-TTCTCACC-
TCCCACCAGCAACCCCCCA 1880
                     | | |   ||| | ||| | | | ||||  || | | |
Db        1388 AGTCACTTTTGACATTGATGCC---
AATGGTATACTCAATGTCTCTGCTGTGG------A 1438
```

```
Qy        1881 CCCAACTCTGGGCCCCAGGCACACGA-----
AGCACAAGTCTCAGGGGACCATTCCCACA 1935
               |   | |  |||     |  | ||| ||     |  ||| | |  || ||| || ||
||
Db        1439 CAAGAGTACGGGAAAAGAGAACAAGATTACTATCACTAATGACAAGGG-
CCGTTTGAGCA 1497

Qy        1936
TTGGGGGATCCTGAGGGAGCCCATCACCGCCTCTTGCATACAACTGTCCACTAGGAGGCA 1995
                        ||| || |  | | ||   |  | ||   | |||   | ||  |
||
Db        1498 -------------
AGGAAGACATTGAACGTATGGTCCAGGAAGCTGAGAAGTACAAAGC- 1543

Qy        1996 CGCCCAGTGTGGGAGAGATGT--
ATGGTCTTGCCTTCCACCTGTAAAAACTGCACATATG 2053
                        || |  | |||| |  | || |  |   || ||    || | | ||| |
Db        1544 -------TGAAGATGAGAAGCAGAGGGACAAGGTGTCATCC----
AAGAATTCACTT--- 1589

Qy        2054 CAAGCCATTTGCACTCTGGAAC-
TGCATGCCGTGAAAACTCCTAATGGTGTGGAACTT-- 2110
                        || | ||| || ||  |  ||| || | ||     |||| | | || | |||||
Db        1590 -GAGTCCTATGCCTTC---AACATGAAAGC------
AACTGTTGAAGATGAGAAACTTCA 1639

Qy        2111 -----
AGTTTGAATTTGAAATCACGCCGCATGCACAAAGGGACAGGCCCAGGCCCGACCT 2165
                        || ||| |||  || |   ||| |  ||| | || | ||   |
|
Db        1640 AGGCAAGATTAACGATGAGGACAAACAG--------AAGATTCTGGACAAG---
TGTAAT 1688

Qy        2166
CAGGTCATCCGCCCGCTGGCTGCAGAGCATCCCTGGGAGCCAAGGCGAGGCCCGTGGAGC 2225
                        | | |||| ||  ||| || | || ||    || | || |   |   ||
Db        1689 GAAATTATCAACTGGCT---TGATAAGAATC------AGACT--
GCTGAGAAGGAAGAAT 1737

Qy        2226
CTGAGCTTTGTGTAGCTCGAGCTTTGTGTAGCTCGTGCACTTATTATGCACCACCTCCCT 2285
                        ||| | |   || ||||  || || |      | |||| |
|||
Db        1738 TTGAACATC-AACAGAAAGAGC----TGGAGAAAG---------TTTGCAAC----
CCCA 1779

Qy        2286
TCAGTCACCACTCCTCTTCCTCCGCCATCCTCATTTATACTGATTGCACACCCCCCGCTC 2345
                        ||| |||||| || ||  |               | |   ||| ||
Db        1780 TCA-TCACCAAG-CTGTACCAGAG-------------
TGCAGGAGGCATGCC-------- 1816

Qy        2346
AAACAACAATGTCCTTATTATGATGACCATCTCGTAGTGGTACATTCCATTCCTATTTAA 2405
                        |  |  |||| |||  |   |  ||  || || |||| |      ||||
Db        1817 -AGGAGGAATG-CCT-----GGGGGATTTCCTGGTGGTGGAGC-------
TCCT------ 1856

Qy        2406
GGTAAGCCCAAAGCCCACTTTTGGATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGCGC 2465
```

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                                ||| ||  |||
Db      1857 -------------
CCCTCTGGTGG---------------------------------- 1867


Qy      2466
CTGCGTTCTTCTGGGTTTGGCTAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATG 2525
                ||| ||| || |||                    ||| | || ||| |||
||||
Db      1868 -TGC-TTCCTCAGGG---------------------CCCACCATTGAA--
GAGGTTGAT- 1901


Qy      2526
TGGGCAAGGGTGTCATTTTCTCGCACAATACAACTCACTGAGGATGCTTCTGTAGAAGTG 2585
                | ||                         |||| | || ||     ||||| |
||
Db      1902 TAAGC------------------------CAACCAAGTGTAGA------
TGTAGCATTG 1930


Qy      2586
AGAAACACGATGAGTACATTCAGAATTACAATAACTCACTCTCACTGGGTAACTTCTCAT 2645
                |||| | | ||||| ||| ||   || ||         | || ||||
|
Db      1931 TTCCACACATTTAAAACATT-TGAAGGACCTAAATTCGT--------AGCAAATTCT-
GT 1980


Qy      2646
GATAGATTTGTATGATCAATACGGGTCTATTTTTATGTCAACTGAACACTGTAGGGTACC 2705
                | || ||| |   | || | ||| | || || || |||| ||             |
Db      1981 GGCAGTTTTAAAAAGTTAA-GCTG--CTA-TAGTAAGT-TACTGGGCA--------
TTC- 2026


Qy      2706 TTCCAGTCTTTTTCAAGATTGTTAAATTGAGACAAGTAATTGAA--
TAATTTGTCCTATT 2763
                || |  ||| ||   || || ||   |  || ||| |   |  ||| |
Db      2027 -TCAATACTTG---AATATGGAACATATGC-
ACAGGGGAAGGAAATAACATTGCACT--- 2078


Qy      2764
TTTATTTTAAAAAAAGTGAATGGACTGAAATGTTAAATGTGAATGTACATTTCTTAATTG 2823
                || ||||         |||| | |||  |  ||| | || ||||||
|
Db      2079 ----TTATAAAC-----------ACTGTATTGTAAGTGGAAAATGCA-
ATGTCTTAAATA 2122


Qy      2824
CAATTTTCTACTGAGTGTTTGCACTATACTTTCTGGAATCTTATTTAACAAAAATAAAG 2883
                ||      ||| | |   || |||| |||          ||     | || |||||
|||
Db      2123 AAA-----CTATTTAAAATTGGCACCATA-------
AAAAAAAAAAAAAAAAAAAAAAAA 2170


Qy      2884 GGAAAAAATTGCTTGA-CT 2901
                || | | |||| || ||
Db      2171 GGCCACATGTGCTCGAGCT 2189


RESULT 14
US-10-478-914-57
; Sequence 57, Application US/10478914
```

  Query Match   29.4%; Score 5053; DB 1; Length 2336;
  Best Local Similarity   42.6%; Pred. No. 0;
  Matches 1300; Conservative   0; Mismatches 869; Indels 886;
Gaps 178;

Qy   2 TGAAATCAGGAAATCAGGCCGGGCGCAGTGGCTCATGC-CTGTAAGCC--
CAGCACTTTG 58
            | | || | | || ||| | | ||| || |||| ||| | | | |
|
Db   12 TTACTTCTGCTCTAAAAGCT--
GCGGAATTCCTCGAGCACTGTTGGCCTACTGGAATGCG 69

Qy   59 GGAGGCGGAGGCGGGTGGATCCATTGAGGTCAGGAGC---TCAAGACC-
AGCCTGGTCAA 114
            | | | ||| | || | || || || || || || |||| ||| | || | |
Db   70 AGCTGAGCAGACAG--
GGCTGCAAGGAAATCTGGCGCGGTTCAATACCTCGTCTAGCC-- 125

Qy   115
CATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAAAAAAATTAGCTGGGCGTGTTGGCG 174
               || || || |||| | | ||| | ||
|
Db   126 -----TGGGTTCCAGTATCTAATTTTTTT------TTTGTTTTAAC---------
TGAC- 164

Qy   175
GGAGCCTGTAGTCCCAGCTACACGGGAGGCTAAGGTGGGAGAATTGCTTGAACCCGGGAG 234
              | || || | | | ||||| |
|||
Db   165 --AAACTCATTTCTCTAC-----------------TGGGA--------------
CAGGAT 191

Qy   235
GCGGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTCCAGCCTGGGCGACAGAGCAAG 294
            || | ||| | |||| | | | |||| || |
||||||
Db   192 GCTG----TGCTG---GCTGGAA--GTTCCATT--TCTAC--------------
AGCAAG 226

```
Qy          295
ACTCTCTCAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGACCACAGTGGTAGC 354
              |  || ||                            ||| | |||    ||||| ||
|
Db          227 AATC-CT--------------------------ATCTGGAAA-----
CACAGAAGTTGT 253


Qy          355 CACCTGGCCTAA--TGCT-GTGTTTTTGTACCTGACAGGGGTCACT-
CATTTTAGGCACA 410
                |  || ||| |  ||| |  |||| |  ||  || ||| |  |
||
Db          254 CCTCTAGCCACAGCAGCTCGAACTTTTTTGATTGTC----GTTGCTGCTTTCT---
CCCA 306


Qy          411
ACTCCTTCATTCTTTGTGAAATTAGTGAGTTTCCTTCTACCCGTCACCAGATTCAATATG 470
                | || |||| |           |||| |  |      |||| |||
Db          307 TCACCCCCATCC--------------------CCTTTTGAC-----
AAAGATCCAA---- 337


Qy          471 TTCTATTAATACAC---CGATAACCACAGGGGAAGGGC-ACTTGTC-
GCTCTCCCACCTG 525
                || | | |  |   || ||||      |   ||| ||| || | ||| ||
|
Db          338 --CTGTAAAAAGTCTTACG-TAAC----AGTTCAGGACTACT--
TCGGTTCTTTTACTGG 388


Qy          526 GTTACCACAGTCTCCATGGGTCTTTTGCCGTGACCACAAATAAAG---
GAAACACT---- 578
                || | ||| ||    |  | |||| |   |   || | ||    ||| | |
Db          389 GTAAGCACTTTCAATTTTTTTTTTTTTAACTAAAAGCCATTTTAAAATTGAATCTGTTGAG 448


Qy          579 ---CATCACTAGTATCTAAGTCGGGCTTTACAGTAACTATGCACCTTCTGTG---
TGCTT 632
                  | | |||| ||||       |    ||| ||||        || || |||   |
||
Db          449 GGGCTTGACTAAAATCTTTTAAGTAATTTG-
TGTAATGGAATACTGTCAGTGGATTTTTT 507


Qy          633
CACCTCACTCTCTACTTCAAACAGCCCATGGAGGGAGGTATTATTATACTCCTTATGTTG 692
                |  |||| |               | | | ||       |||||||
||||
Db          508 CGTCTCATT-----------TCTGCACGTG-------------------CTCCTT-
TGTTC 537


Qy          693 ACAGTGAAGAATCT--------GAGGCCCAGA--
GAGGTTGGGGACTTGAGTAAAGTCAC 742
                ||| |||| ||                ||||| | | ||| ||  |||| | |
|
Db          538 TCAGAACAGAAGCTTTTTATACACATCCCATAACGCAGCTGGAGA---GAGTTATG-
AAG 593


Qy          743 ACAGCCCTGAGAGGCAGGACCAGGGTTCCATTCCTGCTCTATCCAGTTCCA-----
AGCC 797
                |||  | | | || |  | |||| |        ||| | |  ||  |      |
Db          594 TCAGTTATTATAAGGAACACAAAGGTTGCTTTCC-
ATTCTTTGCCTTTAGATAATTAATT 652
```

```
Qy        798 CTTGTGTTTTCCATTATGTTTAGTGCCTCTTTGCTAACAGCA-
ACATCTGCAAGATTTG- 855
              || |||||||   |     | | |  | |||     |  | | | ||    ||||| |
Db        653 TTTTTGTTTTC---TTAAAATGGAG--
TATTTAAAGAAGGAAGAAATTCACAAGAAATAA 707


Qy        856 --TGTTGGTTTTGATGGAGAACTCT--AGCTCAT-
CCACATGCTAGTGCCCAAGTGGTGG 910
               |||||||   | || || |  || |  | |||| |  |   | | ||| |
|
Db        708 ACTGTTGGAGAATTTAGAAAAGTTTGAAGTTTTTACCACCTTTTCTATCTCTAGT-
TTTG 766


Qy        911 AGGGGCCACCTCAGCAGGTGGGTTCTGAATGCAGCCAAGGCTGTCCCCGCAATGGG---T 967
              | ||||| | || |||         ||| ||| ||    || ||||
Db        767 TGTGGCCA----AACACTTG---------TGCCGCCTGGG--------
GCGGTGGGGGTA 805


Qy        968 GAGACTCGCTCCAACTGCCCGCCCTCAGAGCAGGTGCCTAAGTCCTCCCTGG-
CACTGGC 1026
              ||| | ||   || ||        |||| |     ||||| |   | ||| ||
|||
Db        806 GAGGCAAGCATAGACAG---------AGAGGA----
ACTAAGCCAGACATGGACAAAGGC 852


Qy       1027 A--GGCC-TTACCTCACATTGCTAAATTAAAGCAATGCAATT--CCT-CT-
TGGGTAAG- 1078
              |   |||  ||| |  | ||     || | | ||   || |  | |||||
||
Db        853 ACGAGCCAAAACCAGACAGTCCT-------
GGCCGTTCGATAGGCCAGCAGTGGGTGAGA 905


Qy       1079 -AGGAATTCCTCCTTCTTTACTAACTGATCC-------CCAGCAAGGAAAT-
AAAATGTT 1129
              |||   ||  || ||  || |    | |  |        |  | | ||| || |
|||
Db        906 CAGG---
TCAGCCAGCTGCAGGGGCGGGAGCGGGGGGGCGGGTAGGGACATGGATGTGTG 962


Qy       1130 AG--GCTTTAAAAATCCCTACTTTGTCATATC-
AGACTATATTCTAAAACTATATTTGAG 1186
              ||  |||      | | |  ||   ||| ||||| ||||| |||| |||||
Db        963 AGGTGCT---------CATGC---
GTGCGATCGTGACTAGATTCTGAAACT--------- 1001


Qy       1187
CGAAACCTGTCATTGCGTCTAATTTCAAATATACAGAATCTCCTTAAGAGCTGTTGCCTT 1246
              || | ||| ||||      |||| |||   ||| ||||                 ||
Db       1002 ----GCCAGCCAT---------TTTC------CCAG---CTCC------------
GC--- 1024


Qy       1247
ATTTTTTTGTAAAGCCTCTCTGACATCAAATGGGGAGAAATGGTGGCACCTCCAGACACC 1306
              ||||           || ||| || ||     ||||      | ||     |
Db       1025 -----TTTG-----------TGCAATCTAAAGG-----AATG-----CATC----
CCCT 1053


Qy       1307
```

```
CTGAAACTACACACCATTTCTTCCCTGCTCAGCTTCTGCTCAGGAGTTCTGTGAGCTATG 1366
 | ||| |    | |    |||| || | |||   ||        ||||
|
Db      1054 CTGAAGCAG---------TCTTGCCAG---AGC-----CT---------
AGTGAG----G 1083

Qy      1367 GGAAGGCCATTGGTTGTATTTGCTACTTTTACTTTCATCTTCCTCTGC-
TGTAGAGCCAT 1425
              |  ||   ||||                       |  | || |  | | ||
||
Db      1084 GAGAGAAGTATGGT----------------------
AAATACCACAACATATGGAATCA- 1120

Qy      1426
TTAATGTTATTGTCATATGCTGCTGGTGAGGTAAAGGTGGGTCCGGGTGCCTTCCCAGGG 1485
              |  | |  |  |||| | || |  | ||||  |     |   |||
Db      1121 -----GAAAATACCG---GGAACTGGAGTGGGCAAGGGG-----
GAATGC---------- 1157

Qy      1486
GTTAGAGGATGTTCAAAGGGCCGATTTCAGCAGGAGTTCAGAGGGCTTATGATGGATGGT 1545
              |||||| |||     || |   ||| |   |  | | |        ||| ||
|
Db      1158 ---AGAGGGTGT-----GGAAATTTTTA----GTGATCTGG--------AATG--
TGTT 1195

Qy      1546 GAGAGATTTGACAACCACCAGAGCACATGTGCTCTGACC--
CTCTCCTGGGCATTGGTTC 1603
              || ||   ||    | ||| |||     | | ||| |||| ||   || | |
|
Db      1196 GAGTGACAGGAAGTGCCCCA-AGCTTCT---CCCCCACCAACTCTTCT---
CAGTCGCGC 1248

Qy      1604
CTGCTGGTACCGGGCGGTTCAGACCTTCAAATAGGTTGCTTTCAAAAGAGCTTTCAGGCA 1663
              ||||| |   | | |   |  |||||  ||       ||||| ||| ||||  || |
Db      1249 CTGCTTTTGTCTAACTCTTGTAATCTACACACT-ACTGCTTACAA---
AGCTGTCTG--- 1301

Qy      1664 CTTATTGAGAATTAATGTTTAAACAGACATAA--
TAGCCTAGATGAACTCCCAAGAGATC 1721
                                 |||||  ||||| ||    | |||| | |  ||||
|
Db      1302 ---------------AGTTTA---AGACAAAAGAAACCTAAAAG-TCTCCTT----
ACT 1338

Qy      1722      1722
TATTAAATCTTGTGGGCTGAATAAATATCTCGTGCAGGACTGTGCAACAGTAGCCCAGAG 1781
              |  ||  | |||| |||      |          | |||| |||  ||    |  ||
Db      1339 TCATAGTACCTGTGATATG--------------
GAAGGAATGTAAAAGCATGACC----- 1379

Qy      1782
CATCCTGCCTGTGGGCATCCACCTCCCAGGTGAGGGCAGTGGGAAGCTGGCCCGACGGCA 1841
              | |  |||| ||| ||| |||     | |||||    ||| | ||| |
Db      1380 CTTTAAGCCTATGGACAT---TTTTTCAGGTAT--
ACAGGAGAAAGAT----------- 1422

Qy      1842
GCCAGAACTTGTTTCTCACCTCCCACCAGCAACCCCCCACCCAACTCTGGGCCCCAGGCA 1901
                         || | |||             |||| || ||      ||
```

```
Db      1423 ----AAAATAATTT--------------------TCCACAGAAAAATG------
AGAAT 1451

Qy      1902 CACGAAGCACAAGTCTCAGGGGACCATTCCCACATT--
GGGGGATCCTGAGGGAGCCCAT 1959
                 |  ||| | |   ||||| | | |  | ||  |  | || ||||
             |
Db      1452 TATGAATTATATAGTTCAGGTTCCAAATCTAATTTTTAAAAGAATTCTGA--------
TT 1503

Qy      1960 CACCGCCTCTTGCATACAACTGTCCACTAGGAGGCACGCCCAGTGTGGGAGAGATGTATG 2019
                 |  |  | |||   ||||||  | |    |  ||   || | ||   || |   |||
Db      1504 CTGCTACACTT---TACAAATG--CTTAGGTTGGTT--
CCTAATTTGAAGGAG------- 1549

Qy      2020 GTCTTGCCTTCCACCTGTAAAAACTGCACATATGCAAGCCATTTGCACTCTGGAACTGCA 2079
                      || ||| |  ||  |  | ||||| |||||| |||
Db      1550 ------------ACTTGTTTTATTTGGTTA-
ATGCATTGCATTTGAACT----------- 1585

Qy      2080 TGCCGTGAAAACTCCTAATGGTGTGGAACTTAGTTTGAATTTGAAATCACGCCGCATGCA 2139
                    ||    | ||| |     ||| |  | ||||||
Db      1586 -----TGT----TTCTATT-------
TTCTTTGCATAAATTTGG--------------A 1614

Qy      2140 CAAAGGGACAGGCCCAGGCCCGACCTCAGGTCATCCGCCCGCTGGCTGCAGAGCATCCCT 2199
                 |   ||| ||   | |  || | || | |||   |   ||  |         |
Db      1615 CTTTGGG--AGAAAAATGC-------AAAGTAAT----AAGTAGAATGCA-------
CTT 1654

Qy      2200 GGGAGCCAAGGCGAGG------CCCGTGGAGCCTGAGCTTTGTGTAG----
CTCGAGCTT 2249
                 ||| |  || ||||     ||| |  | | |||  ||     |  ||
             |
Db      1655 GGGGGAAAAAAGGAGGATTTTTCCCTT----CATGGG--
TTGGAAAGTATTTTAAAGGGT 1708

Qy      2250 TGTGTAGCTCGTGCACTTATTATGCAC-CACCTCCCTTCAGTCACCACTCCT------
CT 2302
                 ||| |   || || |   |  | || | | | | ||| | || |  | ||
             |
Db      1709 TGTTT---TCTTG-AAAAAACAAGCTCTCTCTTACTTTCTG-
CATCTATGCTATAAAGAT 1763

Qy      2303 TCCTCCGCCATCCTCATTTATACTGATTGCACAC-
CCCCCGCTCAAACAACAATGTCCTT 2361
                 || || || | |  | | | | | || |    |   ||| |||| |||
             ||
Db      1764 AACTATGCTATAATAAATGTAA--
GGTAGAAACTTTAAAGAGAAAATAACAGTGTTCTA 1821

Qy      2362 ATTATGATGACCATCTCGTAGTGGTACATTCCATTCCTATTTAAGGTAAGCCCAAAGCCC 2421
                 |  ||| | |  ||   | |  | |  ||||   ||              | ||
```

```
|
Db        1822 A--GTGAAAAGCTACT-----TAGCATTTTCCCAAACT----------
CACACATTATCA 1864

Qy        2422 ACTTTTGGATTTTCTCGACTGTCCGAGAAAAG--------
TTGTGTAAGCGCCTGCGTTC 2473
               ||     ||    ||  |    |  ||||||||    |   |   ||   ||   ||
||
Db        1865 AC----
AGAAACACTAAAAATTAAGAGAAAAGCGGCCAACTAATTAAATAGCTAGCCTTA 1920

Qy        2474 TTCTGGG---
TTTGGCTAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGC 2530
               || ||||    | || ||||  |    |||| 	       |||| | | |
||||
Db        1921 TTTTGGGGGTATGGGATAGAAAATTAAGTGT---------
GAATAAAATGATACTTGGGA 1971

Qy        2531
AAGGGTGTCATTTTCTCGCACAATACAACTCACTGAGGATGCTTCTGTAGAAGTGAGAAA 2590
               | |      |||||| |  |||   ||| ||||| |        |||
|
Db        1972 ATG--------TTTCTCCCTC-GTAC----CACAAAGGATGTT--------
AGTGGTCAG 2010

Qy        2591 CACGATGAGTACATTCAGAATTACAATAACTC---ACTCTCA--CTGGGTA-AC----
TT 2640
               | | |||| ||  | |  | | ||  |||    | ||| | | || | ||
||
Db        2011 C-CTACGAGTTAATCCTTCCTAGC-
ATGGCTCTGAGCCTTCATGCCGAGCAGACGTTATT 2068

Qy        2641 CTCATGATAGATTTGTATGATCAATACGGGTCT------------
ATTTTTATGTCAACT 2688
               | ||||| |||| | |  || | |   | |            |||| ||
|||
Db        2069 CACATGA-
CGATTCGAAAAGTCCATTCATATATCTCGCTACCTGGATTTGAATAGAAACC 2127

Qy        2689 GAACA------
CTGTAGGGTACCTTCCAGTCTTTTTCAAGATTGTTAAATTGAGACAAGT 2742
               |||      || || ||  ||| ||| | |   | |  ||| || ||
||
Db        2128 AGACAGCAATTCTTTA--GTTCCAGCCA-
CCATTCGCCCCACTGGACAATAGCGATTTGT 2184

Qy        2743 AATTGAATAATTTGTCCTATTTTTATTTTAAAAAAAGTGAATGGA-
CTGAAATGTTAAAT 2801
               | | | |    ||| |  |    | ||| ||  | ||| ||| | |  |
||
Db        2185 --TAGCACAG--AGTCACA---GGCTGTGGGACACAAAGCTTGGAGCTGCA--
GAAAGAT 2235

Qy        2802 GTG------AATGTAC-----ATTTCT---
TAATTGCAATTTTTCTACTGAGTGTTTGCA 2847
               | |      | |     ||| |    |   ||||      || |||
|
Db        2236 GGGGGATTCAGAGAACAGGAAATTACAGGCTCGATGCA------CTCCTGG----
CAGCT 2285
```

```
Qy      2848 CTATACTTTCTGGAATCTTATTTAACAAAAATAAAGGGAAAAAATTGCTTGA-CT
2901
             ||    | |   |     |    || ||||| ||| ||  | |  |||| || ||
Db      2286 CTGAGAATACAAAA-----AAAAAAAAAAAAAAAAAAGGCCACATGTGCTCGAGCT
2335


RESULT 15
US-10-478-914-60/c
; Sequence 60, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 2022
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-60

  Query Match            28.3%;  Score 4867;  DB 1;  Length 2022;
  Best Local Similarity  41.7%;  Pred. No. 2.5e-298;
  Matches 1211;  Conservative   0;  Mismatches  756;  Indels  940;
Gaps  147;

Qy         8 CAGGAAATCAGGCCGGGCGCA-
GTGGCTCATGCCTGTAAGCCCAGCACTTTGGGAGGCGG 66
             | |    ||| || || || ||     |||| |        ||| |   ||
|
Db      2022 CTG-----CAGCTCGAGCACATGTG------
GCCTTTTTTTTTTTTTTTTTTAGATGGAGT 1974

Qy        67 AGGCGGGTGGATCCATTGAGGTCAGGAGCTCAAGACCAGCCTGGTCAAC-
ATGGTGAAAC 125
                        | | || ||                 | |||| ||||   | |||| |
|
Db      1973 T------TTGCTCTTTT----------------
GCCCAGGCTGGAGTGCAATGGCGCGAT 1936

Qy       126
CCCGTCTCTACTAAAAATACAAAAAAAAAATTAGCTGGGCGTGTTGGCGGGAGCCTGTAG 185
             | || ||| ||| || | |                |||| ||| | |  ||
|
Db      1935 CTCGGCTC-ACTGCAACTTCCGCCTC--------CTGG----
GTTCAAGCTATTCTCCTG 1889

Qy       186 TCCCAGCTACACGGGAGGCTAAGGT--------------
GGGAGAATTGCTTGAACCCGG 231
             | |||| |  | | |   ||| ||||          | ||| |||||||||| ||
```

```
                  |
Db      1888
CCTCAGCCTCCTGAGTAGCTGAGGTGAGAGGACTGACGCGAGAGGATTGCTTGAGCCTAG 1829

Qy       232
GAGGCGGAGGTTGCAGTGAGCTGAGATTGCACCATTGCACTCCAGCCTGGGCGACAGAGC 291
                 ||||  ||||||||||||||||| | |  ||| || ||||||| ||||| ||||
                  |||
Db      1828
GAGGTTGAGGTTGCAGTGAGCTGTGTTCACGCCCACTGGACTCCAGGCTGGGTGACAAAGC 1769

Qy       292 AAGACTC--
TCTCAAAAAAAAAAAAAAAGAAAGAAAGAAATCAGAAAATCGACCACAGTG 349
                 ||||| |  ||||||||| ||||| ||| ||| ||| ||| | |||||   | |||
Db      1768
AAGACCCTGTCTCAAAAACAAAAACAAACAAACAAACAAACAAAAAAATAACCAACAAAA 1709

Qy       350
GTAGCCACCTGGCCTAATGCTGTGTTTTTGTACCTGACAGGGGTCACTCATTTTAGGCAC 409
                  | |  ||||  | | |  ||||   |||||          ||||
Db      1708 AAAAC--CCTGAGTTTAAGTTTGATTTTAAGACCTG------------------
TAGGGAC 1668

Qy       410 AACTCCTTCATTCTTTGTGAAATTAGTGAGTTTCCTTCTACCCGTCA-
CCAGATTCAATA 468
                  | |   || |||| |   | ||| || || ||| |  | | || |||
Db      1667 AGCAGATTAGTTCT-----
ACTTTAATGGGTATGCATCATCTGGAAAGCAAGGGTCA--- 1616

Qy       469
TGTTCTATTAATACACCGATAACCACAGGGGAAGGGCACTTGTCGCTCTCCCACCTGGTT 528
                  ||| |  ||| | |  ||||        ||| |   |||  |  | |||
Db      1615 --------TAAAAAGAAGAT----ACA----------TCTT----CACTGGCACC--
ATC 1584

Qy       529
ACCACAGTCTCCATGGGTCTTTTGCCGTGACCACAAATAAAGGAAACACTCATCACTAGT 588
                  || |||||| ||         | || | ||| ||  |||
Db      1583 ACATCAGTCATCA---------------GTCCTTAGATACAG--
AAC------------- 1554

Qy       589
ATCTAAGTCGGGCTTTACAGTAACTATGCACCTTCTGTGTGCTTCACCTCACTCTCTACT 648
                  ||||||| |         | || ||   |||| |     |   ||
Db      1553 ------------CTTTACTG-------ACTCCCTC--AAAACTTC------
CATGCTTC- 1522

Qy       649
TCAAACAGCCCATGGAGGGAGGTATTATTATACTCCTTATGTTGACAGTGAAGAATCTGA 708
                  |||||  ||| |||         | || |    |||
Db      1521 -CAAACTAACCAAGCAG-------------TTCTTCT-------
ACA------------- 1496

Qy       709
GGCCCAGAGAGGTTGGGGACTTGAGTAAAGTCACACAGCCCTGAGAGGCAGGACCAGGGT 768
                  |||||  |          ||  |  ||||           ||
                  ||
```

```
Db      1495 ------------TTGGGATC---------ATCGAATTTCCCT-----------TCA-
TGT 1469

Qy       769
TCCATTCCTGCTCTATCCAGTTCCAAGCCCTTGTGTTTTCCATTATGTTTAGTGCCTCTT 828
              |||   || |||||  |   ||| |   |   | ||| |         |||
|
Db      1468 TCCAACTCTCCTCTAGC---TTCAATATACACATAGACAACCTTA--------GCC-
ATC 1421

Qy       829 TGCTAACAGCAACATCTGCAAGATTTGTGT-
TGGTTTTGATGGAGAACTCTAGCTCATCC 887
              || ||| | || | || ||  | ||||| || |||| | ||
|
Db      1420 TGAAAAC--
CTACTTTTAGAATATTCCCGAGTGGTTCCACGTAAGTCCTCTGCCCAGATTC 1363

Qy       888
ACATGCTAGTGCCCAAGTGGTGGAGGGGCCACCTCAGCAGGTGGGTTCTGAATGCAGCCA 947
              |||       | |||| |       | || |||
||||
Db      1362 ACA------TACCCATAAATT-------CTACTTCA----------------
TAAGCCC 1333

Qy       948 AGGCTGTCCCCGCAATGGGTG-
AGACTCGCTCCAACTGCCCGCCCTCAGAGCAGGTGCCT 1006
              |  |||| |    || |   |||   | | |       | | | |   | |
|
Db      1332
ATACTGTTCTTAAAAAAGAAATAGAAAAAATATATCAATATAACTTTAAAATAAGACACA 1273

Qy      1007
AAGTCCTCCCTGGCACTGGCAGGCCTTACCTCACATTGCTAAATTAAAGCAATGCAATTC 1066
              || ||| ||  ||  | ||       | ||| ||| || ||    || || ||
|
Db      1272 AA--CCTTCATGAAAAT-ATAG-----TCATCAAATT--TATTTT----
CATTGGGATGC 1227

Qy      1067
CTCTTGGGTAAGAGGAATTCCTCCTTCTTTACTAACTGATCCCCAGCAAGGAAATAAAAT 1126
              |  ||  | || |||||||||  | || | | |  |   | |||||
Db      1226 CATTT---TTTGAAGAATTCCTAAGACTAATGTTTCT--
TGACATGCAAG---------A 1181

Qy      1127
GTTAGGCTTTAAAAATCCCTACTTTGTCATATCAGACTATATTCTAAAACTATATTTGAG 1186
              ||||  || ||| |  | ||| |              ||||||  ||   ||   |
||
Db      1180 GTTA-GCATTAATAG--CTTACGTT----------ACTATA-
AATACTGCTGCTTGGAAG 1135

Qy      1187 CGAAAC--
CTGTCATTGCGTCTAATTTCAAATATACAGAATCTCCTTAAGAGCTGTTGCC 1244
              |   || |||| | |   ||| |||   ||| || |||| | || |||     ||
|
Db      1134 CAGTACAACTGTTTTAGAG-----TTTTAAGACTACAGACTTTCATTA----
CTCAAATC 1084

Qy      1245 TTATT---TTTTTGTAAAGCCTC-------
TCTGACATCAAATGGGGAGAAATGGTGGC- 1293
```

```
                   |||||   |  ||||||  ||       ||||  | ||  |||  || || |||
     ||
Db      1083 TTATTCAGTAAATGTAAA-AATCAGAAGGTTCTG--AACAGCTGGTTAGGAA-
GGTAGCC 1028

Qy      1294 -ACCTCCAGACACCCTGAAACTAC-ACACCATTTCTT-
CCCTGCTCAGCTTCTGCTCAGG 1350
                  |  |  ||| |  ||   ||   | | || |||||    | || || |  ||
     |||
Db      1027 AAGATGCAGGAAAGATG--TCTGCGCCTCCTTTTCAAGGGCAGC-
CAACTCTTGAACAGT 971

Qy      1351 AGTTCTGTGAGCTATGGGAAGGCCA-
TTGGTTGTATTTGCTACTTTTACTTTCATCTTCC 1409
                  ||    | || |    |  ||| |||   |  | ||| |    || | ||
     |
Db       970 AG------GTGCCA--AAATATCCACATGGCCTTTATAGCTTC---
CACCTGCGTCACAC 922

Qy      1410
TCTGCTGTAGAGCCATTTAATGTTATTGTCATATGCTGCTGGTGAGGTAAAGGTGGGTCC 1469
                  |  |  |  | |  |  |||||| ||| || ||   |||| ||| |||  |||
Db       921 ACAAAT----AACAAAGTAATGTAAATGACA-----TGCT--
TGAAATAA---------- 883

Qy      1470
GGGTGCCTTCCCAGGGGTTAGAGGATGTTCAAAGGGCCGATTTCAGCAGGAGTTCAGAGG 1529
                  |||  ||  ||          |   | |   || | |||  | ||
Db       882 ------CTTGTCA----------
GCAATACTTTGGCTCAATTATATCA------------ 851

Qy      1530
GCTTATGATGGATGGTGAGAGATTTGACAACCACCGAGCACATGTGCTCTGACCCTCTC 1589
                  |||                | ||||  | | | | |||| |
     ||
Db       850 -CTT-------------TAAACTTTGCTTGCAGCAATA--AAATGT----------
ACTA 817

Qy      1590
CTGGGCATTGGTTCCTGCTGGTACCGGGCGGTTCAGACCTTCAAATAGGTTGCTTTCAAA 1649
                  |||||||  ||          | |||| |||        |  ||||
     |||
Db       816 CTGGGCAAATTATC-----------------TCCAGAACTT--------
TGACTTTAAAA 782

Qy      1650
AGAGCTTTCAGGCACTTATTGAGAATTAATGTTTAAACAGACATAATAGCCTAGATGAAC 1709
                  |  | || | || |||||          || |||
Db       781 AATG--TTAAATCAATTATT--------------------
TCAATATA------------ 756

Qy      1710
TCCCAAGAGATCTATTAAATCTTGTGGGCTGAATAAATATCTCGTGCAGGACTGTGCAAC 1769
                  | ||||| | | ||      || |  ||| ||||
Db       755 -------------AATAAATAAT-TAGGC---------CTCACTAACAG--
CTGT----- 726

Qy      1770
AGTAGCCCAGAGCATCCTGCCTGTGGGCATCCACCTCCCAGGTGAGGGCAGTGGGAAGCT 1829
                  ||||   |  ||                |  | || |||
```

```
                     |
Db      725  -----CCCAACACCTC-------------TAC-
CCACCCT-------------------T 704

Qy     1830  GGCCCGACGGCAGCCAG---
AACTTGTTTCTCACCTCCCACCAGCAACCCCCCACCCAAC 1886
             ||| ||    || | ||    | ||  ||| ||     ||| |||    | | |
                     ||
Db      703  GGCTCGGAAACAACTAGTTAGGCCTGAGTCTTACAATTTTTCAGGAACAAGCTAACAAA- 645

Qy     1887  TCTGGGC--
CCCAGGCACACGAAGCACAAGTCTCAGGGGACCATTCCCACATTGGGGGAT 1944
             ||||  |||||||| |  ||| |  |  || |         ||| |||
Db      644  --AGGGCATCCCAGGCAGAGGAAATAATATGCTGA-------
ATTACCA----------- 605

Qy     1945  CCTGAGGGAGCCCATCACCGCCTCTTGCATACAACTGTCCACTAGGAGGCACGCCCAGTG 2004
             ||||||  |    ||| | ||  |||| |  | |       | ||  |
Db      604  CCTGAGTTA---AGTCAAAGGCTTCTGATTCCT--TGTTCAAAA------
TCACCTA--- 559

Qy     2005  TGGGAGAGATGTATGGTCTTGCCTTCCACCTGTAAAAACTGCAC-
ATATGCAAGCCATTT 2063
             |||| ||||| |    ||| || ||| |  |             |
Db      558  ----------TTATGCTCTTG-TTTCC-----
TAATAATTCCACAAAATGTTCAACT--- 518

Qy     2064  GCACTCTGGAACTGCATGCCGTGAAAACTCCTAATGGTGTGGAACTTAGTTTGAATTTGA 2123
             |||||       ||| |  |||| |  || |       || ||  || ||
Db      517  --ACTCT-------TATGACATTAACACTTCAAGAG--AAAGAGCTAAG-------
CTGA 476

Qy     2124  AATCACGCCGCATGCACAAAGGGACAGGCCCAGGCCCGACCTCAGGTCATCCGCCCGCTG 2183
             | ||       ||| |||| | |    |||     ||  |    | |         ||
Db      475  AGTCT---TTCATTCACATAAAGA-------TGACACAATTTAA--
AAAT---------- 438

Qy     2184  GCTGCAGAGCATCCCTGGGAGCCAAGGCGAGGCCCGTGGAGCCTGAGCTTTGTGTAGCTC 2243
             ||| || ||            |||   || |  | |    |||| |  |        |
Db      437  GCTACAAGGC--------------
AGGTATGGACAAAGTACTATGAGGGTAATAAGGAGG 392

Qy     2244  GAGCTTTGTGTAGCTCGTGCACTTATTATGCACCACCTCCCTTCAGTCACCACTCCTCTT 2303
             || ||  || || |  || |     |        |                      |
                     |||||
Db      391  GA---ATGATTAACACG----CTAAAAAT-------------------------
ATACTCTT 362

Qy     2304  CCTCCGCCATCCTCATTTATACTGATTGCAC-
ACCCCCCGCTCAAACAACAATGTCCTTA 2362
             | |||| |  ||| | |       |  ||  ||     |||||  | |  || |
Db      361  --------AACCTAA--TGAAATGAAAGTACTGCCTTCC---CAAAC--
CGAAGTTC--- 320
```

```
Qy       2363 TTATGATGACCATCTCGTAGTGGTACA-
TTCCATTCCTATTTAAGGTAAGCCCAAAGCCC 2421
                             | |  |||  |||| ||  | |  ||||||| ||| ||||||
Db        319 ---------AAAACAGGTATATTTACATTTAAAATTGTATTTAAAATAA-
TTCAAAGCTT 270

Qy       2422
ACTTTTGGATTTTCTCGACTGTCCGAGAAAAGTTGTGTAAGCGCCTGCGTTCTTCTGGGT 2481
                ||                                        | || ||
Db        269 AC--------------------------------------
CACCAGC----------- 261

Qy       2482
TTGGCTAGATAGGGTTGTGTCCCTCTATGGAATGGAGAGTGATGTGGGCAAGGGTGTCAT 2541
                            ||     |||| |                | || |   ||| |
Db        260 ----------AG--------CCCTTT----------------
TCTGACCGTAGGTAAC-- 237

Qy       2542
TTTCTCGCACAATACAACTCACTGAGGATGCTTCTGTAGAAGTGAGAAACACGATGAGTA 2601
                        |||| |   ||| || | |||||
|||
Db        236 TTTCCCATCAAATTCATC-CACTG----------------------------------
GTA 211

Qy       2602
CATTCAGAATTACAATAACTCACTCTCACTGGGTAACTTCTCATGATAGATTTGTATGAT 2661
                | ||         ||| |  ||| | || |||   ||| ||
Db        210 CCTT---------TATATCCGGCTCAACCTGAGAA-------
ATGGTA----------- 179

Qy       2662 CAATACGGGTCTATTTTTATGTC-------
AACTGAACACTGTAGGGTACCTTCCAGTCT 2714
                || | |||| | ||||| | || ||| ||      |||| |  | || || | | || |
|
Db        178 CAGTTCAGGTGTTCTTCTATCTCAGATAGTAACTAAGTAATGGAGAGAAAATTTC---
CA 122

Qy       2715
TTTTCAAGATTGTTAAATTGAGACAAGTAATTGAATAATTTGTCCTATTTTTATTTTAAA 2774
                      | ||       || ||| ||| ||| | ||| | ||||| |
|||||
Db        121 AATAAAA----ATTTCATTTAGA-AAG-AGTTG--TATTTTATCATC-------
ATTAAA 77

Qy       2775
AAAAGTGAATGGACTGAAATGTTAAATGTGAATGTACATTTCTTAATTGCAATTTTTCTA 2834
                     ||||   || | | | |  || |   |  | |||      ||| ||||
|
Db         76 TAAAG---CTGGCCAGTAG-GCCAACAGTGCTCGAGGAATTC-----
CGCAGCTTTTAGA 26

Qy       2835 -CTGAGTGTTTGCACTATACTTTCTGG 2860
                | || | |||| | | | | ||
Db         25 GC--AGAAGTAACACT-TCCGTACAGG 2


Search completed: March  9, 2010, 15:51:56
Job time : 13.4075 secs
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                              GenCore version 6.3
                   Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                           (without alignments)
                                           1134.946 Million cell
updates/sec

Title:          US-10-572-905-8
Perfect score:  19543
Sequence:       1 gcgggcgggccggcggcgg.........aaaaaaaaaaaaaaaaaaaa
3056

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:      834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      7335755.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                                   SUMMARIES
                    %
Result            Query
   No.    Score  Match Length DB  ID                        Description

-----------------------------------------------------------------------
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     1    7203   36.9   3210  1   US-10-478-914-4            Sequence 4,
Appli
 c   2  6879.5  35.2   3210  1   US-10-478-914-4            Sequence 4,
Appli
     3    6611   33.8   3589  1   US-10-478-914-21           Sequence 21,
Appl
 c   4  6319.5  32.3   3589  1   US-10-478-914-21           Sequence 21,
Appl
     5    6214   31.8   2437  1   US-10-478-914-61           Sequence 61,
Appl
 c   6  6092.5  31.2   2437  1   US-10-478-914-61           Sequence 61,
Appl
     7    5788   29.6   2120  1   US-10-478-914-64           Sequence 64,
Appl
 c   8    5725   29.3   2120  1   US-10-478-914-64           Sequence 64,
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Appl c	9	5415.5	27.7	2495	1	US-10-478-914-20	Sequence 20,
Appl c	10	5339	27.3	2198	1	US-10-478-914-17	Sequence 17,
Appl	11	5283.5	27.0	2495	1	US-10-478-914-20	Sequence 20,
Appl c	12	5269.5	27.0	2336	1	US-10-478-914-57	Sequence 57,
Appl	13	5207.5	26.6	2198	1	US-10-478-914-17	Sequence 17,
Appl	14	5054	25.9	2336	1	US-10-478-914-57	Sequence 57,
Appl c	15	4731.5	24.2	2083	1	US-10-478-914-3	Sequence 3,
Appli c	16	4643	23.8	1946	1	US-10-478-914-62	Sequence 62,
Appl	17	4628	23.7	1946	1	US-10-478-914-62	Sequence 62,
Appl c	18	4627.5	23.7	2022	1	US-10-478-914-60	Sequence 60,
Appl	19	4489.5	23.0	2083	1	US-10-478-914-3	Sequence 3,
Appli	20	4294.5	22.0	2022	1	US-10-478-914-60	Sequence 60,
Appl c	21	4115	21.1	1813	1	US-10-478-914-63	Sequence 63,
Appl	22	3967.5	20.3	1813	1	US-10-478-914-63	Sequence 63,
Appl	23	2437.5	12.5	889	1	US-10-478-914-5	Sequence 5,
Appli	24	2387.5	12.2	816	1	US-10-478-914-15	Sequence 15,
Appl c	25	2375.5	12.2	816	1	US-10-478-914-15	Sequence 15,
Appl	26	2369.5	12.1	867	1	US-10-478-914-6	Sequence 6,
Appli c	27	2359	12.1	867	1	US-10-478-914-6	Sequence 6,
Appli	28	2351.5	12.0	717	1	US-10-478-914-42	Sequence 42,
Appl c	29	2289	11.7	889	1	US-10-478-914-5	Sequence 5,
Appli	30	2274	11.6	839	1	US-10-478-914-16	Sequence 16,
Appl	31	2229	11.4	794	1	US-10-478-914-13	Sequence 13,
Appl c	32	2229	11.4	794	1	US-10-478-914-13	Sequence 13,
Appl	33	2208	11.3	1020	1	US-10-478-914-68	Sequence 68,
Appl	34	2204	11.3	816	1	US-10-478-914-38	Sequence 38,
Appl	35	2203	11.3	839	1	US-10-478-914-16	Sequence 16,
Appl c	36	2195.5	11.2	889	1	US-10-478-914-9	Sequence 9,
Appli c	37	2193.5	11.2	816	1	US-10-478-914-38	Sequence 38,
Appl	38	2175	11.1	1020	1	US-10-478-914-68	Sequence 68,

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Appl
    39  2171.5  11.1   889  1  US-10-478-914-9      Sequence 9,
Appli
    40   2167   11.1   938  1  US-10-478-914-69     Sequence 69,
Appl
  c 41  2156.5  11.0   811  1  US-10-478-914-37     Sequence 37,
Appl
  c 42   2135   10.9   938  1  US-10-478-914-69     Sequence 69,
Appl
  c 43  2126.5  10.9   717  1  US-10-478-914-42     Sequence 42,
Appl
  c 44   2098   10.7   820  1  US-10-478-914-39     Sequence 39,
Appl
    45   2092   10.7   854  1  US-10-478-914-7      Sequence 7,
Appli
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                             ALIGNMENTS

RESULT 1
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match   36.9%; Score 7203; DB 1; Length 3210;
  Best Local Similarity   46.1%; Pred. No. 0;
  Matches 1625; Conservative   0; Mismatches 1095; Indels 802;
Gaps 225;

Qy   1 GCGGGGCGGGCCGGC-GGCGGGAGGCCGGGC-
CGCGGAGCCAGGAGTGACTAGCAGCAGTT 58
              || | |||| | ||| ||||| || | || |||| | || |
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Db   1 GCACTGTTGGCCTACTGGCCCAGGCCTTGCACACG----CAGGTG---CTCTC-----
TT 48

Qy   59
GGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGGAGGCGCGTGGTGCG 118
                |||| |||| || || || | |||| ||
|

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Db        49 ---AGTGC----------TCCCTGGCAAGGATGG----------GAAGGCAT---
GTTCA 82

Qy       119 GGTTTCGGCGGCGGCTGAGGAAGAAGCGCGGGCGGCGCCTTC-GGGAGGC---
GAGCAGG 174
              |   |  ||| || | || ||| |  |  ||| ||| | | ||| |  ||
|
Db        83 GTCCTAGGAGTAGGAAGGGGCAGAGGTGTTGATGGCCCCTACAGAGCGGCCAAGGACAAG 142

Qy       175 CAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGGAGGCGC 234
                 ||| || || | ||| | ||| | || || | |  | | || ||||
|
Db       143 GAGCTGCTGTTCGAAAC--AGC--CTTCCTGCTCCC--
CAACCTGCCTCCCA-------C 189

Qy       235 GTGGCGGCGCTCGGCCT---
CGCGGCGGCGGCGGCGGCAGCGGCCCAGCAGTTGGCGGCG 291
                  | | | || |  | | ||| | ||    | | || |        ||
|
Db       190 CCAACAG-GTTTTGCATATACTCTACTG-GGAAGAGG----GACACACC------
CGAC- 236

Qy       292 AGCGCGTCTGCGCCTGCGCGGCGGGCCCGCGCCCCTCCTCCCCCCCTGGGCGCCCCCGG 351
                 ||    |||| ||| |  ||| ||| | | || | | || |  |||| ||||
|
Db       237 TGCATCACTGC-CCTCCAAGTCTCTCCCTGC-
CCTGTCCAGCATCCAGGAGCACCCCTAG 294

Qy       352 CGGCGTGTGTGAAT-
GGCGGCCTCCGCGGCGGCGGCAGCCTCGGCAGCAGCG------------- 397
                 | |   | |    ||| | || | | |  || | | |||||| || | || |
Db       295 TTGGGGAAGCTTCTGTGACTCCCCCTACAACAGCCTAGGATGGAGTGGGGTTTGTGAACA 354

Qy       398 ---GCC-TCGGCCGCCT-----------CTGGCAG--CCCGGGCCCG-
GGCGAGGGCTC 438
               || |  ||| | ||          ||| ||  ||| |||| | ||| ||
Db       355 AATGCAGAAGGCAGTCTTAGGGAGGTCAGCTGACATGCCCCTGGCCTGTGGCTGGGAAGT 414

Qy       439 CGCTGGCGGCGAAAAGCGCTCCACCGCCCCTTCGGCCGCAGCCTCGGC----
CTCTGCCT 494
               || | ||| ||  || || |||| |   ||  |  | ||| ||     | |||
|
Db       415 AGC-AGAGGC-TAAGGTTCTTCCCCGC----TCTGGGGTTGCC-
AGGAGTAGCACTGGAT 467

Qy       495 CAGCCGCGGCGTCG----TCGCC-CGCGGGGGGCGGCGCC-GAGGC-
GCTGGAGCTGCTG 547
               ||| |  | |   |   ||    || |  | | || |||| ||      || |
Db       468 CAGTC-AGGTGACAGGGCTCTCCTCTCTCTGAGCAGGTCCGGTGGCAGC-----
CTTCAA 521

Qy       548 GAGCACTGCGGCGTGTGCAGAGAGCGCCTGCGACCCGAGAGGGAGCCC--
CGCCTGCTGC 605
               |  | |  || ||| | |    | | ||  |   | | | || |  ||| ||
|
Db       522 GGTCGCCACGCCGTATTCCCTGTATGTCT--GTCCCGAGGGGCAGAACGTCACC--
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CTCA 577

Qy          606 CCTGTTTGCACTCGG--CCTGTAGTGCCTGCTTAGGGCCCGC---GGCCCCCGCC--
GCC 658
                ||||   || || ||  ||||| |       |  ||||| ||    | ||  | ||
|
Db          578 CCTGCAGGCTCTTGGGCCCTGTGG-----
ACAAAGGGCACGATGTGACCTTCTACAAGAC 632

Qy          659 G----
CCAACAGCTCGGGGGACGGCGGGGCGGCGGGCGACGGCACCGTGGTGGACTGTCC 714
                |      |  |||||||| ||   |||| || || | | || |   | |  | |
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Db          633 GTGGTACCGCAGCTCGAGG---GGCGAGGT-GCAGAC--CTGCTC---
AGAGCGCCGGCC 683

Qy          715
CGTGTGCAAGCAACAGTGCTTCTCCAAAGACATCGTGGAGAATTATTTCATGCGTGATAG 774
                  | |  |||| ||     ||     |||| | || |          | ||| ||
|
Db          684 CATCCGCAACCTCACGT-----TCCAGGACCTTC-------------
ACCTGCACCATGG 725

Qy          775
TGGCAGCAAGGCTGCCACCGACGCCCAGGATGCGAACCAGTGCTGCACTAGCTGTGAGGA 834
                 ||| | ||||||||| |  | ||| ||     ||| || || |||  || |||
|||
Db          726 AGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGC--CACGGGCT----
GGA 779

Qy          835 TAATGCC-CCAGCCACCA--
GCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACCTG 891
                |||  || |||||| ||     | ||| |       | |  |  || |
|||||
Db          780 GTCGGCCTCCGACCACCATGGCAAC---------TTCTC--
CATCACCATGCGCAACCTG 828

Qy          892 -------TG--TAGAGGCGCAC-----CAG-CGGGTGAAGTACACCAAGGACCA-
TACTG 935
                       ||  ||| ||| | |      | | |||| | | | ||| | ||||
|||
Db          829 ACCCTGCTGGATAGCGGC-
CTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTC 887

Qy          936 TGCGCTCTACTGGG-CCA----GCCAAGTCTCGGGATGGTGAACGTACTGTCTA--
TTGC 988
                 | ||   || |||  |||     |||| |  | || |       | ||| | |
|||
Db          888 GGAGC---ACAGGGTCCATGGTGCCATGGAGCTGCA-GGTG--
CAGACAGGCAAAGATGC 941

Qy          989 AACGTACACAAGC---ATGAACCCCTTGTGCT----
GTTTTGTGAGAGCTGTGATACTCT 1041
                | | | |   | |     || |||| | | |    |       |||| ||    |
|
Db          942
ACCATCCAACTGTGTGGTGTACCCATCCTCCTCCCAGGAGAGTGAAAGTAAGGGACCAAC 1001

Qy          1042 CACCTGCC------GAG---ACTGCCAGCTCAATGCCCACAAGGACC----
ACCAGTACC 1088
                 | | ||||       | |    ||| || || || ||        ||
||||
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 ||
Db       1002 CTCTTGCCCCTTTTGGGTTCTCTGTTTTCT-TCTGTCCTCA---
TCCTGCACCCAGACCC 1057


Qy       1089 AGTTCTTAGAGGATGCAGTGAGGAACCAGCGCAAGCTC-
CTGGCCTCACTGGTGAAGCGC 1147
              |||        | |  | | |      | || |||||| | |   | | | ||||     |
|
Db       1058 TGTTT----GGAACTCTG-
GCCTCATCACCCCAAGCCCTCAGAACCCCCCGGTCCTCCTC 1112


Qy       1148 CTTGGGGACAAACATGCAACATTGCAGAAGAGCACCAAGGAGGTTCGCAGCTCAATCCGC 1207
              |||       |       || | | |   | || || |          |||||
|
Db       1113 CTTTTCTGCTGCTGCACATCCCTTCTGCTTC-CTCCTTGGTG----------
CAATCC-C 1160


Qy       1208 CAGGTG---
TCTGACGTACAGAAGCGTGTGCAAGTGGATGTCAAGATGGCCATCCTGCAG 1264
              |||  |   ||  | | |    | | ||   |||| |||    || | ||| ||
Db       1161 CAGAAGCCCACTCTCCTTC-----CATCTGCTC-TGGA-GTCT--
CTGCTCCTCTTGACT 1211


Qy       1265 ATCATGAAGGAGC--TGAATAAGCGGGGCCGTGTG--CTGGTCAATGATGCC-
CAGAAGG 1319
              || || ||   || |     || | ||| |   | | |  || |||     |||| ||
Db       1212 CTC-TGGAGTGGCTGTGCCTTGGCAGTGACCTTTGGCCAGGGCAA--
GTGCCTCA----- 1263


Qy       1320 TGACTGAGGGGCAGCAGGAGCGCCTGGAGCGGC--
AGCACTGGACCATGACCAAGATCCA 1377
              ||||  ||| |    |||| ||   ||   || |  | || || ||
|||
Db       1264 TGAC--AGGTACTG--GGTGCCCCAG--GCAGCTAAGTGCCG--CCCTGCCCA----
CCA 1311


Qy       1378 GAAGCACCAGGAGCACATTCTGCGCTTTG---
CCTCTTGGGCTCTGGAGAGTGACAACAA 1434
              |  |   ||      ||     | |||  |  |||||||| |    | | | ||
||
Db       1312 GC--CCCCTATGGCTTGGGAAG-
GCTGGGGGTCCTCTTGGCCAACAGGGTGAAACCCCAT 1368


Qy       1435 CAC-------AGCCC----TTTTGCTTTCTAAGAAGTTGATCTAC-----
TTCCAGCTGC 1478
              || |       | |      || ||      | | | || |      | ||||||
|
Db       1369
CTCTACTAAAAACACAAAAATTAGCCAGGCATGGTGGTGCGCGCCTGTAGTCCCAGCTAC 1428


Qy       1479 ACCGGGCCCT----CAAGATGATTG-
TGGATCCCGTGGAGCCACATGGCGAGATGAAGTT 1533
              |  |   ||     |||||  | | || ||||  |||| |||| ||          ||
|||
Db       1429 TCAAGAGGCTGAGGCAAGAGAATCGCTTGAACCCG-GGAGTCA-----------
GAGGTT 1476


Qy       1534 TCAGTGGGACCTCAATGCCTGGACCAAGAGTGCCGAGGCCTTTGGCAAGATTG-
TGGCAG 1592
```

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                  |||||           |||  || |     | |||   || |   | ||  || ||
||
Db      1477 GCAGTG---------AGCCGAGATC----GCGCCACTGCACT---
CCAGCCTGCTGATAG 1520


Qy      1593 AGCGTCCTGGCACTAACTCAACAGGCCCTGCACC-------CATGGCC----------
CC 1635
                  ||   | | | | || | |||||| |   |   | ||      | ||||
|
Db      1521 AG---
CAAGACTCCATCTCAAAAAAAACAACCCAAAATTTGCCTGGCATGGTGGCAGGCA 1577


Qy      1636
TCCAAGAGCCCCAGGGCCCCTGAGCAAGCAGGGCTCTGGCAGCAGCCAGCCCATGGAGGT 1695
                  ||    | |||     || || | | || |   || ||| ||  |  | |||
|
Db      1578 TCTGTAATCCC---
AGCTACTCGGGAGGCTGAGACATGAGAGCTGCTTGAACCTGGGAG- 1633


Qy      1696
GCAGGAAGGCTATGGCTTTGGGTCAGGAGATGATCCCTACTCAAGTGCAGAGCCCCATGT 1755
                  |||| |        | ||  || | |  |||| | | ||  | | |||   ||
||
Db      1634 GCAGAA-----GTTGCAGTGAGCC--GAGATCA-CACCACTGCACTCCAG---
CCTGGGT 1682


Qy      1756 GTCAG-GTGTGAAACGGTCCC-------------
GCTCAGGTGAGGGCGAGGTGAGCGGC 1801
                  | ||| | || | |||||          ||| |   ||  ||| ||   |
Db      1683
GACAGAGCGAGACTCTGTCCCAAAAAATCAAAAAAATCACTTTTGGTAGAGATGCAC--T 1740


Qy      1802 CTTATGCGC-AAGGTGCCACGAGTGAGCCTTGAACGCCTGG-----------------
AC 1843
                  ||   ||| | ||| | || | |  |||||||||| |||||
||
Db      1741 CT----CGCTATGTTGCCCAGGCTG-
GTCTTGAACTCCTGGGCTCAATTGATCTTCCCAC 1795


Qy      1844 CTGGACCTC---------------ACAGCTGACAGCCAGCCA--
CCCGTCTTCAAGGTCT 1886
                  || ||||||            |||| ||  ||||| |||  ||   | ||| !!
|
Db      1796 CTTGACCTCCAAAGTGCTGGGATTACAGGTGTGAGCCA-
CCATGCCTAGCCTCAGGGAAT 1854


Qy      1887 TCCCAGGCAGTAC-CACTGAGGACTACA--ACCTTATTGTTATTGAACGTG----
GCGCT 1939
                  || |   || || | ||| |   ||  ||| ||| | | | ||    | |
Db      1855 TCTTA-
TAAGAACTCTATGAAGTAGGCATCACCATCTTCTCTGTATCCATGGAAAGAGAG 1913


Qy      1940 GCC----GCTGCA-
GCTACCGGCCAGCCAGGGACTGCGCCTGCAGGAACCCCTGGTGCCC 1994
                  |||   | | |||| |  |    | |||| | | |    | ||| |||
Db      1914 GCCTAGAGATGTATGCTAACTTGC--CCAAG--CT-CACAT-----
AGCCCCAGGGT---- 1959


Qy      1995 CACCCCTGGCTGGCATG----GCCATTGTCAAGGAGGAGGAGACGGAG--
GCTGCCATTG 2048
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```
                        |  |  |||||  |||      ||     |  |  |||||||  ||  |  ||   ||||  ||
Db      1960  --AGCATAGCTGGGATGTTGAGCTGAGGCC--
GGAGGAGAAGTAGCAGTCGCTGGCA--- 2012

Qy      2049  GAGCCCCTCCTACTGCCACTGAGGGCC---CTG----------
AGACCAAACCTGTGCTT 2095
                        |||  |  |  |   |||  |  |||  |||      |||            ||  ||   ||  |  |
Db      2013  GAG-CACACAGGCTG-
CTCTGGGGGATGAGCTGGTGCGTTTAAGGAACAGGCCAGCAC-- 2068

Qy      2096  ATGGCTCTTGC----------GGAGGGTCCTGGTGCTGAG---GGTC-----
CCCGCCT-- 2136
                          ||||   |  ||            |  ||||    |  |||  |||   ||||     ||  |  ||
Db      2069  -
TGGCATTCGCAAGCAGTGGGGAAGGGGAGAGATGCCGAGGTGGTCAGTATCCTGACTTT 2127

Qy      2137  ----GGCCTCACCTAG--
TGGCAGCACCAGCTCAGGGCTGGAGGTGGTGGCTCCTGAGG- 2189
                           |||||    |  |  |          |  |  |  ||     |      ||||  |
||
Db      2128  
CAGAGGCCTTTTTTTGTTTGTTTTAATTTTTGCTAGATTGATATTAAAAACTCATGTGGA 2187

Qy      2190  GTACCTCAGCCCCAGG------TGGTGGCCCGGGAACCCTGGATGACAG-------
TGCC 2236
                         |  |  ||||        |||         |  |  |  ||    |  ||   |||||||
||
Db      2188  GGAACTCA-----
AGGAATGTTTAGAAGACCAAAAGTCCCCAATGACAGGAACAAAAGCA 2242

Qy      2237  
ACCATTTGCCGTGTCTGCCAGAAGCCAGGCGATCTGGTTATGTGCAACCAGTGTGAGTTT 2296
                          ||||  ||   |  |  |             |||  |           ||  ||     ||  ||  |
||
Db      2243  ACCAATT--TTTAACTTTC------------TCTTCTCAT-----
TCCTGTTTTCATTG 2282

Qy      2297  TGTTTCCACCTGGACTGTCACCTGCCGGCCCTGCAGGATGTACCAGGGGAGG-
AGTGGAG 2355
                           ||  ||||  ||  |  |      |||    |    ||  |||||  ||     |||||
|||
Db      2283  ATTTCCCACATGTAGT----CCTTTTG---CT-
CAGGAAGTCTTTGGGGAAATTAAGGAT 2334

Qy      2356  CTGCTCA-CTCTGCCAT--GTGCTCC-----------CTGAC--
CTGAAGGAGGAGGAT 2398
                           ||  |  |||||  ||  |||  ||         |||  |  |||     |  ||||
|
Db      2335  CTTTGAAGCTCTGAAATAGGTGATCAGGTTAGTGGTGTCTGTCAGCTGTC-
TAAGAGGTT 2393

Qy      2399  GGCAGC--CTCAGC-
CTGGATGGTGCAGACAGCACTGGCGTGGTGGCCAAGCTCTCACCA 2455
                           ||  |       |   |  |  |||  ||   ||  |   ||||       ||        ||  ||
Db      2394  
GGAAAATGAACTACTCAAGATAGTCACGAAAATACTGAAAGTTTGATTTTTCTTTC---- 2449

Qy      2456  GCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCC----
CTATTCTGTCACGAACCCTG 2511
                          |  |   |     |||  |||   |  |||    ||||           |  ||  |  ||  ||   |
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Db        2450 -CATATTTGAATTAATTTTTTC-
TGTTTGACTGGAAGGGGTTTTTGTATAACTAAAACCT 2507

Qy        2512 CCGCCCCCTGCATCAGCTGGCTACCGAC--TCCACCTTCT-----------
CCCTGGAC 2557
                | ||   |||| |  | |    |     ||| |  |           || ||
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Db        2508 CAGC-----
GCATAAAGGAGATTTAAAAGGAGCACATGATTTAGTGGGTGGGCCATGAAA 2562

Qy        2558 C---AGCCCGG---------------TGGCA--CCCTGGA-
TCTGACCCTGATCCGTGCC 2596
                |   ||  ||                || ||   ||||| | | | ||   | |
|
Db        2563 CTAGAGATGGGATTTGGGGGTGAATTTGTCAATATCTGGATTTTAATCCAGA--
CATCTC 2620

Qy        2597 CGCCTCCAGGAGAAGTTGTCACCTCCCTACAGCTCC----CCAC------------
AGGA 2640
                || |  ||     ||| |  | || ||| |  |   || |              ||
Db        2621 TGCTAAC--
GAGCCTTTGGTAAGTCACTTCAGATACTTTTCCTCCTTTTTACAAAGAGAG 2678

Qy        2641 GTTTGCCCAGGATGTGGGCC---GCATGTTCAAG--C--AATTCAACAAG-----
TTAAC 2688
                | || |  | | |  ||| |   ||  ||| || |  | |||||| |||||     ||
||
Db        2679 GGCTGGCTTAGTTATTTGCCAAAGCCCCTTCCAGGCCTGAATTCCACAAGTACGATTTAC 2738

Qy        2689 TG-AG-GACAAGGCAGACGTGCA-
GTCCATCATCGGCCTGCAGCGCTTCTTCGAGACGCG 2745
                || || |  |  || ||  ||  ||    ||  || ||  |      || ||||
|
Db        2739 TGTAGTGTCTTATCACTCTTTCATGTC--ACAATAGCGTGGAGC----
ATTAGAGAAAAG 2792

Qy        2746 CATGAAC---------GAGGCC---------TTCGGTGACACCA----
AGTTCTCTGCTG 2783
                | |  ||          |||         || ||| |  |  |||| |  |
Db        2793 CCTAGACTTTTAGTTGATAGCCAGTTGAAATATCATTGATAGAATTTTAGTTTTAGGAAA 2852

Qy        2784 TGCTGG-TGGAGCCCCCGC-------CGATGAGCCTGCCTG-GTGCT--
GGCCTGAGTTC 2832
                ||| | ||    |  ||       | || ||  | || | ||| |||  |
Db        2853 AATTGGTTTGATTTCTAGCTTTATTACTATTAG---GTATGTGAGCTTGGGC---
AAATC 2906

Qy        2833 CCAGGAGCT----GTCTGG-TGGCCCTGGTGATG-GCCCCTGAGGC----
TGGAGCCCCC 2882
                |   | ||  |||| |  | |   ||| | |  ||||| |  |           ||
Db        2907 GCTTAATCTTTGAGTCTAGTTTTCTCTCAAAATGAGAACATTAGGCTAAATGATTTCCGA 2966

Qy        2883 ATGGCCAGCCCAGCCTGGC--TCTGT-
TCTCTGTCCTGTCACCCCATCCCCACTCCC--- 2936
                | ||||| |||  |   ||| | |  ||| || |     || |    |
Db        2967
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GTTTCCAGCTAGTCCTAGAGTTCTATATTTCTACATAGTTGAATTATTTTATCATGCTGT 3026


Qy      2937 --CTGGTGGC-CTGACTCCCACTCCCTGGTGGCCCC---------
ATC----------- 2972
                |||| |    ||||| | ||  | |  || |          ||
Db      3027 TGCTGGGGAATATGACTAACCCT--
TTTGAAGCTACTAATTTTATGTCGAGCTTTAAAGT 3084


Qy      2973 CCCCAGT-----TCCTC--ACGATATGGTTTTTACTTCTGTG----------
GATTTAAT 3015
                || | |     || || | |||| |||  || | ||
|||||||
Db      3085
CCATAATTGTTATCTTCAGAAAATATTATTTGACCTACAGTATGTCCAAATCAATTTAAT 3144


Qy      3016 AAAAAAAACTTC-ACCAGTTCAAAAAAAAAAAAAAAAAAAA 3056
                ||||       || | |||   |||||||||||||||||||||
Db      3145 AAAATCGCTTTATAACAGGAAAAAAAAAAAAAAAAAAAAAAA 3186



RESULT 2
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match             35.2%;  Score 6879.5;  DB 1;  Length 3210;
  Best Local Similarity   43.8%;  Pred. No. 0;
  Matches 1566;  Conservative    0;  Mismatches 1096;  Indels  911;
Gaps  220;

Qy        11 CCGGCGGCGGAGGCC---------------------------GGGCC----
GCCGAGCC 38
                |  ||    | ||||                            ||
|||
Db      3209
CGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTGTTATAAAGC- 3151

Qy        39 AGGAGTGACTAGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGC-----
GCGGCGGGC 93
                |   | | ||    | |||| | | |||| | |||||    |||       | |  |
Db      3150 -GATTTTATTAAATTGATTTGGACATACTGTAG----
```

```
GTCAAATAATATTTTCTGAAGAT 3096

Qy        94 AGC------GGCCCAGGAGGCGCGTGGTGCGGGTTTCGGCGGC----
GGCTGAGGAAGAA 143
             | |      || |    | || ||    |      |    || |    || | ||  |
|
Db      3095
AACAATTATGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATAT 3036

Qy       144
GCGCGGGCGGCGCCTTCGGGAGGCGAGCAGGCAGCAGTTGGCCGTGCCGTAGCAGCGTCC 203
             | |  | | | || |  | |   |  | |    |          |||| |   |
Db      3035 TCCC---CAGCAACAGCATGATAAAATAATTCAACTAT----------
GTAGAAATATAG 2989

Qy       204 CGCGCGCGG-CGGGC-AGCGGCCCAGGAGGCGCGTGGCGGCGCTCGGCCTCGC----
GGC 257
               | |  || || || |  | | | | | |  |  | | ||  |    | |||
|
Db      2988 AACTCTAGGACTAGCTGGAAACTCGGAAATCATTTAGC--
CTAATGTTCTCATTTTGAGA 2931

Qy       258 GGCGGC--
GGCGGCAGCGGCCCAGCAGTTGGCGGCGAGCGCGTCTGCGCCTGCGCG---- 311
             | |  | | | ||  |   ||| || ||  | |  | |   |   ||| |
Db      2930 GAAAACTAGAC-TCAAAGATTAAGCGATTTGC-CCAAGCTCACAT--
ACCTAATAGTAAT 2875

Qy       312 ---GC-GGGCCCCGCGCCCCTCCTCCC---
CCCCTGGGCGCCCCCGGCGGCGTGTGAA-T 363
               || |     |  | || | |  |      |      |  |   |  | | ||
|
Db      2874
AAAGCTAGAAATCAAACCAATTTTTCCTAAAACTAAAATTCTATCAATGATATTTCAACT 2815

Qy       364 GGCGGCCTCCGCGGCGGC--AGC----
CTCGGCAGCAGCGGCCTCGGCCGCCTCTGGCAG 417
             |||  |    |  | |   | |  ||    |||   ||    || ||    || | |
Db      2814 GGCTATCAACTAAAAGTCTAGGCTTTTCTCTAATGCT----CCACG-----
CTATTGTGA 2764

Qy       418 CCCGGGCCCGGGCGAGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCCTTCGGCC-- 475
             | | |  | |||| |   |   |         | ||| | |  |    |   | ||||
Db      2763 CATGAAAGAGTGATAAGACACTAC------
AGTAAATCGTACTTGTGGAATTCAGGCCTG 2710

Qy       476 ---
GCAGCCTCGGCCTCTGCCTCAGCCGCGGCGTCGTCGCCCGCGGGGGGCGGCGCCGAG 532
               |  || | ||| |   || |||| |         |||| |       |
|||
Db      2709 GAAGGGGCTTTGGCAAATAACTAAGCC----------
AGCCCTCTCTTTGTAAAAAGGAG 2660

Qy       533 GCGCTGGAGCTGCTGGAGC---ACTGCGG--
CGTGTGCAGAGAGCGCCTGCGACCCGAGA 587
             |  | || ||| |   |    |   | || ||| |||||| | |||
||
Db      2659 GAAAAGTATCTGAAGTGACTTACCAAAGGCTCGTTAGCAGAGA-TGTCTG--------
GA 2609
```

```
Qy        588
GGGAGCCCCGCCTGCTGCCCTGTTTGCACTCGGCCTGTAGTGCCTGCTTAGGGCCCGCGG 647
                |  || |  ||| |    |  |    | | ||  ||    |   |
||
Db      2608 TTAAAATCCAGATATTGACAAATT--CACCC--CC--
AAATCCCATCTCTAGTTTCATGG 2555


Qy        648 CCCCCGCCGC--CGCCAACAGCTCGGGGGACGGC-------
GGGGCGGCGG--------- 689
              ||| | || |       ||  ||||     |   |        | || ||
Db      2554 CCCAC-
CCACTAAATCATGTGCTCCTTTTAAATCTCCTTTATGCGCTGAGGTTTTAGTTA 2496


Qy        690 -GCGACGGCACCGTGGTGGACTGTCCCGTGTGCAAGCAACAGTGCTT-
CTCCAAAGACAT 747
               |  |  ||          |||  |  ||| ||   ||  | |||| |
Db      2495 TACAAAAACCCC----------TTCCAGT---
CAAACAGAAAAAATTAATTCAAATATGG 2449


Qy        748 CGTGGAGAATTA---TTTCA-----TGCGTGAT-------AGTGG---------
CAGC-- 781
               | |  ||| |   |||||     |  | |||||       ||| |       || |
Db      2448
AAAGAAAAATCAAACTTTCAGTATTTTCGTGACTATCTTGAGTAGTTCATTTTCCAACCT 2389


Qy        782 --AAGGCTGCC-ACCGACGCCCAGGATGCGAACCAGTGCTGCACT-----
AGCTGTGAGG 833
              || || ||   || ||| ||    |  ||||| |  |  |    |||| |
|
Db      2388 CTTAGACAGCTGACAGACACC------
ACTAACCTGATCACCTATTTCAGAGCTTCAAAG 2335


Qy        834 AT-----AATGCCCCAGCCACCAGCTACTGTGTGGAGTGCTCGGAGCCT--
CTGTGTGAG 886
              ||     | | | |||||| ||   ||      | ||     | ||    ||||
||
Db      2334 ATCCTTAATTTCCCCAAAGACTTCCT----------
GAGCAAAAGGACTACATGTGGGAA 2285


Qy        887 ACCTGTGTAGAGGCGCACCAGCGGGTGAAGTACACCA-----------
AGGACCATACTG 935
              |  || | || |  | |  |  | ||||  | |||| |       | ||  |
Db      2284
ATCAATGAAAACAGGAATGAGAAGAGAAAGTTAAAAATTGGTTGCTTTTGTTCCTGTCAT 2225


Qy        936 TG--------CGCTCTACTGGGCCAGCCAAGT----
CTCGGGATGGTGAACGTACTGTC- 982
              ||        | ||| || |  ||   |||  ||| | ||    || ||
||
Db      2224 TGGGGACTTTTGGTCTTCTAAACATTCCTTGAGTTCCTCCACAT-
GAGTTTTTAATATCA 2166


Qy        983 -TATTGCAACG---TACACAAGCATGAA----CCCCT---TGTGCTGTTTTGTGA-
GAGC 1030
               | | ||||     | |||| || ||   || ||   || | |   ||| |
|
Db      2165 ATCTAGCAAAAATTAAAACAAACAAAAAAAGGCCTCTGAAAGT-
CAGGATACTGACCACC 2107
```

```
Qy       1031 TGTGATACTCTCACCTGCCGAGACTGCCAGC-----TCAATGCCCACAAGGACC--
ACCA 1083
              |   |    |||||  |||  ||    |||||   ||      ||  |||    |   |   ||   |
Db       2106 TCGGCATCTCTCCCCTTCC-
CCACTGCTTGCGAATGCCAGTGCTGGCCTGTTCCTTAAAC 2048

Qy       1084 GTACCAGTTCTT-----AGAGGATGCAGTGAG--
GAACCAGCGCAAGCTCCT-------- 1128
              |  ||||||  ||  |       |||| |   ||| |       ||||||     ||| |||
Db       2047 GCACCAGCTCATCCCCCAGAGCAGCCTGTGTGCTCTGCCAGCGACTGCTACTTCTCCTCC 1988

Qy       1129 GGCCTCACTGGTGAAGCGCCTTGGGGACAAACATGCAACATT--
GCAGAAGAGCACCAAG 1186
              ||||||||  |  |  ||    ||         ||   ||||  ||  |   ||   |   ||   |   |
Db       1987 GGCCTCA--GCTCAACATCC-------CAGCTATGCTACCCTGGGCT-
ATGTGAGCTTGG 1938

Qy       1187 G-AGGTTCGCAGCTCAATCCGCCAGGTGTCTGACGTACAGAAGCGTG--TGCA-
AGTGGA 1242
              |  |  |||  |||   |   |||   |  |||   |||   ||| | | |        | ||   |  ||  ||
Db       1937 GCAAGTTAGCA--TACATCT-CTAGGCCTCT--CTTTC-----
CATGGATACAGAGAAGA 1888

Qy       1243 TGTCAAGATGGC--CATCCTGCAGATCATGAAGGAG----
CTGAATAAGCGGGGCCGTGT 1296
              ||    ||||  |   |  ||  |||| | ||  ||       |||    |  ||   |||
Db       1887 TG--GTGATGCCTACTTCATAGAGTTCTTATAAGAATTCCCTG---
AGGCTAGGCATGGT 1833

Qy       1297 GCTGGTCAATGATG----CCCAGAA----GGTGACTGAG--GGGCAG--CAG--
GAGCGC 1342
              |  |  |||     ||     |||||| |      ||  |      ||  ||| ||    ||    ||||
Db       1832 G--
GCTCACACCTGTAATCCCAGCACTTTGGAGGTCAAGGTGGGAAGATCAATTGAGC-C 1776

Qy       1343 CTGGAG--CGG---CAGCACTGGAC--
CATGACCAAGATCCAGAAGCACCA--------- 1386
              |  |||||  |      ||||  |||| |  | ||       ||||
Db       1775 CAGGAGTTCAAGACCAGC-
CTGGGCAACATAGCGAGAGTGCATCTCTACCAAAAGTGATT 1717

Qy       1387 -------------GGAGCACATTCTGCGCTTTGCCTCTTGGGCT------
CTGGAGAGTG 1427
              || || ||||  ||||  || |  |     ||||       |   |   |
Db       1716 TTTTTGATTTTTTGGGACAGAGTCT-
CGCTCTGTCACCCAGGCTGGAGTGCAGTGGTGTG 1658

Qy       1428 ACAAC--AACACAGC-
CCTTTTGCTTTCTAAGAAGTTGATCTACTTCCAGCTGCACCGGG 1484
              |    |    |||  || || |||  |    |  | | | |             |||  |||  ||
Db       1657 ATCTCGGCTCACTGCAACTTCTGCCTCCCAGG-------------
TTCAAGCAGCT----- 1615

Qy       1485
```

```
CCCTCAAGATGATTGTGGATCCCGTGGAGCCACATGGCGAGATGAAGTTTCAGTGGGACC 1544
            |||   ||| |   |  | |||||  |  ||               ||    || |||
Db      1614 --CTC---ATGTCTCAGCCTCCCGAGTAGC------------
TGGGATTACAG------- 1579

Qy      1545 TCAATGCCTGGACCAAGAGTGCCGAGGCC---TTTGGCAAG---
ATTGTGGCAGAGCGTC 1598
                 |||||||| |||  ||| ||||||||     ||||| |   || || | |
                 |||
Db      1578 ---ATGCCTG--CCACCA-TGCC-
AGGCAAATTTTGGGTTGTTTTTTTTGAGATGGAGTC 1526

Qy      1599 CTGGCACTAACTCAACAGGC---CCTGCACCCATGGCCC--------
CTCCAAGAGCCCC 1647
                 | || |||  ||| |||||     ||||     |||| |        ||| |
                 ||
Db      1525 TT-GCTCTA--TCAGCAGGCTGGAGTGCA---
GTGGCGCGATCTCGGCTCACTGCAACCT 1472

Qy      1648 AGGGCCCCTGAG--CAAGCAGGGCTCTGGCAGCAGCC-----
AGCCCATGGAGGTGCAGG 1700
                 | | || | |  |||||     |||| ||  |||||     ||     ||| |
                 ||||
Db      1471
CTGACTCCCGGGTTCAAGCGATTCTCTTGCCTCAGCCTCTTGAGTAGCTGGGACTACAGG 1412

Qy      1701 AAGGCT---------ATGGC-----TTTGGGT-----------
CAGGAGATGATCCCTAC 1735
                 ||        ||||     |||| ||               || | |   ||||
Db      1411
CGCGCACCACCATGCCTGGCTAATTTTTGTGTTTTTAGTAGAGATGGGGTTTCACCCTGT 1352

Qy      1736 T---
CAAGTGCAGAGCCCCATGTGTCAGGTGTGAAACGGTCCCGCTCAGGTGAGGGC--- 1789
                 | ||||| || |||| |||        | |||| |   | |||||
Db      1351 TGGCCAAG---AGGACCCC------CAG--------
CCTTCCCAAGCCATAGGGGGCTGG 1309

Qy      1790 -GAGGTGAGCGGCCTTATGC-GCAAGGTGCCACGAGTG--
AGCCTTGAACGCCTGGACCT 1845
                 | |  | ||||| |  || || || || | ||| |  || ||||      || |
                 |||
Db      1308
TGGGCAGGGCGGCACTTAGCTGCCTGGGGCACCCAGTACCTGTCATGAGGCACTTGCCCT 1249

Qy      1846 GGACC----TCACAGCTGACAGCCAGCCAC-CC-----GTCTT------
CAAGGTCTTCC 1889
                 || |    |||| || |    ||||||| ||     |||       || | |
                 |||
Db      1248 GGCCAAAGGTCACTGCCAAGGCACAGCCACTCCAGAGAGTCAAGAGGAGCAGAGAC-
TCC 1190

Qy      1890 CAGGCAGT--------------
ACCACTGAGGACTACAACCTTATTGTTATTGAACGTGG 1935
                 ||||                | |||| ||| | ||| |   |   | |
                 |
Db      1189 AGAGCAGATGGAAGGAGAGTGGGCTTCTGGGGATTGC-
ACCAAGGAGGAAGCAGAAGGGA 1131

Qy      1936 CGCTGCCGCTGCAGCT----------
```

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ACCGG---------------------------- 1956
        |  |||  ||  ||||           |||||
Db      1130 TG-
TGCAGCAGCAGAAAAGGAGGAGGACCGGGGGGTTCTGAGGGCTTGGGGTGATGAGGC 1072


Qy      1957 -------CCAGCCAGGGACTGCGCCTGCAG------------
GAACCCCTGGTGCCCCA 1996
              |||  |||||  |||  |  |||||         |||   |    |  |||
                                                                  |
Db      1071 CAGAGTTCCAAACAGGGTCTGGG--
TGCAGGATGAGGACAGAAGAAAACAGAGAACCCAA 1014


Qy      1997 ------CCCCTGGCTGG--CATGGC---
CATTGTCAAGGAGGAGGAGGAGACGGAGGCTGCCA 2045
              |    |   ||  ||| |  ||||  |    ||  |  ||   |  |||||||   |  |
||||
Db      1013 AAGGGGCAAGAGGTTGGTCCCTTACTTTCACTCTCCTG--
GGAGGAGGATGGGTACACCA 956


Qy      2046 ---------TTGGAGCCCCT---CCT-ACTGCCACTG-AGGGCCCTGAGACCA---
AACC 2088
                     |||  ||   ||   |||  ||||  |||  ||  ||  ||  ||||   |
                                                                      ||
Db      955
CACAGTTGGATGGTGCATCTTTGCCTGTCTGCACCTGCAGCTCCATGGCACCATGGACCC 896


Qy      2089
TGTGCTTATGGCTCTTGCGGAGGGTCCTGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAG 2148
             ||||||     |   ||  |||  ||||  ||      |  ||  ||  ||||   ||
|||
Db      895 TGTGCT------CCGAGTGGTGGTGCCTGAT-CT-----CCACCACCAGGCAGCA-
GTAG 849


Qy      2149 TGGCAGC--ACCAGC----TCAGG----GC-TGGAGGTGGTG-----
GCTCCTGAGGGT- 2191
               |||  ||   |||||     |||||     ||  |||  |||  |      ||  ||
|||
Db      848 AGGCCGCTATCCAGCAGGGTCAGGTTGCGCATGGTGATGGAGAAGTTGC-
CATGGTGGTC 790


Qy      2192 --------ACCTCAGCC------------CCAGGTGGTGGCCCG----
GGAACCCTGGAT 2227
                      ||  |||||         ||||||  |||||   |     ||  |  |||||
              |
Db      789
GGAGGCCGACTCCAGCCCGTGGCGCTGAGCCAGGTCGTGGCTGGTGTTGGCAGCCTGG-T 731


Qy      2228 GACAGTGCCACCAT-TTGCC-GTGTCTG-
CCAGAAGCCAGGCGATCTGGTTATGTGCAAC 2284
              |     |||  ||||  |||  |||   |  | | |  |    |   | |  ||  ||| ||
Db      730 G-----GCCTCCATGGTGCAGGTGAAGGTCCTGGAACGTGAGGTTGCGG--
ATGGGCCGG 678


Qy      2285 CAGTGTGAGTTTTGTTTCCACCTGGACTGTCACCTGCCGGCCCTGCAGGAT---
GTACCA 2341
               |  |  ||||                || || |||  |||||   ||  ||||    |  |
||||||
Db      677 CGCTCTGAG------------CAGGTCTG-CACCT--CGCCCCT-
CGAGCTGCGGTACCA 634
```

```
Qy      2342 GGGGAGGAGTGGAGCTGCTCAC-TC-TGCCATGTGCTCCCTG---------
ACCTGAAGG 2390
               |   || ||   | |||| || |||| | ||  | |         |||| 
|||
Db       633 ----
CGTCTTGTAGAAGGTCACATCGTGCCCTTTGTCCACAGGGCCCAAGAGCCTGCAGG 578


Qy      2391 AGGAGGATGGCAGCCTCAGCCT--GGATGG---
TGCAGACAGCACTGGCGTGGTGGCC-- 2443
               |||| || |   ||  ||| ||| |  |||  |  || |||||| | ||
Db       577 T-GAGGGTGACGTTCTGCCCCTCGGGACAGACATACAGGGAATAC-
GGCGTGGCGACCTT 520


Qy      2444 --
AAGCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTC 2501
               | ||| |||| | ||| ||     | ||| |  |    | |||
Db       519 GAAGGCTGCCACCGG---ACCTGC-----TCAGAGAGAG----GAGAGCC-----
CTGTC 477


Qy      2502 ACGAACCCTGCC--
GCCCCCTGCATCAGCTGGCTACCGACTCCACCTTCTCCCTGGACCA 2559
               |  ||||| ||    || |||  | ||||| |       ||| |
|
Db       476 A-----CCTGACTGATCCAGTGCTACTCCTGGCAAC--------------
CCCAG----A 440


Qy      2560 GCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCT----
CCAGGAGAAGTTGT 2615
               || || ||| |    | | ||| | | || |||    ||||| | |
|||
Db       439 GCGGGGAAGAACC-----TTAGCCTCTGCTACTTCCCAGCCACAGGCCAGGGGCA--
TGT 387


Qy      2616 C-----
ACCTCCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCCGCATGTTCAA 2670
               | |||||||| ||  ||||||| ||      || |
Db       386 CAGCTGACCTCCCTAAGACTGCCTTCTGCA-TTTGTTCA------------
CAAACCC-- 342


Qy      2671 GCAATTCAACAAGTTAACTGAGGACAAGGCAGACGTGCAGTC-
CATCATCGGCCTGCAGC 2729
               || | || | ||| | |||   || | |   ||| | || | | |
|
Db       341 -CACTCCATCC--TAGGCTGTTGTAGGGGGAGTC--
ACAGAAGCTTCCCCAACTAGGGGT 287


Qy      2730 GCTTCTTCGGAGCACGCGCATGAACGAGGCCTTCGGTGACACCAAGTTCT---
CTGCTGTGC 2786
               ||| ||   || ||   || || |||       | |||    || |    ||| ||
Db       286 GCTCCT---GGATGC---
TGGACAGGGCAGGGAGAGACTTGGAGGGCAGTGATGCAGT-C 234


Qy      2787 
TGGTGGAGCCCCCGCCGATGAGCCTGCCTGGTGCTGGCCTGAGTTCCCAGGAGCTGTCTG 2846
               |||| ||| | |        || | |         | | |  || | |||
Db       233 GGGTGTGTCCCTCTTC----------CCAGTAG------
AGTATATGCAAAACCTGTTGG 190
```

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Qy       2847 GTGGCC--CTGGTGATGGCCCCTG-
AGGCTGGAGCCCCCATGGCCAGCCCAGCCTGGCTC 2903
              ||||    |  |||   ||  |  ||||||   |   ||    |||| |  | || |
Db        189 GTGGGAGGCAGGTTGGGGAGCAGGAAGGCTGTTTCGAACAG---CAGCTC--
CTTGTCCT 135

Qy       2904 TG--TTCTCTGTCCTGTCACCCCATCCCCACT-
CCCTGGTGGCCTGACTCCCACTCCCT 2960
              ||   ||||||  | | |  || | ||  || ||  |||||           ||| |||||
Db        134 TGGCCGCTCTGTAGGGGC-CATCAACACCTCTGCCCCT-----------
TCCTACTCCTA 87

Qy       2961 GG--TGGCC---CCATCCCC-CAGTTCCT-----
CACGATATGGTTTTTACTTCTGTGGA 3009
              ||  ||  |   || |||| |  | |  | ||     ||| |   |       |  ||| |
Db         86 GGACTGAACATGCCTTCCCATCCTTGCCAGGGAGCACTAAGAG-----
AGCACCTGCGTG 32

Qy       3010 TTTAATAAAAAAAAACTTCACCAGTT--CAAAA 3040
              |           ||  ||   |||||  | | |
Db         31 T------GCAAGGCCTGGGCCAGTAGGCCAACA 5


RESULT 3
US-10-478-914-21
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match           33.8%;  Score 6611;  DB 1;  Length 3589;
  Best Local Similarity   42.8%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches 1272;  Indels  864;
Gaps  210;

Qy          2 CGGGGCGGGCCG-----------GCGGCGGAGG---CCGGGC---
CGCGGAGCCAGGAGT 44
              | ||    |||             | |||  ||   ||| |   ||| |   || |
|
Db          6 CTGGATTCGCCATCATTTTGCACACTGCGAGGGGCTCCGTGTGTGCGC----
CCTGTCTT 61
```

```
Qy          45
GACTAGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGG 104
             || || |    |    || || |      |   | || |||| | | |   || | ||   || |
|
Db          62 GTCTGGCCGTCCTCATCCCTTCCCCCACCCCCTGCCGC-
CACTCCGACCCGCTCCCAAAG 120

Qy          105 AGG---CGC-
GTGGTGCGGGTTTCGGCGGCGGCTGAGGAAGAAGCGCGGGCGGCGCCTTC 160
                || | |   |   | || || || |    |||||      | |  ||| ||||
Db          121 TGGCTTCACAATAGT-CGGTCCTCGGCG---------------
GTGTAGGCTGCGC---- 160

Qy          161 GGGAGGCGAGCAGG-
CAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAG 219
                  | |||| | || ||  ||    || ||   |||    | |   |
Db          161 -------
ACCAGGTCCACACTTAAGCGAAATCAAGGAGACCCCCTTCTACTTCTACCTT 212

Qy          220 CGGCCCAGGAGGCGCGTGGCGGCGCT-
CGGCCTCGCGGCGGCGGCGGCGGCAGCGGCCCA 278
                 ||   || ||  |  |||  ||| ||  | |    || |   || | |||| |
Db          213 TGGGTTTGGT-GCTCAATGCGAAGCTGCTGCAACTCAGACACGCCTAAGTCAAC--
TCAT 269

Qy          279
GCAGTTGGCGGCGAGCGCGTCTGCGCCTGCGCGGCGGGCCCGCGCCCCTCCTCCCCCCC 338
                 ||||      || ||    || | |  | |         || |   | || ||     |
||
Db          270 GCAGAAAAAGGAGA-AAAGTTTTGGTATAC---
AAATGCTCTCAGTCCAGCCAGACACCA 325

Qy          339 TGGGCGCCCCCGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCA--
GCCTCGGCAGCAGC 396
                  |    ||| | | ||| |||| |||| || |  ||||      || | |||| | |
|
Db          326 AG-------CCGAAAGGTTGTG-CTGGCTGCAACCGAAAGATCAAGGAC-
CGGTATCTTC 376

Qy          397 ----GGC-CTCGGCCGCCTCTGGC----
AGCCCGGGCCCGGGCGAGGGCTCCGCTG---- 443
                     ||| || |    |||||    || | |    || | | || | |||| | ||||
Db          377 TAAAGGCACTGGACAAATACTGGCATGAAGACTG---CCTGAAGTGTGC-
CTGCTGTGAC 432

Qy          444 ----GC---GGCGAAAAGCGCTCCACC---
GCCCCTTCGGCCGCAGCCTCGGCCTCTGCC 493
                     ||   ||    | | |||||||||      | ||     ||    | | ||    ||| ||
|
Db          433 TGTCGCTTGGGGGAGGTGGGCTCCACCCTGTACACTAAAGC--
TAATCTTATCCTTTGTC 490

Qy          494 TCAG-------CCGCGGCGTCGTCG--CCCGCGGGGGGCGGCGCCGAGGCGCTGGAG-
CT 543
                 |||        | | ||| |  |    |||| | |||| |    ||| ||
Db          491 GCAGAGACTATCTGAGGC-TCTTTGGTGTAACGGGAAACTGCGCTGC----
CTGTAGTAA 545

Qy          544 GCTGGAGCACTGCGGCGTGTGCAGAGAGCGCCTGCGACCCGAG---
AGGGAGCCCCGCCT 600
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                  |||      ||    | | | | || |||  | |  |||| || ||   | |     ||
     Db      546 GCT----CATCCCTGCCTTTG-AGATGGTG-
ATGCGTGCCAAGGACAATGTTTACCACCT 599

Qy      601 G--CTGCCCTGTTTGCAC-TCGGC-CTGTAGTGCCTGC---
TTAGGGCCCGCGGC----- 648
              |  |||| |||||| ||| ||  |||| |  |     || | |   | | |
     Db      600 GGACTGC----TTTGCATGTCAGCTTTGTAAT--
CAGAGATTTTGTGTTGGAGACAAATT 653

Qy      649 ---CC---------CCG----CCGCCGCCA-ACAG-CTCGGGGGACGG---
CGGGGCGGC 687
                      ||          |   ||  |||| || | ||  | ||| ||        |
     Db      654
TTTCCTAAAGAATAACATGATCCTTTGCCAGACGGACTACGAGGAAGGTTTAATGAAAGA 713

Qy      688 GGGCGACGGCACCGTGGTGGACTGTCCCGTGTGCA-AGCAACAGTGCTTCTCCAAAG-
AC 745
                  || | |  || ||| ||| | |  ||  |  || ||| |    | ||| ||
     Db      714
AGGTTATGCACCCCAGGTTCGCTGATCTATCAACATCACCCCATTAAGAATACAGAGCAC 773

Qy      746 ATCGTGGAGAATTATTTCATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGCC--
CAGG 803
                   | |      | ||| |||  | |    ||  |   || ||| |   || |
     Db      774
TACATTCTTTTATCTTTTTTGCTCCACATGTACATAAGAATTGACACAGGAACCTACTGA 833

Qy      804 AT-GC---GAACCAGTGCTGCA--
CTAGCTGTGAGGATAATGCCCCAGCCACCAGCTACT 857
                  || || || || ||| || | ||| |        || | | |
     Db      834 ATAGCGTAGATATAGGAAGGCAGGATGGTTATATGGAATA---
AAAGGCGGACTGCATCT 890

Qy      858 GTGTGGAGTGCTCGGAGCCTCTGT---
GTGAGACCTGTGTAGAGGCGCACCAGCGGGTGA 914
                  || || |||      ||| ||| | |      ||| ||       | |    ||
     Db      891 GTATGTAGTG-
AAATTGCCCCAGTTCAGAGTTGAATGTTTATTATTAAAGAAAAAAGTAA 949

Qy      915 AGTACACCAAGGAC------------CATACTGTGCGCTCT------
ACTGGGCCAGCCA 956
                  ||||| | |        | | ||| | |     ||| ||| |
     Db      950 TGTACA--
TATGGCTGGATTTTTTTGCTTGCTATTCGTTTTTGTGTCACTTGGCATGAGA 1007

Qy      957 AGTCTC----GGGATGGTGAACGTACTGTCTATTGCAACGT-----
ACACAAGCATGA-- 1005
                  || |     || |  | | | || |  ||||| ||  |    ||||| | |
     Db      1008 TGTTTATTTTGGACTATTGTATATAATG--
TATTGTAATATTTGAAGCACAAATGTAATA 1065

Qy      1006 ----------------ACC---------CCTTGTGCTGTTTTGTGAGAGCTG----
```

```
TGATA 1037
                            |||          || | ||||  ||||| |  | ||       |
 ||
Db      1066 CAGTTTTATTGTGTTACCATTTGTGTTCCATTTGCTTCTTTGT-
ATTGTTGCATTTAGTA 1124

Qy      1038 CTCTCACCTGCCGAGACTGCCAG---
CTCAATGCCCACAAGGACCACCAGTACCAGTTCT 1094
              | ||| ||  | ||| ||     |  |  | |||| |      ||||| | ||
|
Db      1125 CAATCA-GTGTTTAAACTTACTGTATATTTATGCTTTCTGTATTTACCAG---
CTATT-T 1179

Qy      1095 TAGAGGATGCAGTGAGGAACCAGCGCAAGCTC------
CTGGCCTCACTGGTGAAGCGCC 1148
              || | || || |    | ||  |    |         |   |||||| ||| |
|
Db      1180 TAAATGA-
GCTGTAACTTTCTAGTAAAGAATTGAAAAGCAAATCTCACTAATGATACACA 1238

Qy      1149 TTGGGGACAAACATG-----CAACAT----------------
TGCAGAAGAGCACCAAG- 1186
              |   || || |   ||||||                  |   |||    |||
 ||
Db      1239
GATAGATAAAGCAAGTCTATCAACATTAAAAATACTAAAAAATAAAGACACACACAGAGC 1298

Qy      1187 --------GAGGTTCGCAGCTCAAT-CCGCCA------GGTGTCTGAC---
GTAC----- 1223
                 || | | | || | |||| |        | |||| |   || |
Db      1299
ATTTTAGTGACATCCACTACTTATTGCCGCTATGAGTTAGAGTCTATCAGTGTTCTTGTT 1358

Qy      1224 AGAAGC----
GTGTGCAAGTGGATGTCAAGATGGCCATCCTGCAGATCATGAAGG----A 1275
              | | |       | | | || |    || |    |     |    ||| ||
 |
Db      1359 ATAACCCCCTATTTTCAGG-
GGGTTAAAAATCAGCTTTAAAAAAATACATAAAAATTTCA 1417

Qy      1276 GCTGAATAAGCGGGGCCGTGTGCTG-----GTCAATGATGCCC-----
AGAAGGTGACTG 1325
              || |  ||||    | | |     || ||  ||||     |||| |
 |||
Db      1418 TCTTA--AAGCACTTTCATTTTATACCAACGTGAAAAGTGCCATTTTTAGAA--
TAACTT 1473

Qy      1326 AGGGGC--AGCAGG----------AGCGCCT-------GGAGCGGCAGCACTGG-
ACCAT 1365
                || | |||||          |   |||        | || |   ||| ||
 ||
Db      1474 TAAAGCTTAACAGGTTTCCTTTTAATATCCTTTTTTTGTGTGC-
TCTTTACTTACACAAT 1532

Qy      1366 GACCAAG--------ATCCAGAAGCACCAGGAGCACATTCTGCG--CTT-
TGCCTCTTGG 1414
              | |   |        | ||| ||||       | || | |  || |||||
 ||||
Db      1533 GGCTTTGTTTTGCTTTTTCAGCCACACC-------CCTTATGTGAACTAGTGCCT-
TTGG 1584
```

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Qy      1415 G----------------CTCTGGAGAGTGAC----AACAAC----
ACAGCCCTT-----T 1445
                 |              ||  || || ||   || | |   || | ||
Db      1585
GTATCACGTAAAATTTTTTCCAAAGGGTTACTTTAAAAATCTGTTACCACAATTATGAGA 1644

Qy      1446 TGCTTTCTAAG----AAGTTGATCTACTTCCAG--------
CTGCACCGGGCCCTCAAGA 1493
                 || ||| ||||    || || | || |||| |      |||| | |  | ||| |
                                                                         |
Db      1645
TGATTTTTAAGTGATAAATTAAACTTCTTCTTGTATAAATTCTGCCCAGATCTCTCCACA 1704

Qy      1494 TGA-TTGTGGATCCCGTGGAGCCACATGGCGAGATGAA----------------
GTTTC 1535
                  ||  || || |  || |  | |   ||||||   || ||
                 |||
Db      1705 AGAGCTGAGGGTTTCAT--
AACTTTATGGCTTAATAAATGTATGACACTGAAAAGATTTG 1762

Qy      1536 AGTGGGACCTCAATGCCTGGA---CCAAGAGTGCCGAGGCCTTTG--GC-
AAGATTGTGG 1589
                 |||| ||| || | |||  | | || || |      | ||| || | ||| ||
Db      1763 AGTGTGA-ATCTA---CTGAAATCACTATAATGC-----
ACATTGAAGCTATGATGGTAT 1813

Qy      1590 CAGAG-CGTCCTGGCACTAACTCAACAGGCCCTGCA-----
CCCATGGCCCCTCC----- 1638
                 ||| ||  | |||   |  |  || |  ||     | ||| |    || |
Db      1814 TTGAGTAGTGAGGTTACTT--
TTGATCGGAGCAACATAATGCTCATAGAATCTTCTAGAA 1871

Qy      1639 -AAGAGCCCCAGGGCCCCTGAGCAA--GCAGGGCTCTGG---------------
CAGCA- 1679
                 |||||   || |   ||| || || | | || |            | |
Db      1872
GAAGAGAAACAAAGGGATTGATAAAATGCTGAGAACTAGTGATTATATATTTTTCTGTAT 1931

Qy      1680 --GCCAGCCC-----ATGGAGGTGCAGGAAG--------------------------
GCT 1706
                 || | |       |  | || ||  |||
                 ||
Db      1932
TTACCTGACATTTATTTTAATGTTCAAAAAGTAAACACTTTAAGTTTGATGTGTTTTACT 1991

Qy      1707 ATGGCTTTGGGTCAGGAGATGATCCCTACTCAAGT--------------
GCAGA-----G 1747
                 |  | |||  | | |   || | | || |||||                 || ||
                 |
Db      1992 CTCTCATTGTTTTAAGTAAT--
TGCCAACTCAGAATACATCATTCTTAGGCTGAAATTTG 2049

Qy      1748 CC---CCATGTGTCAGGTGTGAAACGGTCCCG-CTCAGGTGAGGGC-------
GAGGTGA 1796
                 |   |||| | | | |||||| || |   || | |||| ||          || |
Db      2050 TCTTTCCATTTTTTAAG-
GTGAAATAGTACTACCTTACGTGATAGCATACAAAGAAGAAA 2108
```

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Qy        1797 GC----------GGCCTTAT-GCGCAAGGTGCCACGAGTGAGCCTT--
GAACGCCTGGAC 1843
               ||          |   |||| | | | |    | | |   || | |     |
Db        2109
GCTCTAGAAAGAGAAATTATGGAGAATGATTATTTAAATTACAATTAAGGAAATGAGAAT 2168

Qy        1844 CTGGACCTCACAGCTGA-CAGCCAGCCACCCGTCTTCAAGGTCT----TCCCAG--
GCAG 1896
                 ||  || | |  | || |  ||| | | |  |||| | |    |||| |
Db        2169
ATGATCCCCTCTTCCGAGTTGCCCACAAACTTGCTTCTTTGCTTTTGCTCCCTGTAATAG 2228

Qy        1897 TACCACTGAGGACTACAACCTTATTGTTATTGAACGTGGCGCTG------------
CCGC 1944
                 || |||    | |||| |    | | ||| ||  ||| | |             |
Db        2229 AACTACT-----TTTCAACAAATCTAATTTTGCAC--
GGCACCGTTAACCATATTTTCAC 2281

Qy        1945 TGCAGCTACCGGCCAGCCA-GGGACTGCGCCTGC----
AGGAACCCCTGGTGCCCCACCC 1999
                | |||| | |    || | ||| | ||  | |             | || |    |
Db        2282 TACAGCAAACTTAGTGCTATGGGTTTTCTTTTTCTTTGTTTTTTTCTTGAT------
CAC 2335

Qy        2000 CTGGCT-GGCATGGCCATTGTCAAGGAGGAGGAGACGGAGGCTGCCATTGGA----
GCCC 2054
                 || | ||| |    |||| || ||      |     ||| | |    |
Db        2336 TTGTATAGGAAACAACATTTTCCAG----------
TGTTATTTGCATATATATTTTGTCC 2385

Qy        2055 CTCCTA---CTGCC--ACTGAGGGCCCTGAGA--
CCAAACCTGTGCTTATGGCTCTTGCG 2107
                ||| |   ||| |||   | | | |    | |||||        ||||
Db        2386 TTCCAATATATGCATTACAGATGAAAATTAAATGTTATACCTG-------
AATTCTTGGG 2438

Qy        2108 GAGGGTCC------TGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAGTGGCAGCAC-
CAG 2160
                 ||| ||      |   ||||| |    |||| |   | || |   ||
Db        2439 TTGGGGCCAAAATATTAAGCTGAAAATAAT--
GCTGGTGTGGATTTGTTTTAAAACAAAG 2496

Qy        2161 CTCAGGGCTGGAGGTG---GTGGCTCCTGAGGGTACCTCAGC---CCCAGGTGGTGG-
CC 2213
                 ||    || | || |    ||| || ||   | |||| |     ||    |||
Db        2497
CTTTATTATGAACATGCATGTGAATCTGGATATTGCCTCTTATTTTTAAGAAAATGGTTC 2556

Qy        2214 CGGGAACCCTGGATGACA---GTGCCACCATTTGC--C--------
GTGTCTGCCAGAAG 2260
                 | ||| || |||| |    |    ||| ||| |            | |||| | ||
```

```
Db      2557
TGTGAAAAGTGAATGATATGTATTTTTCCAAATGCTTCATGGTTAGGAGTCTTCAAGTT- 2615

Qy      2261 CCAGGCGATCTGGTTATGTG--CAACCAGTGTGAG----------------
TTTTGTTT 2301
             ||| |    |  | |||| |    || |  |  ||               ||| |
Db      2616
CCATGTTCCCCAGATTTGAGATATACTAAAGAAAGAAATTCAAAAGTAGCTATTTGGGGC 2675

Qy      2302 CCACCTG---GACTGTCA------
CCTGCCGGCCCTGCAGGATGTACCAGGGGAGGAGTG 2352
             ||||    ||| | |   |||    |||  |||| ||   |||  || |     ||
                                                                        |
Db      2676 CCACAAAAATAACTATTATTTTAGCCTTAGAGCCTTACA-
CTTGTTTCATGAAGAGAAAG 2734

Qy      2353 GAGCTGC-TCACTCTGCCATGTGCTC----CCTGACC-------------
TGAAGGAG-- 2392
             || ||| | ||  | |  |   |     |  | |||            || ||||
Db      2735 GACTTGCATAAC----
CAAAATAAACAAAGCAAGACAAATTAAAAATATGTGGGGGAGAG 2790

Qy      2393 ----GAGGA---TGGCAGCCT-----CAGCCTGGATGGTGCAGA-
CAGCACTGGCGTG-- 2437
             | |  |   |||     ||    |||||  | |||| |   | |  || || | ||
Db      2791 ATCAGTGAAAAGTGGTTTTCTTAATGCAGCCCTGCTGGTCCCCATTAACAATTGCTTGAA 2850

Qy      2438 ------------------------GTGGCCAAGCTCTCA-
CCAGCCAACCAGCGGAAATGT 2473
                                     | | || ||| | ||| | |    | |
                                                                       |
Db      2851
ATTCACATGGGATGTAAAATTATAATTGTCAGGATCTTATTCAGATGATCTTTTAAGGT-T 2909

Qy      2474 GAGCGTGTACTGCTGGCCCTATTC----TGTCACGAACCCTG---------------
CCG 2514
              |  |   || ||||     | || |||||  | | ||                     |
Db      2910
TAACTGGTTTTGCTTTTGTTTATCTATATGTCAAAATACTTGTAAATTGGGAACAAACTT 2969

Qy      2515 CCCCCTGCATC-AGCTGGCTACCGACTCCACCTTCTCCCTG---
GACCAGCCCGGTGGCA 2570
             | | || | |   |         | |||    |||| | ||| |   ||||| | |
Db      2970 CTCTCAGCTTCTTGAAGTTGTTCAACT-
ATCCTTGCCACTGGAAGACCAAACAAGGTTTT 3028

Qy      2571 CCCTGGATCTGACCCTGATCCGTGCCCGCCTCCAGGAGAAGT-
TGTCACCTCCCTACAGC 2629
             | |||   ||    || | | |        ||   ||||||| | ||    | |
                                                                        |
Db      3029 CACTG---CTTTTTCTTTTACATAATATGCT----
GAGAATTATTTCTTATGCTTTTTAC 3081

Qy      2630 TCCCCACAGGAGTTTGC-CCAG-------GATGTGGGCCGCA---
TGTTCAAGCAAT--- 2675
             || | ||| | |  | |  | |         |||   |||| |   |||| |    || 
Db      3082
TACAAACAAAATTACTCACCTGGATTAAAGATTAAGGCCTTAATCTGTTTAGATTATCTT 3141
```

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Qy        2676 ---
TCAACAAGTTAACTGAGGACAAGGCAGACGTGCAGTCCATCATCGGCCTGCAGCGCT 2732
                   ||  || |  | |     | ||| || | |   |||   ||| | |    ||
|
Db        3142 TAATCTCCATGAAATCGTGAAATAAGAC--
AAGAATAGTGTTTCAGCTGTAGGCCATTTT 3199

Qy        2733 TCTTCGAGACGCGCATGAA-
CGAGGCCTTCGGTGACACCAAGTTCTCTGCTGTGCTGGTG 2791
                    |  | |   || || |  | | || |||   |||| ||  ||  |  |
||
Db        3200 ACAGCTAATTGCCCATAAATTGTAGCATTTATTGACCTGAAGTACTAAGC--
TAATTGTC 3257

Qy        2792 GAGCCCCCGCCGATGAGCCTGCCTGG--TGCTGGC--
CTGAGTTCCCAGGAGCTGTCTGG 2847
                    |  | |    |||| |||| || || | ||  |||||    | |||
|
Db        3258 TTGACTACTC---AAAGCC--CCTGAATTGTTGTCAACT---TTCCCCTTTG-
TGTTGTG 3308

Qy        2848 TGGCCCTG--GTGATGGCCCCTG-AGGCTGGAGCCCCCA--TGGCCAGCCCAGCCTG-
GC 2901
                    | ||||| || || |  | || | |||  ||| |||  || || | | |   |
Db        3309
TAGCCCTAACGTCATTTAGCTTGTTGTCTGATGCCTCCAGTAGGACACCTCCGATGGAGC 3368

Qy        2902 TCTGTTCTCTGTCCTGTCACCCCATCCCCACTCCCCTGGTGGCCTGACTCCCA----
CTC 2957
                    | || ||| | |    |  ||  |  ||  || ||||   | | || ||| ||
||
Db        3369 TTTGATTTCTGAGCAG----CGAAAGCTCCCTTCCTAAGATGCAT--
CTCGCATAGGCTG 3422

Qy        2958 CC-----TGGTGGCCC---CATCCCCCAGTTCCTCA---
CGATATGGTTTTTTACTT---C 3003
                    ||    || || ||  || || ||| |  || |   |  | ||   | ||
|
Db        3423 CCTATGATGAAGGACCGTGCA-
CCTCCACTCCAACAGAGTGCTGAGTTTAAAAGTTGACC 3481

Qy        3004 TGTGGATTTAAT----------------AAAAAAAACTTCACCAG------
TTCAAAAAA 3041
                    ||||  |  ||||                   || |||  ||  | |
||||||||||
Db        3482
TGTGTTTGTAATTTCACTTTCATCTTGCTTAATAAATATCTGCTGGATTCTTTCAAAAAA 3541

Qy        3042 AAAAAAAAAAAAAAA 3056
                    |||||||||||||||
Db        3542 AAAAAAAAAAAAAAA 3556


RESULT 4
US-10-478-914-21/c
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
```

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;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match             32.3%;  Score 6319.5;  DB 1;  Length 3589;
  Best Local Similarity   40.4%;  Pred. No. 0;
  Matches 1545;  Conservative   0;  Mismatches 1195;  Indels 1083;
Gaps  224;

Qy         1 GCGGGGCGGGCC-----GGC--------------------------------
GGCGGAGG 23
             || |  || ||     |||                              |   ||
Db      3587 GCAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAAAGAAT 3528

Qy        24 CCGGGCCGC-------GGAGCCAG----GAGTG-----
ACTAGCAGCAGTTGGCCGTGCC 67
             ||  || |         ||| ||      ||||     || | || ||| |    | |
Db      3527 CC-AGCAGATATTTATTAAGCAAGATGAAAGTGAAATTACAAACA-
CAGGTCAACTTTTA 3470

Qy        68 GTAGCAGCGTCCCGC--GCGCGGCGG-GCAGCGGCCC--------AGGAGGC----
GCGT 112
                 ||||    | |    |  |  ||  || ||| ||| ||        |||   ||
|||
Db      3469 AACTCAGCACTCTGTTGGAGTGGAGGTGCA-
CGGTCCTTCATCATAGGCAGCCTATGCGA 3411

Qy       113 GGTGC----------GGG---TTTCGGCGGCGGCTGAGGAA--
GAAGCGCGGGCGGCG-- 155
             | |||         |||  |||| || ||| || || | ||  |||| |   ||| |
Db      3410 GATGCATCTTAGGAAGGGAGCTTTC----
GCTGCTCAGAAATCAAAGCTCCATCGGAGGT 3355

Qy       156 --CCTTCGGGAGGCGAGCAGGCAGCAGTTGGC--
CGTGCCGTAGCAGCGTCCCGCGCGCG 211
                ||| | |||||| | ||| || ||   ||     || |||    || | |   |
|
Db      3354 GTCCTACTGGAGGC-ATCAGACAACA---AGCTAAATGACGTTAGGGCTACAC-
AACACA 3300

Qy       212 GCGGG---------CAGCGGCCCAGGAGGC---GCGTGG---CGGC-----
GCTCGG--C 249
             |||         || |    |||| |||   | | ||    | |     ||| |
|
Db      3299 AAGGGGAAAGTTGACAACAATTCAGG-
```

```
GGCTTTGAGTAGTCAAGACAATTAGCTTAGTAC 3241

Qy         250 CTCGCGGCGGCGGCGGCGGCAGC-----GGCCC--AGCAGT----TGG----CGGC--
GA 292
               ||  | |       || ||     |||   ||| ||   |||    | ||
|
Db      3240
TTCAGGTCAATAAATGCTACAATTTATGGGCAATTAGCTGTAAAATGGCCTACAGCTGAA 3181

Qy         293 GCGC-------GTCT------
GCGCCTGCGCGGCGGGCCCCGCGCCCTCCTCCCC---- 335
               | |     |||| |  |    ||  |     |      || |
Db      3180
ACACTATTCTTGTCTTATTTCACGATTTCATGGAGATTAAAGATAATCTAAACAGATTAA 3121

Qy         336 --CCCTGGGC---GCCCCCGGCG---
GCGTGTGAATGGCGGCCTCCGCGGCGGCAG---- 383
               || |     || || |    | || || |       || | |
Db      3120
GGCCTTAATCTTTAATCCAGGTGAGTAATTTTGTTTGTAGTAAAAAGCATAAGAAATAAT 3061

Qy         384 CCTCGGC------------AGCAGCGGCCTCGGCCGCC---TCTGG-CAGCCCG-
GGCCC 426
               ||| ||       || |   ||   |    ||  | |||| | || | |||
Db      3060
TCTCAGCATATTATGTAAAAGAAAAAGCAGTGAAAACCTTGTTTGGTCTTCCAGTGGCAA 3001

Qy         427 GGGCGAGGGCTCCGCT------GGCGGCGAAAAG--CGCTCC------
ACCGCCCCTTCG 472
               ||      |  |  ||       || | || |||   | |||        ||        ||
Db      3000
GGATAGTTGAACAACTTCAAGAAGCTGAGAGAAGTTTGTTCCCAATTTACAAGTATTTTG 2941

Qy         473 GC-----------------CGCAGCC---TCGGCC-----------TCTGCCTCAG--
CC 499
               |            |  | || |  ||          |||| | ||
||
Db      2940
ACATATAGATAAACAAAAGCAAAACCAGTTAAACCTTAAAAGATCATCTGAATAAGATCC 2881

Qy         500 GCGGCG--------
TCGTCGCCCGCGGGGGGCGGCGCCGAGGCGCTGGAGCTGCTGGAGC 551
               | |       |  | || |            | | ||    | | |||
|
Db      2880 -TGACAATTATAATTTTACATCCATGTG----AATTTCAA---
GCAATTGTTAATGGGGA 2829

Qy         552 ACTGC--GGC-
GTGTGCAGAGAGCGCCTGCGACCCGAGAGGGAGCCCCGCCTG------- 601
               | ||  ||| |  |      | |   ||        | ||     |||| | |
Db      2828 CCAGCAGGGCTGCATTAAGAAAACCACTTTTCACTGATCTCTC-
CCCCACATATTTTAA 2770

Qy         602 ------CTGCCCTGTT-----------TGCA--------
CTCGGCCTGTAGTGCCTGCTT 636
               ||| ||||       ||||        ||| | ||| |   | |
Db      2769 TTTGTCTTGCTTTGTTTATTTTGGTTATGCAAGTCCTTTCTCTTCATGAA--
ACAAGTGT 2712
```

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Qy        637 AGGGCCC----GC----------------------GGCCCCCGC-
CGCCGC--------- 660
              | ||| |     ||                    |||||||    ||  |
Db       2711 AAGGCTCTAAGGCTAAAATAATAGTTATTTTTGTGGGCCCAAATAGCTACTTTTGAATT 2652

Qy        661 ---------------CAACAGCTCGGGGGACGGCGGGGCGGCGGGCGACGGC--
ACCGTG 703
                             || || ||||| ||  |  |  ||| |  |||
||
Db       2651 TCTTTCTTTAGTATATCTCAAATCTGGGGAACATGGAAC--
TTGAAGACTCCTAACCATG 2594

Qy        704 G------TGG----------------------ACTGTCCCGTGTGC--------
AAGC 725
                     |||                     || |  || | |
|||
Db       2593 AAGCATTTGGAAAAATACATATCATTCACTTTTCACAGAACCATTTTCTTAAAAATAAGA 2534

Qy        726 AACAGT-----GCTTCTC---
CAAAGACATCGTGGAGAATTATTT--------------- 762
                || |     | ||| |   ||    ||| |  ||   || |||
Db       2533 GGCAATATCCAGATTCACATGCATGTTCATAATAAAGCTTTGTTTTAAAACAAATCCACA 2474

Qy        763 CATGCGTGATAGTGGCAGC----AAGGCTGCCACCGACGCCCAGGATGCG-----
AAC-- 811
              |  || ||| |  ||||     |  || ||| || || ||| || |           |||
Db       2473 CCAGCATTATTTT--CAGCTTAATATTTTGGCCCCAAC-
CCAAGAATTCAGGTATAACAT 2417

Qy        812 -----------CAGTGCTGCACTAGCTGTGAGGATA--------
ATGCCCCAGCCACCAG 852
                         | ||  ||||      ||  |||| |        ||||      |||
Db       2416 TTAATTTTCATCTGTAATGCATATATTGGAAGGACAAAATATATATGCAAATAACACTGG 2357

Qy        853
CTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACCTGTGTAGAGGCGCACCAGCGGGT 912
              | ||||      || |     ||| |  | ||| |      |||    ||  || |
Db       2356 AAAATGT------TGTTT----CCTATACAAGTGATC----AAGAAAAAAACAA--
AGAA 2313

Qy        913 GAAGTACACCAAGGACCATA------CTG---------
TGCGCTCTACTGGGCCAGCCAA 957
                       ||| | ||| |    |  ||      |||      |  |  || | |||
|||
Db       2312 AAAGAAAACCCATAGCACTAAGTTTGCTGTAGTGAAAATATGGTTAACGGTGCCGTGCAA 2253

Qy        958 GTCTCGGGATGGTG-
AACGTACTGTCTATTGCAACGTACACAAGCATGAACCCCTTGTGC 1016
                         | |   || || ||| ||| |||| |||   |  || ||||| |
||
Db       2252 AATTAGATTTGTTGAAAAGTAGT-TCTATTACAGGGAGCAAAAGCAAAGA-------
AGC 2201
```

```
Qy      1017 TGTTTTGTGAG-AGCT----------
GTGATACTCTCACCTGCCGAGACTGCCAGCTCA 1064
                  ||||||  |  | ||          |  |||  |||||  |  ||    |  ||   |  |
                                                                              |
Db      2200 AAGTTTGTGGGCAACTCGGAAGAGGGGATCATATTCTCATTT-
CCTTAATTGTAATTTAA 2142

Qy      1065 ATGCCCACAAGGACCACCAGTACCAGTTCTTAGAGGATGC-----
AGTGAGGAACCAGCG 1119
                  ||  |   ||      |||  |  ||  |||||||       ||  |  |||
                                                                              ||
Db      2141 ATAATCATTC--TCCATAATTTCTCTTTC-TAGAGCTTTCTTCTTTGTATGCTATCA-
CG 2086

Qy      1120 CAAG------------CTCCTGGCCTCACTGGTGAAGC--------
GCCT---------- 1149
                  |||              |  |||        |  |||   |  |          ||||
Db      2085 TAAGGTAGTACTATTTCACCT-
TAAAAAATGGAAAGACAAATTTCAGCCTAAGAATGATG 2027

Qy      1150 -----TGGG--GACAA--ACATGCAACATTGC---AGAAGAGCAC------
CAAGGAG-G 1190
                     ||  |  |||  ||  |  ||||  |    ||  |  |||         |    ||
                                                                              |
Db      2026
TATTCTGAGTTGGCAATTACTTAAAACAATGAGAGAGTAAAACACATCAAACTTAAAGTG 1967

Qy      1191 TTCGC----AGCTCAATCCGCCAGGTGTCTG--ACGTACAGAAGCGTGT------
GCAAG 1238
                  ||  |     |  || |     |  ||||  |  |  ||||||||  | |          |
                                                                              ||
Db      1966
TTTACTTTTTGAACATTAAAATAAATGTCAGGTAAATACAGAAAAATATATAATCACTAG 1907

Qy      1239 TGGATGTCAAGATGGCCATCC------
TGCAGATCATGAAGGAGCTGAATAAGCGGGGCC 1292
                  |        ||  |  ||||     |  |    ||  ||  ||  ||     ||         |
                                                                              ||
Db      1906 TTCTCAGCATTTTATCAATCCCTTTGTTTCTCTTCTTCTAGAAG----
ATTCTATGAGCA 1851

Qy      1293
GTGTGCTGGTCAATGATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGC--G 1350
                  |  ||  ||  ||          |   ||  ||||    ||  |      |  |    ||     |  |
Db      1850 TTATGTTGCTCC-----GATCAAAAGTAACCTCA----CTACTCAAATACC---
ATCATA 1803

Qy      1351 GCAGCACTGGACCATGACCAAGATCCAGAAGCACCAGGAGCACA----
TTCTGCGCTTTG 1406
                  ||  ||  ||  |  |           |  |||  ||    ||      ||  |     |||  |  |
                                                                              |
Db      1802
GCTTCAATGTGCATTATAGTGATTTCAGTAGATTCACACTCAAATCTTTTCAGTGTCATA 1743

Qy      1407 CC--TCTTGGGCTCTGGAG-AGTGACAACAACACAGCCCTTTT---
GCTTTCTAAGAAGT 1460
                  |    |  |||  ||  |      |  |||  |  ||| |||  |     |    |||  |
Db      1742 CATTTATTAAGCCATAAAGTTATGAAACC--
CTCAGCTCTTGTGGAGAGATCTGGGCAGA 1685
```

```
Qy      1461 TGATCTACTTCCAGCTG----------CACCGGGCCCTCA--
AGATGATTGTGGATCCCG 1508
                 | ||| || | ||| ||| || |||||| |
                                                     |
Db      1684
ATTTATACAAGAAGAAGTTTAATTTATCACTTAAAAATCATCTCATAATTGTGGTAACAG 1625

Qy      1509 --------TGGAGCCACATGGCGAGATGAAGTTTCAGTGGGACCTCAATGC-
CTGGACCA 1559
                     | | || ||| | || ||| ||| ||| || || || |
                                                              ||
Db      1624 ATTTTTAAAGTAACCCTTTGG---
AAAAAATTTTACGTGATACCCAAAGGCACTAGTTCA 1568

Qy      1560 -------AGAGTG--------------CCGAGGCCTTTG------------
GC------- 1579
                  | ||| | | ||| |||          ||
Db      1567
CATAAGGGGTGTGGCTGAAAAAGCAAAACAAAGCCATTGTGTAAGTAAAGAGCACACAAA 1508

Qy      1580 --AAGATTGTGGCAGAGCGTCCTG----GCACTAA-------CTCAACA-
GGCCCTGCAC 1625
                  ||| | | | | |||| || ||| || || | ||| ||
                                                       |
Db      1507
AAAAGGATATTAAAAGGAAACCTGTTAAGCTTTAAAGTTATTCTAAAAATGGCACTTTTC 1448

Qy      1626 CCATGG----
CCCCTCCAAGAGCCCCAGGG------------------------------ 1651
                 | | | | ||| || | |
Db      1447
ACGTTGGTATAAAATGAAAGTGCTTTAAGATGAAATTTTTATGTATTTTTTTAAAGCTGA 1388

Qy      1652 --------CCCCTGAGCAAGCAGGG------------
CTCTGGCAGCAGCCAGCCCATGG 1691
                 |||||||  | ||| | ||| || | | | |||
                                                     |
Db      1387
TTTTTAACCCCCTGAAAATAGGGGGTTATAACAAGAACACTGATAGACTCTAACTCATAG 1328

Qy      1692 AGG--------------TG---
CAGGAAGGCTATGGCTTTGGGTC--------------- 1719
                  ||        || | || ||| || | || |||
Db      1327 CGGCAATAAGTAGTGGATGTCACTAAAATGCTCTG--
TGTGTGTCTTTATTTTTTAGTAT 1270

Qy      1720 ------AGGAGATGATC---
CCTACTCAAGTGCAGAGCCCCATGTGTCAGGTGTG----- 1765
                 | ||| | | || | | | | ||| || || ||
Db      1269 TTTTAATGTTGATAGACTTGCTTTATCTA--
TCTGTGTATCATTAGTGAGATTTGCTTTT 1212

Qy      1766 -------------AAACGGTCCCGCTCA-------------
GGTGAGGGCGAGGTGAGCGG 1800
                 || | | | ||||| ||| | | | |||
Db      1211 CAATTCTTTACTAGAAAGTTACAGCTCATTTAAAAATAGCTGGTAAATAC--
AGAAAGCAT 1154

Qy      1801 CCTTATGC-GCAAGGT--GCCAC-GAGTGAGCCTTGAACGCCTGGAC----------
```

```
CTG 1846
                     ||| | ||| |    ||| || || |      | |   ||
                                                              ||
Db       1153
AAAATATACAGTAAGTTTAAACACTGATTGTACTAAATGCAACAATACAAAGAAGCAAATG 1094

Qy       1847 GACCTCACA-GCTGACAGCCAGCCACCCGTCTTCAA---GGTCTTCCCA---
GGCAGTAC 1899
                  || | || | |  | ||| |   | | || ||  |   |  |||| |      ||
                                                                  ||
Db       1093 GAACACAAATGGTAACA-
CAATAAAACTGTATTACATTTGTGCTTCAAATATTACAATA- 1036

Qy       1900 CACTGAGGACTACA-ACCTTATTGTTATTGAACGTGGCGC-
TGCCGCTGCAGCTACCGGC 1957
                  || |    ||| | ||| | |      |  | ||| |   || | |   | | |
                                                                  ||
Db       1035 CATTATATACAATAGTCCAAAATAAACAT-
CTCATGCCAAGTGACACAAAAACGAATAGC 977

Qy       1958 CAGCCAGGGACTGCGCCTGCAGGAACC--CCTGGTGCC---------------
CCACCCC 2000
                   ||| |   | | |   | | | |   | || |   || |  |              || |
                                                                  |
Db       976
AAGCAAAAAAATCCAGCCATATGTACATTACTTTTTTCTTTAATAATAAACATTCAACTC 917

Qy       2001 TG-
GCTGGCATGGCCATTGTCAAGGAGGAGGAGACGGAGGCTGCCATTGGAGCCCCTCCT 2059
                  ||  ||||   ||| ||| |||          | || || | |          | |||
                                                                  |
Db       916 TGAACTGG---GGCAATT-TCACTAC-----ATACAGATGCAGTC-------
CGCCTTTT 873

Qy       2060
ACTGCCACTGAGGGCCCTGAGACCAAACCTGTGCTTATGGCTCTTGCGGAGGGTCCTGGT 2119
                  | | | |    | | |    |||| |    | |  ||| ||  | |||  ||||
Db       872 ATTCCATATAACCATCCTG----CCTTCCTATATCTAC-
GCTATTCAGTAGGTTCCT--- 821

Qy       2120 GCTGAGGGTCCCCGCCTGGCCTCACCTAGTGGCAGCACCA------------------
GC 2161
                    | |||   ||    |    ||| |  | |||| |||| |
                                                              ||
Db       820 -----GTGTCAATTCTT---ATGTACATGTGG-
AGCAAAAAAGATAAAAGAATGTAGTGC 770

Qy       2162 TCAGGG--CTGGAGGTGGTGGCTCCTGAGGGTACCTCAGC--
CCCAGGTGGTGGCCCGGG 2217
                  || |     || | | |||     || | ||  |||||    || || ||| ||
Db       769 TCTGTATTCTTAATGGGGTG----ATGTTGATAGATCAGCGAACCTGG--GGT-
GCAT--- 719

Qy       2218 AACCCTGGATGACAGTGCCACCATTTGCCGT-
GTCTGCCAGAAGCCAGGCGATCTGGTTA 2276
                   |||| |   | |      || | |  ||| ||| | |  | || | ||||
                                                              ||||
Db       718 AACCTTCTTTCATTAAACCTTCCT----CGTAGTCCGTCTG--GCAAAG-
GATCATGTTA 666
```

```
Qy        2277 TGTGCAACCAGT--GTGAGTTTTGTTTCCACCTGGA-----CTG-
TCACCTGCCGGCCCT 2328
               |       |   |   |   |||||  |||| |   |      ||| | ||    | | |
|
Db         665 T------
TCTTTAGGAAAAATTTGTCTCCAACACAAAATCTCTGATTACAAAGCTGACAT 612


Qy        2329 GCAGGATGTACCAG--GGGAGGAGTGGAGCT--
GCTCACTCTGCCATGTGCTCCCTGACC 2384
               |||       |||| ||| |   |||    |||    ||||   ||| ||
|
Db         611 GCAAAGCAGTCCAGGTGGTAAACATTGTCCTTGGCACGCATCACCAT---
CTCAAAGGC- 556


Qy        2385 TGAAGGAGGAGGATGGCAGCCTCAGCCTG-
GATGGTGCAGACAGCACTGGCGTGGTGGCC 2443
                 | ||| ||| |  |  ||| |  | | |       ||| | | | |
|
Db         555 --AGGGATGAGCTT----ACTACAGGCAGCGCAGTTTCCCGTTACAC---
CAAAGAGCCT 505


Qy        2444 AAGCTCTCACCAGCCAACCAGCGGAAATG-TGAGC----
GTGTACTGCTGGCCCTATTCT 2498
                  | | |     | | |  || ||| | | |||    ||||||| |  ||
|
Db         504 CAGATAGTCTCTGCGA--CAAAGGATAAGATTAGCTTTAGTGTACAG--
GG--------T 457


Qy        2499 GTCACGAACCCTGCCGCCCC-------CTGCATCAGCTGGCTACCGACT--
CCACCTTC- 2548
               |   || ||| || |||    |  |  |||| ||| |   | |
||||
Db         456 G----GAGCCC-
ACCTCCCCCAAGCGACAGTCACAGCAGGCACACTTCAGGCAGTCTTCA 402


Qy        2549 TCCCTGGACCAGCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCTCCAGGAG 2608
               | | | |  | ||| |  | |||   |||| | |||   | |     ||||       | | |
|
Db         401 TGCCAGTATTTGTCCAGTG----CCTTTAGAAGATACCGGTCCTTGAT--
CTTTCGGTTG 348


Qy        2609 AAGTTGTCACCTCCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCC---
GCATG 2665
                 ||    ||| ||| | |  |       || | | |  |  | | | | |     |
||
Db         347 CAGCCAGCACAACCTTTCGGCT------
TGGTGTCTGGCTGGACTGAGAGCATTTGTATA 294


Qy        2666 TTCAAGCAATTCAAC-----------
AAGTTAACTGAGGACAAGGCAGACGTGCAGTCCA 2714
                   || | ||| |     |||| ||| ||| |  | | || |||||
||
Db         293 CCAAAACTTTTCTCCTTTTTCTGCATGAGTTGACTTAGG-CGTGTCTGAGTTGCAG--
CA 237


Qy        2715 TCATCGGCCTGCAGCGCTTCTTCGAGACGCGCATGAACGAGGCCTTCGGTGACACCAAG- 2773
                  | || || |   ||| |      |  | | |  | | | |     || || | ||
|
```

```
Db        236 GCTTC-GCATTGAGCAC-----C-
AAACCCAAAGGTAGAAGTAGAAGGGGGTCTCCTTGA 184

Qy       2774 -TTCTCTGCTGTG-----CTGGT--GGAGC---
CCCCGCCGATGAGCCTGCCTGGTGCTG 2822
                |||  ||   |||    ||||| | |||   |  ||||||| ||   |  |  ||   ||
Db        183 TTTCGCTTAAGTGTGGACCTGGTGCGCAGCCTACACCGCCGAGGA--
CCGACTATTG--- 129

Qy       2823 GCCTGAGTTCCC---AGGAGC-TGTCTG-GTGGC-
CCTGGTGATGGCCCCTGAGGCTGGA 2876
                |||   | |    ||||| ||| | ||||| | || | |||      | || ||
Db        128 ---TGAAGCCACTTTGGGAGCGGGTCGGAGTGGCGGCAGGGGGTGGGGGAAG-
GGATGAG 73

Qy       2877 GCCCCCATGGCCAGCCCAGCCT-
GGCTCTGTTCTCTGTCCTGTCACCCCATCCCCACTCC 2935
                || | |    |||||| | || |  ||| |                  ||| |      |||
|||
Db         72 GAC-----GGCCAGACAAGACAGGGCGC--------------ACACACGGAGCCC-
CTCG 33

Qy       2936 CCTGGTGGCCTGACTCCCACTCCCTGGTGGCCCCATCCCCCAG 2978
                |  |||         |     || ||| |  |||| ||
Db         32 CAGTGTG------------CAAAATGATGG-CGAATCCAGTAG 3


RESULT 5
US-10-478-914-61
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match            31.8%;  Score 6214;  DB 1;  Length 2437;
  Best Local Similarity  44.4%;  Pred. No. 0;
  Matches 1418;  Conservative   0;  Mismatches  870;  Indels  906;
Gaps  202;

Qy          8 GGGGCCGGCGGCGGAGGCCGGGCCGCGGAG--
CCAGGAGTGACTAGCAGCAGTTGGCCGTG 65
                |  |  |  | ||        || |||||   ||       |  |||| | ||||||||
|
```

```
Db          1 GTTACTTCTGC--TCTAAAAGCTGCGGAATTCC-------TCGAGCA-CTGTTGGCC-
TA 49


Qy         66 CCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGC-
CCAGGAGGCGCGTGGTGCGGGTTTC 124
              | |    | || | ||| | | || || |||| |        |   ||
|
Db         50 CTG----GGTGTACTGTG-GAGACTGTCAAAGTCTCCCGGAGCC--------
CAATTTCC 96


Qy        125 GGCGGCGG------
CTGAGGAAGAAGCGCGGGCGGCGCCTTCGGGAGGCGAGCAGGCAGC 178
              || ||||       |||| |||||| |  | || || |    | ||    |
||
Db         97 GGAAGCGGTGAGTTCTGA--AAGAAGTTC---CTGCACCGTAGTTTCCCAAGT---
CTGC 148


Qy        179 AGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGGGCAGCGGCCCAG-
GAGGCGCGTG 237
                |  || || |  || | ||||||| | |     ||||| |||   |
Db        149 GAAT-CCCCAACCATG--AGCGCCTCGGGCGT-
ACTGTCCTTTACCCAGCAAGGATGGGA 204


Qy        238 GC-
GGCGCTCGGCCTCGCGGCGGCGGCGGCGGCAGCGGCCCAGCAGTTGGCGGCGAGCGC 296
                || || ||| ||||    |   ||     ||| || ||  | | | | || ||
||
Db        205 GCAGGTGCT-GGCCAAAGTGAAACG-----GGCTGTGGTTTACCTG--
GACGCCGCCTGC 256


Qy        297 GTC-
TGCGCCTGCGCGGCGGGCCCCGCGCCCCTCCTCCCCCCCTGGGCGCCCCGGCGGC 355
                | |  | ||||| ||| |        ||| ||     | || ||
|||
Db        257 GCCGAGAGCCTGCACTGGGG---CTGCG-----GATCCACCCGT-----
CTCCTGGAGGC 303


Qy        356 GTGTGAATGGCGGCCTCCGCGGCGGCAGCCTCGGCAGCAGCGGCCTCGGCCGCCTCTGGC 415
                | ||||    || |||||     | | | |                | | ||| |
Db        304 G-GTG---GGGGGCC----------CTGACT------------------
GTCACCTGCGAG 332


Qy        416
AGCCGGGCCCGGGCGAGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCCTTCGGCC 475
                || || ||||      | |  | ||| | |  | ||     | ||||
|||
Db        333 AGTTCGAGCCC-------GACGCAATTGGTGGTG----GAGCCAAGCAGCCC--
AAGGCA 379


Qy        476 GCAGCCTCGGC--
CTCTGCCTCAGCCGCGGCGTCGTCGCCCGCGGGGGGCGGCGCCGAGG 533
                |   |  | | ||      |||||||  | | | || | ||||| |  |  | ||
Db        380 G-TGTTTGTGCTGAGCTGCCT--GCTGAAAGGCCG--GACCGTGGAGATC--
CTACGGGA 432


Qy        534 CGCTGGAGCTGCTGGAG-CACTGC--
GGCGTGTGCAGAGAGCGCCTGCGACCCGAGAGGG 590
                |       | ||||| || |||| |  |   |   ||| | | | |     | ||| |||
```

```
Db       433 CATC--ATCTGCCGCAGTCACTTCCAGTATTGTGTGGTGGTCAC-----
AACCGTGAG-- 483

Qy       591
AGCCCCGCCTGCTGCCCTGTTTGCACTCGGCCTGTAGTGCCTGCTTAGGGCCCGCGGCCC 650
           || |  |||| |||    | | | | | |  | | |         || | |||||
Db       484 ----CCAC--GCTGTCC----ACCTCACAGCTAATCATGTC---------
CCAGCGGCGG 524

Qy       651
CCGCCGCCGCCAACAGCTCGGGGGACGGCGGGGCGGCGGGCGACGGCACCGTGGTGGACT 710
           | || |||             | || || |||||| || |
Db       525 CAGCGGGCC-------------
GAGATGGAGGGGCAGCAG---------------------- 550

Qy       711
GTCCCGTGTGCAAGCAACAGTGCTTCTCCAAAGACATCGTGGAGAATTATTTCATGCGTG 770
               || |||| | |||| | |                | |||||||          ||
           |||
Db       551 --CCGGTGTTCGAGCAGCTG------------------GAGGAGAAG------
CTGTGTG 584

Qy       771 ATAG---TGGCAGCAAG-GCTGCCACCGACGCCCAGGATGCGAACCA-
GTGCTGCACTAG 825
           |  |   |||| ||| | ||   | | |    ||| ||| || | | ||| || | |  |
           |
Db       585 AATGGATGGGCAACATGAACTAC-----ACGGCC--
GAGGTGTTCCATGTCCCGTTATTG 637

Qy       826
CTGTGAGGATAATGCCCCAGCCACCAGCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGA 885
               ||          ||||||           ||| ||||||    || || ||
Db       638 CT----------TGCCCC---------------TGT----TGCTC---
CCCACTTTG--- 662

Qy       886
GACCTGTGTAGAGGCGCACCAGCGGGTGAAGTACACCAAGGACCATACTGTGCGCTCTAC 945
                   ||| ||      |||||  || |      || || | | ||
           |
Db       663 --CCT-TG-------ACTCCAGCTTTTGCA------------TCC---
CTTTTCCCACTGC 698

Qy       946 TGGGCCAGCCAAGTCTCGGGATGGTGAACGTACTGTCTATTGC---
AACGTACAC----A 998
               |   ||  |||       |||| ||| || ||    ||  ||   | || |||
           |
Db       699 T--ACC--CCA-------GGAT-
GTGCACCTCCTTAATAGCGCCCGACCGGACAAGAGGA 746

Qy       999
AGCATGAACCCCTTGTGCTGTTTTGTGAGAGCTGTGATACTCTCACCTGCCGAGACTGCC 1058
               ||| | | ||           || | | ||||     ||| || |
           ||
Db       747 AGCTGGGAAGCC-------------TGGGTGATGTGG---ACTCCACTAC-------
GCT 783

Qy       1059
AGCTCAATGCCCACAAGGACCACCAGTACCAGTTCTTAGAGGATGCAGTGAGGAACCAGC 1118
             | |    |||| || | | | |  ||| ||        |||||
Db       784 AAC------CCCA----GAGCTGCTGCTGCAGATC-----
```

```
AGATGC------------- 814


Qy        1119
GCAAGCTCCTGGCCTCACTGGTGAAGCGCCTTGGGGACAAACATGCAACATTGCAGAAGA 1178
                 |  ||   |  | |||||||  |      | |   || |    |||||||     |
||
Db        815 -CTAGTGTCAGGCCTCAGT------TCTCTGTGTG-----------AACATT---
TAGGA 853


Qy        1179
GCACCAAGGAGGTTCGCAGCTCAATCCGCCAGGTGTCTGACGTACAGAAGCGTGTGCAAG 1238
              |  ||   |||||                         ||TGTTT |    | ||| ||  || |
Db        854 GTAC--GGGAGG------------------AGTGTTT----TGCTGTAG---
GTTCCT- 884


Qy        1239 TGGATGTCAAGATGGCCATC-
CTGCAGATCATGAAGGAGCTGAATAAGCGGGGCCGTGTG 1297
                     | ||||   || |||| ||||| |||| |||  ||   | | | ||   ||
Db        885 --TAAGTCA----GGTCATCGCTGCGGATC-TG-----GCCAATTATGC----
CC----- 923


Qy        1298
CTGGTCAATGATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGCGGCAGCAC 1357
                 |||  ||| ||   |   |||| ||||      || ||||||     | |    ||||
||
Db        924 CTG--CAAAGA--ACAGGAAGAAGACT-----GCTGCAGG-----CAG----
GGCATCAG 965


Qy        1358 TGG--ACCATGACCAAGATCCAGAAGCAC-
CAGGAGCACATTCTGCGCTTTGCCTCTTGG 1414
                 |||       || || | || | | |  |||||||||     | |    | ||
|||
Db        966 TGGTTTTTGTGGACAGAACCCTGGATCTCACAGGAGCA--------
GTTGGACATCATGG 1017


Qy        1415 -----
GCTCTGGAGAGTGACAACAACACAGCCCTTTTGCTTTCTAAGAAGTTGATCTACT 1469
                          || | |||| | || |||| |   |||| ||                     |
|
Db        1018 AGACAACTTAGTAGAG-AAGATCATTTCAGCACT----------------------
TCC- 1053


Qy        1470 TCCAGCTGCACCGGGCC-CTCAAGATGAT-TG-
TGGATCCCGTGGAGCCACATGGCGAGA 1526
                 ||||||    || || | ||| |||||| || ||| |  | ||        || ||||
Db        1054 -CCAGCT--CCCAGGCCACACAA-ATGATGTGATGGTTAACATG-------
ATAGCG--- 1099


Qy        1527 TGAAGTTTCAGTGGGACCTCAATGC-
CTGGACCAAGAGTGCCGAGGCCTTTGGCAAGATT 1585
                          |||| |||| ||    |||   | ||  ||||        |    ||
|
Db        1100 ----------------CTCACTGCACT---CCAT-
ACTGAGGAGGAAAATTATAATGTG 1138


Qy        1586 GTGGCAGAGCGTCCTGGC--
ACTAACTCAACAGGCCCTGCACCCATGGCCCCTCCAAGAG 1643
                 || |||        || ||| ||  || | |||              |   || | ||| |
||
Db        1139 GTTGCA------CCAGGCTGTCTTTCACAA----------TTCAGTGACACCAC----
```

AG 1178

```
Qy         1644
CCCCAGGGCCCCTGAGCAAGCAGGGCTCTGGCAGCAGCCAGCCCATGGAGGTGCAGGAAG 1703
                   ||| |||| | |||| || | || ||| ||| ||||
Db         1179 --CCAAAGCCCTATGGGAAGCTTTACT----
GAACACTAAGCACAAAGAGG--------- 1223


Qy         1704
GCTATGGCTTTGGGTCAGGAGATGATCCCTACTCAAGTGCAGAGCCCCATGTGTCAGGTG 1763
                           || | |||| |||| | ||| |          ||
|||
Db         1224 ---------------CA-GTGATGG---------AAGTTCGGAGAC------
ATCTAGTG 1252


Qy         1764
TGAAACGGTCCCGCTCAGGTGAGGGCGAGGTGAGCGGCCTTATGCGCAAGGTGCCACGAG 1823
                   ||| ||| | ||         ||| | | ||| | | || | |
|
Db         1253 -GAAGCGG-CAAGC-----------AGAGAAAACCTGCC--
AATCAAGATGAGTATGGGG 1297


Qy         1824
TGAGCCTTGAACGCCTGGACCTGGACCTCACAGCTGACAGCCAGCCACCCGTCTTCAAGG 1883
                   ||| |   || || |||| | |||| | | || | ||||
|||||||||
Db         1298 AGAGTC----ACACCGGGAC----AGCTCATGTCCTATATTCAGC------
TCTTCAAGA 1343


Qy         1884 TCTTC--CCAGGC-----
AGTACCACTGAGGACTACAACCTTATTGTTATTGAACGTGGC 1936
                   | | | | || | | | || || |||| | || ||| | || |
||
Db         1344 ACAACCTCAAAGCTCTAATGAATCATTGTGGCCT-CCTCCAGCTTG-
GACTGGCCACAGC 1401


Qy         1937 GCTGCCGCTGCAGCTAC--CGGCCAGCCA---
GGGACTGCGCCTGCAGGAACCCCTGGT- 1990
                   | |||| || | | | |||| ||||| | | | || | ||
Db         1402 TCAAACGTTGAAACACCCACAGACTGCCAAGTGGGAC--AACTTTCTGG--
CTTTTGAAA 1457


Qy         1991 -GCCCCACC--CCTGGC--TGGCATGGC--
CATTGTCAAGGAGGAGGAGACGGAGGCTGC 2043
                   || || | | || ||| | | || |||| | | | |
|||||
Db         1458
GGCTCCTTCTTCAGAGCATTGGGGAGTCAGCAATGTCCGTTGTGTTAAATCAGCTGCTGC 1517


Qy         2044 CATTG---GAGCC----CCTCCTACTGCCACTGAGG------GCCCTGAG-----
ACCAA 2085
                   | || |||| | | | ||| |||| ||||||||| |
|
Db         1518
CCATGATTAAGCCTGTAACCCAGAGAACCAACGAGGACTACAGCCCTGAGGAACTGCTGA 1577


Qy         2086 ACCTGTGCTTATGGCTCTTGCGGAGGGTCCTGGTGCT-
GAGGGTCCCGCCTGGCCTCAC 2144
                   ||| | ||| | | | ||| || ||| | | || | |
Db         1578 TCCTTCTCATATATATTT--------
```

```
ATTCTGTCACTGGAGAGCTCACGGTAGACAAAGA 1629


Qy        2145 CTAGTG-GCAGCACCAGCTCAGGGC-
TGGAGGTGGTGGCTCCTGAGGGTACCTCAGCCCC 2202
               | ||| | |||| | | | |  | | | |  |||||| |   ||| ||| | || |
Db        1630 CCTGTGTGAAGCAGAAGAAAAAGTCAAGAAAGCATTGGCTC----AGGT-
CTTCTG---- 1680


Qy        2203
AGGTGGTGGCCCGGGAACCCTGGATGACAGTGCCACCATTTGCCGTGTCTGCCAGAAGCC 2262
                             | | | |||||||     || |||| |||     |||| | ||
Db        1681 -----------TGAGGAATCTGGAT-----TGTCACC-TTTG------
CTGCAAAAAATT 1717


Qy        2263 AGGCGATCTGGTTATGTGCAACCAGTGTGAGTTTT---GTTTCCA------CC-
TGGACT 2312
               | || |||| | ||| | ||| | ||| |||| || |    |||        || ||||
Db        1718 A--
CGGACTGGGACTCTTCAATTAATCTGACATTTCACAAATCCAAAATTGCCGTGGATG 1775


Qy        2313
GTCACCTGCCGGCCCTGCAGGATGTACCAGGGGAGGAGTGGAGCTGCTCACTCTGCCATG 2372
                 | | | | | |||| ||| | |   ||||||| |  | |||
Db        1776 AACTCTTTACTTCACTTCGGGATATTGC----------TGGAGCT-
CGGAGTCT------ 1818


Qy        2373 TGCTCCCTGACCTGAAGGAGGAGGATGGCAGCCTCAGCCTGGATG-
GTGCAGACAGCACT 2431
                       |||||||              ||| | || ||| || || |
||
Db        1819 ----------CCTGAA-----------ACAGTTTAAGTCTGTATATGTTC--------
CT 1849


Qy        2432 GG----CGTGGTGGCCAAGC-TCTCACCAGCCAACCAGCGGAAATGT--
GAGCGTGTACT 2484
               || | |    ||| || ||| | |||| | |       | ||| ||| ||
|
Db        1850 GGAAATCATACCCACCAGGCATCTTATAAGCC----------
ATTGTTGAAGCAAGTTGT 1899


Qy        2485 GCTGGCCCTATTCTGTCACGAAC--CCTGCCGCC----
CCCTGCATCAGCTGGCTACCGA 2538
               | || ||||  || |||  ||| ||   || |        | | || || || |
|
Db        1900
GGAGGAAATATTTCATCCCGAGAGGCCAGATTCCGTTGATATTGAACACATGTCTTCAGG 1959


Qy        2539 CTCCACC-
TTCTCCCTGGACCAGCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCC 2597
               | ||| ||||| | |        || |||| |   ||| ||| |||
||
Db        1960 CCTCACTGATCTCCTTAAAACT----GGATTTAGCATGTTCATGAAGGTGAGCCGG--
CC 2013


Qy        2598
GCCTCCAGGAGAAGTTGTCACCTCCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGG 2657
               | ||| |    || |  | | ||||| |    ||||     | ||
||
Db        2014 TCATCCTAG------TGACTACCCCCTCCTGATCCTC-------TTTGTGGTAGGTG-
GG 2059
```

```
Qy        2658
GCCGCATGTTCAAGCAATTCAACAAGTTAACTGAGGACAAGGCAGACGTGCAGTCCATCA 2717
                |  |  ||    ||         ||||  ||    ||  ||  |   |  ||   |
||||
Db        2060  GTCACAGTCTCTG----------AAGTGAA-AATGGTCAAAG--ATCTTGTGG--
CATCG 2104


Qy        2718  TCG--GCCTGCAGCGCT--
TCTTCGAGACGCGCATGAACGAGGCCTTCGGTGACACCAAG 2773
                |  |   |||  |  |   |     |   |||  |  |  ||    ||||   |||   |   |  |||
|
Db        2105  TTGAAGCCAGGAACCCAGGTAATCGTGCTGTCCA--CACGACTCCT--
GAAGCCACTTAA 2160


Qy        2774  TTCTCTGCTGTGCTGGTG-GAGCCCCCG-
CCGATGAGCCTGCCTGGTGCTGGCCTGAGTT 2831
                      ||  |||  ||||  |     ||   |  |  ||||      ||||     |   |  |  |||   |
|
Db        2161  CATTC--CTGAGCTGTTATTTGCAACTGACCGA-----CTGC---
ATCCAGACCTTGGCT 2210


Qy        2832  CCCAGGAGCTGTCTGGTGGCCCTGGTGAT--GGCC-
CCTGAGGCTGGAGCCCCCATGGCC 2888
                      |   ||||   |       ||    |  |||   |  ||   ||  | |||||||      ||
||
Db        2211  TCT--GAGCATCC-----
GCTAAGAAGATAAGACCTACTCAAGCTGGAAATGCCGATGCA 2263


Qy        2889
AGCCCAGCCTGGCTCTGTTCTCTGTCCTGTCACCCCATCCCCACTCCCCTGGTGGCCTGA 2948
                         |                    ||  ||||  |  ||  ||  |  |  ||||  |            ||
|
Db        2264  A----------------TTTTCTGCCACCACTCCCAAATACTC-CTCCAC----
AACCAGC 2302


Qy        2949  CTCCCACTCCCTGGTGGCCCCA----------TCCCCCAG-----------TTCCT-
CAC 2986
                         ||||  ||  ||   |  ||     |          ||   ||  |              |  |||  |
|
Db        2303
GTCCCTGTCACTAATTGCGAGAATGATGGAATTCTGCCTGAAGGGTCTTGATACCTACTC 2362


Qy        2987  GATATGGTT-TTTACTT------
CTGTGGATTTAATAAAAAAAACTTCACCAGTTCAAAA 3039
                         |   |||   |||  |||        |||||   |  |  |  |||||||||     |   ||   ||
|
Db        2363
AGTGAGGTACTTTGCTTGGATTGCTGTGATTCTTAAAAAAAAAAAAAAAAAAAGGCCACAT 2422


Qy        3040  AAAAAAAAAAAAAA 3053
                         |         |
Db        2423  GTGCTCGAGCTGCA 2436


RESULT 6
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
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  Query Match           31.2%;  Score 6092.5;  DB 1;  Length 2437;
  Best Local Similarity   43.7%;  Pred. No. 0;
  Matches 1392;  Conservative    0;  Mismatches  879;  Indels  911;
Gaps  208;


Qy        12 CGGCGGCGGAGGCCGGGC-CGCGGAGCCAGGAGT--------------
GACTAGCAGCAG 56
             |  || ||      || || |  |  |||      |             || |
||||||
Db      2437 CTGCAGC-----
TCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTAAGAATCACAGCAA 2383


Qy        57 TTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGC--
GGCCCAGGAGGCGCGTGG 114
             |           ||  |||| || || |  |  || | |  | |||   |||| |
Db      2382 T--------CC-AAGCAAAGTACCTCACTGAGTAGGTATCAAGACCCTTCAGGC-
AGAAT 2333


Qy       115 TGCGGGTTTCGGCGGCGGCTGAGGAAGAAGCGC------
GGGCGGCGCCTTCGGGAGGCG 168
              | |    ||| ||       | | || |||       || || |  ||      ||
|
Db      2332 TCCATCATTC-TCGCAATTAGTGACAGGGACGCTGGTTGTGGAGGAGTATT----
TGGAG 2278


Qy       169 AGCAGGCAGCAGTTGGCCGTGCCGTAGCAGCG--TCCCGCGCGGCGGGC--
AGCGGCC 224
               |  ||||| |  | ||          | | ||   ||| ||  | | || |  |
|
Db      2277 TGGTGGCAGAAAATTGC--------
ATCGGCATTTCCAGCTTGAGTAGGTCTTATCTTCT 2226


Qy       225 CAGGAGGCGCGTGGCGGCGCTCGGCCTCGCGGCGG-CGG-CGGCGGC----
AGCGGCCCA 278
              || | || | || | || | ||| | || | ||| | | ||    | | ||
||
Db      2225 TAGCGGATGCTCAGAAGC-
CAAGGTCTGGATGCAGTCGGTCAGTTGCAAATAACAGCTCA 2167


Qy       279 GCAGT------TGGCGGCGAGCG-
CGTCTGCGCCTGCGCGGCGGGCCCCGCGCCCCT--C 329
```

```
                        |  |  |        ||||   |   |  |  |||  ||  |  |  ||  ||          ||  |  |  |||
|
Db      2166  GGAATGTTAAGTGGCTTCAGGAGTCGTGTG-GACAGCACGAT--
TACCTGGGTTCCTGGC 2110


Qy       330
CTCCCCCCCTGGGCGCCCCCGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCAGCCTCGG 389
                    ||  |    |  |||  |      |   |  ||  |  |          |  ||
|
Db      2109  TTCAAC-----GATGCCACAAG------ATCTTTGAC--CATTTTC-------
ACTTCAG 2070


Qy       390
CAGCAGCGGCCTCGGCCGCCTCTGGCAGCCCGGGCCCGGGCGAGGGCTCCGCTGGCGGCG 449
                 |  |  | ||      || |||     ||     ||  |  ||  ||     |  ||  |
|
Db      2069  AGACTGTGACC----
CCACCTACCACAAAGAGGATCAGGAGGGGGTAGTCACTAG----G 2018


Qy       450
AAAAGCGCTCCACCGCCCCTTCGGCCGCAGCCTCGGCCTCTGCCTCAGCCGCGGCGTCGT 509
                 |  ||     ||  |  |  |||||    ||          |||   |  ||         ||
|
Db      2017  ATGAG---GCCGGCTCACCTTCATGAACA-----------TGCTAAATCC----
AGTTTT 1976


Qy       510  CGCCCGCGGGGGGCGGCGCGGAGGCGCTGGAGC----
TGCTGGAGCACTGCGGCGTGTGC 565
                    ||  |  |     |||| ||| ||      ||  |   |  ||| |
||
Db      1975  -----AAGGAGATCAG---TGAGGC-
CTGAAGACATGTGTTCAATATCAACGGAATCTG- 1926


Qy       566  AGAGAGCGCCTGCGACCCGAGAGGGAG---------
CCCCGCCTGCTGCCCTGTTTGC-- 614
                     ||||   |  || ||  |  |            |  |   |  ||||  |         |  ||
Db      1925  -------GCCT----
CTCGGGATGAAATATTTCCTCCACAACTTGCTTCAACAATGGCTT 1877


Qy       615  --ACTCGGCCTGTAGTGCCTGCTTAGGGCCCGCGGCCCCCGCCGCCGCCAACAG-
CTCGG 671
                       |    |||||  |  |   ||  ||      ||  |    |       |  |  |   |||  |   ||
|
Db      1876  ATAAGATGCCTGGTGGGTATGATTT---
CCAGGAACATATACAGACTTAAACTGTTTCAG 1820


Qy       672  GGGACGGCGGGGCGGCGGGCGACGGCACCGTGGTGGACTGTCCCG-
TGTGCAAGCAACAG 730
                     |  |||         |  |   ||  || |||            | |   ||||   |||  ||| |||
||
Db      1819  GAGAC------TC--CGAGCTCCAGC----------AATATCCCGAAGTG-AAGTAA-
AG 1780


Qy       731
TGCTTCTCCAAAGACATCGTGGAGAATTATTTCATGCGTGATAGTGGCAGCAAGGCTGCC 790
                     |  |  ||||  |  | ||   |||       ||||       ||||  |  || |||          ||
Db      1779  AGTTCATCCACGGCAATTTTGG------ATTT-----GTGA-
AATGTCAGATTAATTG-- 1734


Qy       791
```

```
ACCGACGCCCAGGATGCGAACCAGTGCTGCACTAGCTGTGAGGATAATGCCCCAGCCACC 850
            ||  |||||  | ||| |||           | | |   |||||
||
Db     1733 -AAGAGTCCCAGTCCGTAATTTTTTGCAGCA---------
AAGGTGACAATCCAGATTCC 1684

Qy      851 AGCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACCTGTGTAGAGGC----
GCACCA 906
                 || |     | | |||||  ||      || | || |     |
|
Db     1683 T--CACAG------AAGACCTGAGCCAATG--------CTTTCTTGA--
CTTTTTCTTCT 1642

Qy      907 GCGGGTGAAGTACACCAAGGAC----CATACTGTGCGCTCTACTGGGCCAGCC-
AAGTCT 961
                 ||       | ||| ||| |      ||| ||| ||||| | | ||  || |
|
Db     1641 GC--------
TTCACACAGGTCTTTGTCTACCGTGAGCTCTCCAGTGACAGAATAAATAT 1590

Qy      962
CGGGATGGTGAACGTACTGTCTATTGCAACGTACACAAGCATGAACCCCTTGTGCTGTTT 1021
                 | ||| ||  | | | |     | ||| ||  | |  ||| ||  ||
||
Db     1589 ---ATATGAGAAGGATCAG-CAGT-------TCCTCAGGGCTGTAGTCCTCGT--
TGGTT 1543

Qy     1022 TGTGAGAGCTGTGATACTCTCACCTGCCGAGACTGCCAGCTCAATGCCCACAA-
GGAC-- 1078
                 ||| | ||| |   |  ||||| | |  |   | | |||| | |  ||||| ||||
Db     1542 ------CTCTGGGTTACAGGCTTAATCATGGGCAG-
CAGCTGATTTAACACAACGGACAT 1490

Qy     1079 ------CACCAGTACCAGTTCTTAGAGGATGCAGTGAGGAACC-----
AGCGCAAGCTCC 1127
                 | ||   ||| || | || ||          |||| ||     |  || ||
Db     1489 TGCTGACTCC----CCAATGCTCTGAAGA-------
AGGAGCCTTTCAAAAGCCAGAAAG 1441

Qy     1128 TGGCCTCACTGGTGAAGC-
GCCTTGGGGACAAACATGCAACATTGCAGAAGAGCACCAAG 1186
                 | | |||| |    || | || |         | |||| ||       ||||
Db     1440 TTGTCCCCACTTG-----GCAGTCTGTGGG----TGTTTCAACGTT-----
TGAGCT----- 1399

Qy     1187
GAGGTTCGCAGCTCAATCCGCCAGGTGTCTGACGTACAGAAGCGTGTGCAAGTGGATGTC 1246
                 |  || || ||| |   | | |  ||| |           ||    |||
||
Db     1398 -------GTGGC-CAGT---CCAAG---CTGGAG----GAGGC-----CACAATGAT-
TC 1363

Qy     1247
AAGATGGCCATCCTGCAGATCATGAAGGAGCTGAATAAGCGGGGCCGTGTGCTGGTCAAT 1306
                 |  | || | | |   || |||||||||||||     || | || ||| |
Db     1362 ATTAGAGCTTTGAGGTTGTTCTTGAA-GAGCTGAATAT---
AGGACATGAGCTG------ 1313

Qy     1307 GATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGACGGCAG-----
CACTGGA 1361
```

```
                  |||  |   ||||||         |   ||      |  || ||  |||||       |  |||
Db        1312  ---TCCCGGT--GTGACTCT----
CCCCATACTCATCTTGATTGGCAGGTTTTCTCTG-- 1264


Qy        1362  CCATGAC-CAAGATCCAGAAG-CACCAGGAGCACATTCTGCGCTTTGCCTC-
TTGGGCTC 1418
                  | | | | |      | ||| | | ||    | || | | | |  |||||| |||
|||
Db        1263  -CTTGCCGCTTCCACTAGATGTCTCC----GAACTTCCATCAC--
TGCCTCTTTGTGCTT 1211


Qy        1419  TGGAGAGTGACAACAACACAGCCCTTT-TGCTTT--CTAAGAAGT----------
TGATC 1465
                  || || || || |  | ||| |  ||||| || | |  ||        |||
Db        1210  ---AGTGT-
TCAGTAAAGCTTCCCATAGGGCTTTGGCTGTGGTGTCACTGAATTGTGAAA 1155


Qy        1466
TACTTCCAGCTGCACCGGGCCCTCAAGATGATTGTGGATCCCGTGGAGCCACATGGCGAG 1525
                  || | | |||     || | | ||||         || | |
Db        1154  GACAGCCTGGTGCA-----ACCACATTATAATTTT-------------CCTCCT--
CAGT 1115


Qy        1526  ATGAAGTTTCAGTGGGACCTCAATGCCTG--
GACCAAGAGTGCCGAGGCCTTTGGCAAGA 1583
                  ||| || ||||| | | | || | |||      |      |  | ||||
Db        1114  ATGGAG-TGCAGTGAG--CGCTAT-CATGTTAACCAT------
CACATCATTTG------ 1071


Qy        1584  TTGTGGCAGAGCGTCCTGGCACTAACTCAACAGGCC--
CTGCACCCATGGCCCCTCCAAG 1641
                  ||||||    |    || |    || ||  |  || || |  | | |     |||||
Db        1070  -TGTGGCCTGGGAGCTGGGGAAGTGCTGAAATGATCTTCT-
CTACTAAGTTGTCTCCATG 1013


Qy        1642  A-GCCCCAGGGCCCCTGAGCAAG-
CAGGGCTCTGGCAGCAGCCAGCCCATGGAGGTGCAG 1699
                  | | | |  || ||||| |  ||||| |||| |  ||    |  |||
Db        1012  ATGTCCAACTGCTCCTGTGAGATCCAGGGTTCTGTCCACA--
AAAACCA----------- 966


Qy        1700
GAAGGCTATGGCTTTGGGTCAGGAGATGATCCCTACTCAAGTGCAGAGCCCCATGTGTCA 1759
                              ||              |||| |||| |  ||||||     ||
|||
Db        965   -----------CT-----------GATG--CCCTGC-C---TGCAG-----CA---
GTCT 942


Qy        1760  GGTGTGAAACGGTCCCGCTCAGGTGAGGGCGAGGTGAGCGGCCTTATGCGCAAGGTGCCA 1819
                  |         ||| || | ||   || ||          ||| || || | || |
||
Db        941   TCT---------TCCTGTTCT--TTGCAGG----------GGCATAATTGGCCAGAT-
CCG 903


Qy        1820  CGAGTGAGCCTTGAACGCCTGGACCT--
GGACCTCACAGCTGACAGCCAGCCACCCGT-C 1876
                  |        ||| |||   ||| ||| |  ||| |  ||||| | |  |  ||  ||||||
|
```

```
Db        902 C-----AGCGATGA---CCT-GACTTAAGGAACCTACAGC--
AAAACACTCCTCCCGTAC 854

Qy       1877 TTCAAGGTCTTCCCAGGCAGTACCACTGAGGACTACAACCTTATTGTTAT-
TGAACGTGG 1935
              |  |  |  |  | | ||| |||  ||| | ||||||| | | ||  |  | | || |||
Db        853 TCCTAAATGTTCACA--CAG-AGAACTGAGGCCTGACAC----
TAGGCATCTGAT----- 806

Qy       1936
CGCTGCCGCTGCAGCTACCGGCCAGCCAGGGACTGCGCCTGCAGGAACCCCTGGTGCCCC 1995
                  |||| || |||||| |      |  ||| |||  |   ||| ||        |
Db        805 --CTGCAGCAGCAGCT---------CTGGGGTTAGCG--TAGTGGAGTCC-----
ACATC 764

Qy       1996 ACCC---CTGGCTGGCATGGCC-
ATTGTCAAGGAGGAGGAGACGGAGGCTGCCATT---- 2047
              ||||   || |  || | ||  ||  |||||      | ||  ||| || |||
Db        763 ACCCAGGCTTCCCAGCTT--CCTCTTGTCC---------GGTCG--GGC-
GCTATTAAGG 718

Qy       2048 -
GGAGCCCCTCCTACTGCCACTGAGGGCCCTGAGACCAAACCTGTGCTTATGGCTCTTGC 2106
              || || |||| |  | | |||   |  |||       ||
|||
Db        717 AGGTGCACATCCTGGGGTAGCAGTGGGAAAAGGGA-----------------------
TGC 680

Qy       2107 GGAGGGTCCTGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAGT-
GGCAGCACCAGCTCAG 2165
                  |  | |||| |   |||            |  ||| || |||| |||
|
Db        679 AAAAG---CTGGAGTCAAGG-----------------
CAAAGTGGGGAGCAACAG----G 644

Qy       2166 GGCTGGAGGTGGTGGCTCCTGAGGGTACCTCAGCCCCAGGTG--------
GTGGCCCGGG 2217
              |||  |   |  || | || | |  ||||| |||    |||         || ||||
Db        643 GGCAAGCAATAACGGGACATG-GAACACCTCGGCC----
GTGTAGTTCATGTTGCCC--- 592

Qy       2218 AACCCTGGATGACAGTGC--
CACCATTTGCCGTGTCTGCCAGAAGCCAGGCGATCTGGTT 2275
              | | |  | ||| ||  | | |  |  ||||  ||| | |||
Db        591 ATCCAT---TCACACAGCTTCTCC---TCCAG---
CTGCTCGAACACCGGC--------- 550

Qy       2276 ATGTGCAACCAGTGTGAGTTTTGTTTCCACCTGGACTGTCACCTGCCGGCCCTG---
CAG 2332
                   |||  ||          |||| || | |   |||||| | ||
||
Db        549 ---TGCTGCCC-------------CTCCATCTCGGCCG----
CTGCCGCCGCTGGGACAT 510

Qy       2333
GATGTACCAGGGGAGGAGTGGAGCTGCTCACTCTGCCATGTGCTCCCTGACCTGAAGGAG 2392
              |||  |    | | |||||      | | | ||||| |
|
Db        509 GATTAGCT----GTGAGGTGGA----------CAG-CGTG-
```

```
GCTCAC-----------G 478

Qy        2393 GAGGATGGCAGCCTCAGCCTGGATGGTGCAGACAGCACTGGC--GTGGTGGCC---
AAGC 2447
                | | || | || || |      ||| |    ||| ||   |||   || || ||   |
|
Db         477 GTTG-TGACCACCACA-CAATACTGGAAGTGACTGC---
GGCAGATGATGTCCCGTAGGA 423

Qy        2448 TCTCACCAG-
CCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTCACGAA 2506
                |||| | | || ||                | | || ||  |  || |||
||
Db         422 TCTCCACGGTCCGGCCT-----------------TTCAGCAGG--CAGCTCAG-
CACAAA 383

Qy        2507 CCCTGCCGCCCCCTGCATCAGCTGGCTACCGACTCCACCTTC-TC---
CCTGGACCAGC- 2561
                | ||||| |    ||||      ||||| ||  | |||  || | ||   |  | ||
|
Db         382 CACTGCCTTGGGCTGCT-----TGGCT-
CCACCACCAATTGCGTCGGGCTCGAACTCTCG 329

Qy        2562 CCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCTCCAGGAGA-
AGTTGTCACCT 2620
                | |||| || | | ||    | |||    ||   |||||||||||||| | | ||
||
Db         328 CAGGTGACAGTCAGG----GCCCC----CC---
ACCGCCTCCAGGAGACGGGTGGATCC- 281

Qy        2621
CCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCCGCATGTTCAAGCAATTCAAC 2680
                    ||| ||||| |            ||| | |||| |              ||
Db         280 ----GCAG--CCCCAGTG---------CAGGCTCTCGGC-----------
GC-------- 255

Qy        2681
AAGTTAACTGAGGACAAGGCAGACGTGCAGTCCATCATCGGCCTGCAGCGCTTCTTCGAG 2740
                             |||| | ||| ||| | |  | | | ||| |   | |||
Db         254 ----------------AGGC-
GGCGTCCAGGTAAACCACAGCCCGTTTCACTT------- 219

Qy        2741
ACGCGCATGAACGAGGCCTTCGGTGACACCAAGTTCTCTGCTGTGCTGGTGGAGCCCCCG 2800
                                   | ||| |    |||           | |||
Db         218 -------------TGGCC------AGCACC-------------TGCT---------
CCCA 200

Qy        2801 CCGATGAGCCTGCCTGGTGCTGGCCTGAGTTCCC-
AGGAGCTGTCTGGTGGCCCTGGTGA 2859
                  |      |  | ||| |||  || | |   ||| ||| |||        | ||||
Db         199 TC------CTTGCTGGGTAAAGGACAGTACGCCCGAGGCGCT----------
CATGGTTG 156

Qy        2860
TGGGCCCCTGAGGCTGGAGCCCCCATGGCCAGCCCAGCCTGGCTCTGTTCTCTGTCCTGTC 2919
                    ||   |  || || ||  | | ||       | || ||   || | |||
||
Db         155 GGGATTCGCAGACTTGGGAAACTACGGT--------GCAGGAACTTCTTTCAGAAC--
```

TC 106

```
Qy      2920 ACCCCATCC--CCACT---CCCCTGGTGGC-----CTGACTCCC----
ACTCCCTGGTGG 2965
             ||| | ||| | | | || || | |    | | ||||   || ||| |
||
Db       105
ACCGCTTCCGGAAATTGGGCTCCGGGAGACTTTGACAGTCTCCACAGTACACCCAGTAGG 46

Qy      2966
CCCCATCCCCCAGTTCCTCACGATATGGTTTTTACTTCTGTGGATTTAATAAAAAAAACT 3025
             || |||| | ||| || | ||| | | ||| | | | ||
Db        45 ------CCAACAGT---GCTCGA---GG-----
AATTCCGCAGCTTTTAGAGCAGAAGTA 3

Qy      3026 TC 3027
               |
Db         2 AC 1
```


RESULT 7
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match   29.6%; Score 5788; DB 1; Length 2120;
  Best Local Similarity 43.2%; Pred. No. 0;
  Matches 1299; Conservative   0; Mismatches 734; Indels 974;
Gaps 192;

Qy   57 TTGGCC-
GTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGGAGGCGCGTGGT 115
             | |||| || | | || || | | || | | ||
|
Db   1 TAGGCCTGTAC---GGAAGTGTT-------------
ACTTCTGCTCTAAAAGC------T 38

Qy   116
GCGGGTTTCGGCGGCGGCTGAGGAAGAAGCGCGGGCGGCGCCTTCGGGAGGCGAGCAGGC 175
             |||| ||| || ||| | | | |||| | ||||
||
```

```
Db         39 GCGGAATTCCTCG-------------AGCACTGTTG--GCCTACTGGAG-------
TGC 75

Qy        176
AGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGGCGGGCAGCGGCCCAGGAGGCGCG 235
                    |  ||| |||         || |    || || ||| |         ||
||||||
Db         76 TGAAGTAGGC---------GCGG----ACGTGCCCGGTG---------CC---
TGGCGCG 110

Qy        236 TGG----
CGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCAGCGGCCCAGCAGTTGGCGGCG 291
                   |||     ||||| |||  | |||| ||||| ||    |||     ||| ||
|
Db        111 TGGTAGCAGGCGCCCGGTGCCCCGGC--CGGCGAAGACCATGGC------
GTTCATGGTG 162

Qy        292 AGCGCGTCTGCGCCTGCGCGGCGGGCCCCGC-
GCCCCTCCTCCCCCCCTGGGCGCCCCCG 350
                  |    |     | ||  ||||| ||| |     ||| | ||||| |||
Db        163 AAGAC-------CATGGTGGGCGG--CCAGCTGAAGAACCT----
CACTGGGAGCC---- 205

Qy        351
GCGGCGTGTGAATGGCGGCCTCCGCGGCGGCAGCCTCGGCAGCAGCGGCCTCGGCCGCCT 410
                         ||  ||||||          | |     || ||  | || |  | |
Db        206 --------TGGGAGGCGGC----------
GAGGATAAGGGAGATGGGGACAAGTC----- 242

Qy        411 CTGGCAGCCCGGGC-
CCGGGCGAGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCCT 469
                         ||||||| || | |||| | ||    | || || |
Db        243 --GGCAGCCGAAGCTCAGGGCATGAGC----
CGGGAGGAGTA------------------ 278

Qy        470
TCGGCCGCAGCCTCGGCCTCTGCCTCAGCCGCGGCGTCGTCGCCCGCGGGGGGCGGCGCC 529
                          ||  |         |  |||| ||  | ||||                  |
Db        279 -----CGAGG----------AGTATCAGAAGCAAC-TCGT----------------
GGAA 306

Qy        530
GAGGCGCTGGAGCTGCTGGAGCACTGCGGCGTGTGCAGAGAGCGCCTGCGACCCGAGAGG 589
                     |||  | |||||| | |  ||||        ||  || |||| |  ||
||||
Db        307 GAGAAGATGGAGCGG--GATGCAC-----AGTTCACACAGAG-GAAGGC------
AGAGC 352

Qy        590
GAGCCCCGCCTGCTGCCCTGTTTGCACTCGGCCTGTAGTGCCTGCTTAGGGCCCGCGGCC 649
                     | ||| | |||| |  |     |||| || | | | |        || ||
||
Db        353 GGGCCAC-ACTGCGGAGC------CACTT--CC----GAGACAAAT----
ACCGGCTACC 395

Qy        650 CCCGCCGCCGCCAACAGCTCGGGGGACGG--
CGGGGCGGCGGGCGACGGCACCGTGGTGG 707
                      | |     || ||||| | | | |  |  | ||| ||    || | |||||
|
Db        396 CAAG--AACG-AGACAGAT-GAGAGCCAGATCCAGATGGCAGG---
```

```
TGGAGACGTGGAG- 447


Qy        708 ACTGTCCCGTGTGCAAGCAACAGTGCTTCTCCAAAGACATCGTGGAGAA-----
TTATTT 762
              ||| |||| | || || | || ||    | |||| ||||| |           |
Db        448 -CTGCCCCGGGAGCTGGCCAAGATG-
ATCGAGGAGGACACAGAGGAGGAGGAGGAGAAGG 505


Qy        763 CATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGCCCAGGATGCGAACCAGTGCTGCAC 822
                || | || | | |||||| | |||       || | || ||||| | |||
|||
Db        506 CCTCAGTCCTTG-GGCAGCTGGCCAGCCT------TCCTGGCT-TGAACCTGGGCT-
CAC 556


Qy        823 TAGCTGTGAGGATAATGCCCCAGCCACCAGCTACTGTGTGGAGTGCTCGGAGC-
CTCTGT 881
              |        |||| || |||| |||||    |||| || | ||| ||| ||
|
Db        557 TC-----AAGGACAAGGCCCAGGCCAC-----ACTG---GGGGATCTC-
AAGCAATCAG- 601


Qy        882 GTGAGACCTGTGTAGAGGCGCACCAGCGGGTGA--AGTACACCAAGG--
ACCATACTGTG 937
              ||| || || | | ||    |||| ||| |  |  |||
Db        602 -------CTGAGAAGTGTCACGTCA---
TGTGACCACTTCCCCGGGGTTACC-------- 643


Qy        938 CGCTCTACTGGGCCAGCCAAGTCTCGGGATGGTGAACGTACTGTCTATTGCAACGTACAC 997
              | || ||||||| | || || |||| |||| |||| | | | | | | | ||
|
Db        644 CACTGGGCTGGGCCC-CCATG---AGGGC---TAAGAGTG-
TGTCAACTTCCAGGGACCC 695


Qy        998 AAGCATGAACCCCTTGTGCTGTTTTGTGAGAGCTGTGATACTCTCACCTGCCGAGACTGC 1057
              |        || || || |          | ||| ||    | | | |  ||||
|
Db        696 A------TACTCCATTTG-----------GGGCTTTGTT----
TCCCTTGCC-------C 727


Qy        1058 CAGCTCAATGCCCACAAGGACCACCAGTACCAGTTCTTAGAGGATGCAGTGAGGAACCAG 1117
               || | | || |||| ||      | || || |   ||||
||
Db        728 CATCCTAGTTCC----AAGACCT----TTCCCATCC-------ATGC-------
CCCAAG 765


Qy        1118 CGCAAGCTCCTGG------
CCTCACTGGTGAAGCGCCTTGGGGACAAACATGCAACATTG 1171
               | | | |||| ||||        |||| |        ||| ||||
Db        766 C-CTATCTTCTGGTTTCTTCCTCTC--------CGC--
TGGG------------------ 796


Qy        1172 CAGAAGAGCACCAAGGAGGTTCGCAGCTCAATCCGCCAGGTGTCTGACGTACAGAAGCGT 1231
               || ||| || ||    || |||  ||| || ||| |  |||| || | ||  |||
|
Db        797 -AGTAAAGTCCCCA------TCTTCACTCTACCCTTCAGGACCCTCCC---
```

```
CACCAGC-T 845


Qy         1232
GTGCAAGTGGATGTCAAGATGGCCATCCTGCAGATCATGAAGGAGCTGAATAAGCGGGGC 1291
                   ||  |||||         |||| ||  |||| || ||    ||||| ||
|
Db          846 CAGCCTGTGGA---------GGCCTCCC--AAGAT--TGTAG-----
GAATAGGC----C 883


Qy         1292
CGTGTGCTGGTCAATGATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGCGG 1351
                   | |               |||
Db          884 CAT---------------
CCCT------------------------------------ 890


Qy         1352 CAGCACTGGACCATG--ACCAAGATCCAGAAGCAC-
CAGGAGCACATTCTGCGCTTTGCC 1408
                    | |||| |||||   ||||| |||    |||| |||||||||  | | |    |
|
Db          891 ---CTCTGG--CCATGGCCCCAAGTTCC---TGCACACAGGAGCACCCACAGAG---
AGAC 940


Qy         1409
TCTTGGGCTCTGGAGAGTGACAACAACACAGCCCTTTTGCTTTCTAAGAAGTTGATCTAC 1468
                    |      | | |||       |||| ||  |||      | ||| |||
Db          941 AC----ACACAGGA-------CACAAAC--
CCCTGGCACGTTCAGAGA----------- 976


Qy         1469
TTCCAGCTGCACCGGGCCCTCAAGATGATTGTGGATCCCGTGGAGCCACATGGCGAGATG 1528
                    ||| ||  | | | | |                    |||||         |||
Db          977 ---CAGAAGCCACAGACAC---------------ATCCC-------------
GGC------ 1000


Qy         1529 AAGTTTCAGTGGGAC-
CTCAATGCCTGGACCAAGAGTGCCGAGGCCTTTGGCAAGATTGT 1587
                    |||   ||| | ||                            |||||||
Db         1001 -----ACAGACAGACACACA--------------------
CGAGGCC-------------- 1022


Qy         1588
GGCAGAGCGTCCTGGCACTAACTCAACAGGCCCTGCACCCATGGCCCCTCCAAGAGCCCC 1647
                    ||| ||| || | ||    || | ||||    ||| | | || |||         |
|
Db         1023 -----AGCTCCCTTGCG-TGTC----CAGCCCCT----CCA-GACACCACCA-----
CTC 1062


Qy         1648
AGGGCCCCTGAGCAAGCAGGGCTCTGGCAGCAGCCAGCCCATGGAGGTGCAGGAAGGCTA 1707
                    || | | ||||||  || || ||  |||||  || | ||        |||| |||
Db         1063 AGAAACTCTGAG--AG-AGAGCATGGGCAGACACC--CTCA-------
GCAGACAGG--- 1107


Qy         1708 TGGCTTTGGGTCAGGAGATGATCCCTAC---TCAAGTGC---
AGAGCCCCATGTGTCAGG 1761
                    ||| | | ||  |       || | ||    |   || |   | ||||||
Db         1108 AGGCCTGAGTTCCAG------
TCTCCACCTTTATTGTTCTTGAAAGCCCC---------- 1151


Qy         1762
```

```
TGTGAAACGGTCCCGCTCAGGTGAGGGCGAGGTGAGCGGCCTTATGCGCAAGGTGCCACG 1821
                 ||  | | ||| |                      ||||||||
Db      1152 --TG-------CTCTCTCTG-----------------
AGCCTTAT-------------- 1170

Qy      1822 AGTGAGCCTTGAACGCCTG-
GACCTGGACCTCACAGCTGACAGCCAGCCACCCGTCTTCA 1880
             || | ||| || | | ||| | | |||| | | | |     ||||
Db      1171 --------TTCATCATCTGTAAAATGGGAATGTC--
CTGAATGACTTCTAAGGCTCTTTC 1220

Qy      1881
AGGTCTTCCCAGGCAGTACCACTGAGGACTACAACCTTATTGTTATTGAACGTGGCGCTG 1940
             || | | ||| ||| ||   | | | ||| || |     ||| |  |  ||
|
Db      1221 TGGCTTGAACTGTCAGAGCC----AAGCCCACATCCCTC-----CTTGGGCAGG--
GCAG 1269

Qy      1941
CCGCTGCAGCTACCGGCCAGCCAGGGACTGCGCCTGCAGGAACCCCTGGTGCCCCACCCC 2000
             | ||||| || | ||| |||| | |||| ||| || | |  || ||| | |
Db      1270 CAGCTGCTGCCA-CAGCCT-CCAGCGGCTGCCACTGTGGG--
CTCTGGGAGCCGGAGCGA 1325

Qy      2001 TGGCTG---GCATGGCC-
ATTGTCAAGGAGGAGGAGACGGAGGCTGCCATTGGAGCCCCT 2056
             | |||| | ||| | || |||||| |  | | | | ||     |||
||
Db      1326 T-GCTGTGTGAGAGGCAGAGTGCCAAGGATGAAG---
CTGGCACTGAACAGTAAGCGGCT 1381

Qy      2057 CCT-ACTGCCACTGAGGGCCCTGAGACCAAAC-----
CTGTGCTTATGGCTCTTGCGGAG 2110
             || | | || || ||||||| | ||| |     |||| ||    | || ||
||
Db      1382 CCAGGCCTCCTCT--GGGCCCAGGGCCCAGCCAATTTCTGTTCT----
GTTCCTGTAGAA 1435

Qy      2111 GGTCCTGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAGTGGCAGCAC-
CAGCTCAGGGCT 2169
             | || ||| | ||  | |    |||| | |   || | |||||||
|
Db      1436 CGCTCT----CTG-GATTCCATAGCTGGAATCTCCT--------
CTCTTAGCTCAG---T 1479

Qy      2170 GGAGGTGGTGGCTCCTGA---GGGTACCT-CAGCCCCA---GGTGGTGGC--
CCGGGAAC 2220
             | |       ||| |   | || ||| |   ||||     | |||| || |||
Db      1480
GAAAAATAAAAATCCCAAATGGTGTGCCTACCTTCCCACTTCTTACTGGCTTCCAGGAGT 1539

Qy      2221
CCTGGATGACAGTGCCACCATTTGCCGTGTCTGCCAGAAGCCAGGCGATCTGGTTATGTG 2280
             | |||| || ||| |   ||| |   ||| | ||||| | | |  ||| |
|||
Db      1540 CTTGGAGTTCATAGCCCC------CCGAGCCTGCCTTAA---AGGGG---------
TGT- 1580

Qy      2281
CAACCAGTGTGAGTTTTGTTTCCACCTGGACTGTCACCTGCCGGCCCTGCAGGATGTACC 2340
```

```
                    |  |||                    || ||       ||||| | |    || ||
|
Db      1581 CCTCCA---------------CCCCC--------CACCTACAG---
CTTCA--------C 1606

Qy      2341 AGGGGAGGAGTGGAGCTGCTCACTCTGCCATGTG---------CTCC----
CTGACCTGA 2387
                   ||| | |||| ||     ||    | ||| | |        |||| |||  ||
Db      1607 AGGAGGGGAGAGG----
GCATCCAGTGCTAGGAGTAGAAGTGTCTCCAGCTCTGTTCTCT 1662

Qy      2388 AGGAGGAGGATGGCAGCCTCAGCCTGGAT---
GGTGCAGACAGCACTGGCGTGGTGGCCA 2444
                   ||      |||      |||||| | |||| | |    ||| |  ||
Db      1663 TGG--------GGC--------CCTGGGTGAAGGTGGGGTCTG---GGGC-
TTATGAAAT 1702

Qy      2445
AGCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTCACG 2504
                 || ||||   ||      |  | | | |||  ||||         |||   ||| |||
|
Db      1703 AGGTCT---GGGCTTTGAGGAGG--ATG-GAGC----------
AGCCTCATTATGTGGGG 1746

Qy      2505 AACCCTGCCGCCCCCTGCATCAGCTGGCTACCGACTCCACCTTCTCCCTG-
GACCAGCCC 2563
                   ||    |  | || |||        |||              || ||| |||||
|
Db      1747 AAGATGG--GGCCTCTG-------GGGCG---------------TCACTGAGACCA--
CA 1780

Qy      2564 GGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCTCCAGGAGAAGTTGTCACCTCCC 2623
                   |||||  || ||  |||   ||| |||  ||| ||| ||    || |    || |  |
|||
Db      1781 GGTGGGGCCGGGG--------CTGGACCGCAGCTGTCT-
TGGGTGCCTGTGCCTGCACCC 1831

Qy      2624
TACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCCGCATGTTCAAGCAATTCAACAAG 2683
                   |||| ||          ||| ||        | |              ||| | |||
|||
Db      1832 -----CTCCTCA----------CCCTAGAGACGG-----------
AAGATGTGCAAAAAG 1865

Qy      2684
TTAACTGAGGACAAGGCAGACGTGCAGTCCATCATCGGCCTGCAGCGCTTCTTCGAGACG 2743
                 | | || |  | |||| |||| || |||| ||||        ||| | | ||    | ||
|
Db      1866 ---AAAGAAGGAAGGGCA-AC-TGCATTCCA------GCC--CCACACT-----
GTGATG 1907

Qy      2744 CGCATGAACGAGGCCTTCGGTGACACCAAGTTCTCTGCTGTGCTGGTGGAGCCCCCG-
CC 2802
                   ||| | |  | ||||  | |||   ||||| |||| |     |||| |
Db      1908 ACTTTGAGCCTGTCCTT---TCCCTCCTTGAGC-CTGTCTTGCTTGT----
CCCCTGTAA 1959

Qy      2803 GATGAGCCTGCCTGGTGCTGGCCTGAGTTCCCAGGAGCTGT-------
CTGGTGGCCCTG 2855
```

```
               ||||  |   ||       |   |||    ||||   |   ||       |  ||  |
   |
Db       1960 AATGAACAGTCC-----C---CCT---
CTCCCCCAAATAGTAATAATACATGTTTCAAAG 2008

Qy       2856 GTGATGGCCCCTGAGGCTGGAGCCCCCATGGCCAGCCCAGCCTGGCTCTGT-
TCTCTGTC 2914
               |  || ||  |  |   ||  |  |||  |  |  ||    |     |||  |||
   ||
Db       2009 --GGTGACCATTTA---TAAAG--
CATATGACAAACCATATCAATAAATGTAACTCATTC 2061

Qy       2915 CTGTCACCCCATCCCCACT---
CCCCTGGTGGCCTGACTCCCACTCCCTGGTGGCCCCAT 2971
               |  |  |     |      |     || |  |||         |  |   |||  || | |
Db       2062 TTTTAAAAAAAAAAAAAAAAGGCCACATGTG----------
CTCGAGCTGCAGGTCGCGG 2111

Qy       2972 CCCCCAG 2978
               ||  |  ||
Db       2112 CCGCTAG 2118


RESULT 8
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match            29.3%;  Score 5725;  DB 1;  Length 2120;
  Best Local Similarity  41.9%;  Pred. No. 0;
  Matches 1305;  Conservative    0;  Mismatches  702;  Indels 1104;
Gaps  194;

Qy         45
GACTAGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCC---- 100
               |  |||||       ||||| | |  | ||  | || ||  |          | ||||
Db       2120 GTCTAGC-------GGCCGCGAC----CTGCAGCTCGAGCAC------
ATGTGGCCTTTT 2078

Qy        101 ----------------CAGGAGGCGCG-----
TGGTGCGGGTTTCGGCGGCGGCTGAGG 138
```

```
                                   |  |||     |        || |  ||  || |  |      |||
Db       2077 TTTTTTTTTTTTTAAAAGAATGAGTTACATTTATTGATATGG--
TTTGTCATATGCTTTAT 2020

Qy        139 AAGAAG-CGCGGGCGGCGCCTTCGGGAGGCGAGCA--------------
GGCAGCAGTTG 183
                ||   |  |    |         |||| |  || |  |  |              || ||   |
|
Db       2019 AAATGGTCAC--------CCTTT--
GAAACATGTATTATTACTATTTGGGGGAGAGGGGG 1970

Qy        184 GCCGTGCC-
GTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGGAGGCGCGTGGCGGC 242
                |  || |  |  |   ||| |   |  || |  || |  |          | |||||  | |
|
Db       1969 ACTGTTCATTTTACAG-GGGACAAGCAAGACAGGCT-----
CAAGGAGGGAAAGGACAG- 1917

Qy        243 GCTC---
GGCCTCGCGGCGGCGGCGGCGGCGGCCCAGCAGTTGGCGGCGAGCGCGTC 299
                ||||   |  | || | | |  ||       || |     |||||
Db       1916 GCTCAAAGTCATCACAGTGTGGG--------
GCTGGAATGCAGT--------------- 1881

Qy        300
TGCGCCTGCGCGGCGGGCCCCGCGCCCCTCCTCCCCCCCTGGGCGCCCCCGGCGGCGTGT 359
                |||  ||| | |      ||    |  | || ||||  ||
|||
Db       1880 TGC--CCTTC-CTTCTTTCTTTTTGCACATCTTCCGTCTCTAGG-------------
GTGA 1836

Qy        360
GAATGGCGGCCTCCGCGGCGGCAGCCTCGGCAGCAGCGGCCTCGGCCGCCTCTGGCAGCC 419
                |  | || ||   |    | |    |||| |  | ||||  |
|||||
Db       1835 GGAGGGGTGCAGGCAC--AGGCACCCAAGACAGCTGCGGTC-------------
CAGCC 1792

Qy        420 CGGGCCCGGGC-
GAGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCCTTC------- 471
                | |||||   | | | |||| | || | ||| | ||| |   ||| |
Db       1791 CCGGCCCCACCTGTGGTCTCAG-TGACGCCCCAGAG-
GCCCCATCTTCCCCACATAATGA 1734

Qy        472 GGCCGCAGCCTCGGCCTC--TGCCTCAGCCGCGGCGTCGT-
CGCCCGCGGGGGGCGGCGC 528
                ||| || ||| | ||     ||| |  ||  || | ||||         || |
|
Db       1733 GGCTGCTCCATCCTCCTCAAAGCC-CAGAC-CTATTTCATAAGCCC--------
CAGACC 1684

Qy        529
CGAGGCGCTGGAGCTGCTGGAGCACTGCGGCGTGTGCAGAGAGCGCCTGCGACCCGAGAG 588
                |  | | |    || |     | | |||            | | | || | |||
Db       1683 C----CAC-----CTTC----ACCCAG-GGC------------
CCCAAGAGAACAGAGCT 1650

Qy        589
GGAGCCCCGCCTGCCCTGTTTGCACTCGGCCTGTAGTGCCTGCTTAGGGCCCGCGGC 648
                ||||| | | || || || |  | ||||| |        |||| ||
```

```
Db      1649 GGAGACACTTCTACT--CC---TAGCACTGG-------
ATGCCCTCT------------ 1615

Qy       649
CCCCGCCGCCGCCAACAGCTCGGGGGACGGCGGGGCGGCGGGCGACGGCACCGTGGTGGA 708
             ||||  ||    |         |   |  ||||  |   ||  |   |||  | ||  |
||
Db      1614 CCCCTCCTGTG----AAGCT-----GTAGGTGGGG-GGTGGAGGAC-
ACCCCTTTAAGG- 1567

Qy       709
CTGTCCCGTGTGCAAGCAACAGTGCTTCTCCAAAGACATCGTGGAGAATTATTTCATGCG 768
             |  | | ||| |      |  |        |   |  ||   |||| ||||| || |||             |
||
Db      1566 CAGGCTCGGGGG------GCTATG-AACTCC-AAGAC-TCCTGG-----------
AAGCC 1527

Qy       769 TGATAGTGGCAGCAAGGCTGCCACCGACGCCCA----
GGATGCGAACCAGTGCTGCACT- 823
             |  | ||   |  | ||||  |  |||        |||     ||||     |     |   |
||||
Db      1526 AGTAAGAAGTGGGAAGGTAGGCAC-----ACCATTTGGGATTTTA----
TTTTTCACTG 1476

Qy       824 AGCT--
GTGAGGATAATGCCCCAGCCACCAGCTACTGTGTGGAGTGCTCGGAGCCTCTGT 881
             ||||   |  ||||| | |          |||||||      |||| |
Db      1475 AGCTAAGAGAGGAGATT---------CCAGCTA-----
TGGAAT--------------- 1446

Qy       882
GTGAGACCTGTGTAGAGGCGCACCAGCGGGTGAAGTACACCAAGGACCATACTGTGCGCT 941
                                ||||  |  |    | |   ||  |   ||  ||  |     |
|
Db      1445 ----------------------CCAGAGAG---CGTTCTACAGGAACAGAAC--
AGAAAT 1413

Qy       942 CTACTGGGCC---AGCCAAGTCTCGGGATGGTG-
AACGTACTGTCTATTGCAACGTACAC 997
                |||||||    ||| ||   || |||| |    | |||||| |  |||
||
Db      1412 TGGCTGGGCCCTGGGCCCAGAGGAGGCCTGGAGCCGCTTACTGTTCAGTGC------
CAG 1359

Qy       998 AAGCATGAACCCCTTGTGCTGTTTTGTGAGAGCTGTGATACTCTCAC-
CTGCCGAGACTG 1056
                           |||    |||||             |  || ||  |    | ||   | ||    |
||
Db      1358 CTTCAT-----CCTTG-------------GCACTCTG--CCTCTCACACAGCATCG-
CT- 1321

Qy      1057 CCAGCT--
CAATGCCCACAAGGACCACCAGTACCAGTTCTTAGAGGATGCAGTGAGGAAC 1114
                           || |||   ||  ||||||| |  |         ||      ||| || |||
Db      1320 CCGGCTCCCAGAGCCCACAGTGGCAGCCG---------CT----
GGAGGCTGTGG----- 1279

Qy      1115
CAGCGCAAGCTCCTGGCCTCACTGGTGAAGCGCCTTGGGGACAAACATGCAACATTGCAG 1174
                           ||||    ||||  ||| ||| ||||                 || ||  || |   |         ||     |||
```

```
Db       1278 CAGC---AGCTGCTGCCCT----------GC-CCAAGGAGGGATGTGGGC----
TTG--- 1240

Qy       1175 AAGAGCACCAAGGAGGTTCGCAGCTCAATCCGCCAGGTGTCT-----
GACGTACAGAAGC 1229
              || |  |        ||| |||| ||   | | | |     | | | ||| |
                                                                        |
Db       1239 ----GCTCTGA---------
CAGTTCAAGCCAGAAAGAGCCTTAGAAGTCATTCAGGA-C 1194

Qy       1230
GTGTGCAAGTGGATGTCAAGATGGCCATCCTGCAGATCATGAAGGAGCTGAATAAGCGGG 1289
                 |             ||      |||| |  ||||| ||||          ||||||
Db       1193 AT-------------TC-------CCATTTTACAGATGATGA--------
AATAAG---- 1166

Qy       1290
GCCGTGTGCTGGTCAATGATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGC 1349
                                        || ||||      |||     |||||| ||
Db       1165 --------------------GCTCAGA--------GAG----
AGCAGGGGC--------- 1147

Qy       1350
GGCAGCACTGGACCATGACCAAGATCCAGAAGCACCAGGAGCACATTCTGCGCTTTGCCT 1409
                                  || || ||| |   |   |   ||| ||
||||
Db       1146 ----------TTTCAAGAACAATA-AAGGTGGAGACTGGAACTCA----------
GGCCT 1108

Qy       1410 CTTGGGCTCTG--GAGAGTGACAACAACACAGCCCTTTGC----
TTTCTAAGAAGTTGA 1463
                   | ||    ||||  ||| ||| |   | |     || ||  |    ||||| ||   ||
                                                                        |
Db       1107 CCTG---TCTGCTGAGGGTGTCTGC--
CCATGCTCTCTCTCAGAGTTTCTGAGTGGTGGT 1053

Qy       1464
TCTACTTCCAGCTGCACCGGGCCCTCAAGATGATTGTGGATCCCGTGGAGCCACATGGCG 1523
                 || | |    ||||| |    || ||||| |     ||| | || ||| | ||
Db       1052 -----GTCTGGAGGGGCTGGACACGCAAG--------GGAGC---TG--
GCCTCGTG--- 1014

Qy       1524
AGATGAAGTTTCAGTGGGACCTCAATGCCTGGACCAAGAGTGCCGAGGCCTTTGGCAAGA 1583
                 || || |     || || |  || ||||| | | | | | ||| | | ||  |
Db       1013 ------TGTGTCTG-------TCTGTGCCGGG---ATGTGT-
CTGTGGCTTCTGTCT--- 974

Qy       1584 TTGTGGCAGAGCGT-CCTGGCACTAACTCAACAGGCCCTGCACCCATG-
GCCCCTCCAAG 1641
                  | || ||| || |  |        |   |      ||||  || | | |||
                                                                        |
Db        973 ------CTGAACGTGCCCAGGGGTTTTGT------GTCCTG----
TGTGTGTCTCTCTGTGTG 930

Qy       1642
AGCCCCAGGGCCCCTGAGCCAAGCAGGGCTCTGGCAGCAGCCAGCCCATGGAGGTGCAGGA 1701
                 |        || |||| |   ||||| |     || |        | | ||||||     |||
Db        929 GGT------GCTCCTGTG--TGCAGGAACTTGG---------GGCCATGGC----
CAGAG 891
```

```
Qy        1702 AGGCTATGGCTTTGGGTCAGGAGATGATCCCTACTCAAGTGCAGAGCC-
CCATGTGTCAG 1760
               |||     ||| |              || ||||| |   ||    ||| |||
|||
Db         890 AGGGATGGGCCT--------------ATTCCTACAATCTTGGGAGGCCTCCA-----
CAG 850


Qy        1761 GTGTGAAACGGTCCCGCTCAGGTGAGGGCGAGGTGAGCGGCCTTATGCGCAAGGTGCCAC 1820
                        |            | |  | |||| |         ||| | ||| | || | |||
|
Db         849 G-----------CTGAGCTGGTGGG--------GAGGGTCCTGAAGGGTAGAGTG--
AA 812


Qy        1821 GAGTGAGCCTTGAACGCCTGGACCTGGACCTCACAGCTGACAGCCAGCCACCCGTCTTCA 1880
                        ||  | ||| |            ||| |||| || ||   ||  ||| |
|
Db         811 GATGGGGACTTTA-----------------
CTCCCAGCGGGAGAGGAAGAAACCAG-----A 773


Qy        1881 AGGTCTTCCCAGGCAGTACCACTGAGGACTACAACCTTATTGTTATTGAACGTGGCGCTG 1940
                        || |    |||      || ||   | |   ||  | | | |||
||
Db         772 AGAT------AGGCT-------TGGGG-------
CATGGATGGGAAAGGTCTTGGAACT- 734


Qy        1941 CCGCTGCAGCTACCGGCCAGCCAGGGACTGCGCCTGCAGGAACCCCTGGTGCCCCACCCC 2000
                                        ||| | || |  |||| |       ||||||
Db         733 -----------------------AGGATGGGGCAAG--GGAAAC---
AAAGCCCCA---- 706


Qy        2001 TGGCTGGCATGGCCATTGTCAAGGAGGAGGAGAC---
GGAGGCTGCCATTGGAGCCCCTC 2057
                               | |||| | | | |   ||| | || ||         |
|||
Db         705 -------------------AATGGAGTATGGGTCCCTGGAAGTTGACA-------
CACTC 672


Qy        2058 CTA-CTGCCAC-
TGAGGGCCCTGAGACCAAACCTGTGCTTATGGCTCTTGCGGAGGGT-- 2113
                        || |  || | || |||||| |         ||           | | ||||
Db         671 TTAGC--CCTCATGGGGGCCCAG--------CC-----------------
CAGTGGGTAA 639


Qy        2114 -
CCTGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAGTGGCAGCACCAGCTCAGGGCTGGA 2172
                        || || | ||  | ||  | | |               ||||| | |||
||
Db         638 CCCCGGGGAAGTGGTCACATGACGTGACACTTCT-----------
CAGCTGATTGCTTGA 590


Qy        2173 GGTGGTGGCTCCTGAGGGTACCTCAGCC----CCAGGTGGTGGCCCGGGAAC---
CCTGG 2225
                        | |    | || | |  ||| |||   || | |   |||| || |   ||
||
Db         589 GAT----CCCCCAGTGTG-
```

```
GCCTGGGCCTTGTCCTTGAGTGAGCCCAGGTTCAAGCCAGG 535


Qy       2226 ATGACAGTGCCACCATTTGCCGTGTCTGCCCAGAAGCC--
AGGCGATCTGGTTATGTGTCAA 2283
              | | | | |||||              ||||| | | | |||| ||| | |    |
Db        534 AAGGCTG-GCCA------------GCTGCCCAAGGACTGAGGCCTTCTCCTCCT---
CCT 491


Qy       2284 CCAGTGTGAGTTTTGTTTCCACCTGGACTGTCACCT--
GCCGGCCCTGCAGGATGTACCA 2341
              || ||||        ||| |||   | ||| || ||| || |
||
Db        490 CCTCTGTG---------TCCTCCT---CGATCATCTTGGCCAGCTC-----------
CC- 455


Qy       2342
GGGGAGGAGTGGAGCTGCTCACTCTGCCATGTGCTCCCTGACCTGAAGGAGGAGGATGGC 2401
                             || || |||        ||| || |||| ||||| |
||||
Db        454 ---------GGGGCAGCT-------CCACGT-CTCC---
ACCTGCCATCTGGATCTGGC 416


Qy       2402
AGCCTCAGCCTGGATGGTGCAGACAGCACTGGCGTGGTGGCCAAGCTCTCACCAGCCAAC 2461
                   |||| ||| | ||        || |   ||| ||| | |
Db        415 T--CTCA-TCTGTCTCGT---------TCTTG---
GGTAGCCGGTATTTGTCT------- 378


Qy       2462
CAGCGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTCACGAACCCTGCCGCCCCCTG 2521
               ||||| ||             ||| | | | | | ||| | |||| ||
Db        377 ---CGGAAGTG------------GCT--CCGCAGTGTGGCCCG--
CTCTGCCTTCCTCTG 337


Qy       2522 CATCAGCTG-
GCTACCGACTCCACCTTCTCCCTGGACCAGCCCGGTGGCACCCTGGATCT 2580
                   | | ||| || || ||||| |||||| ||| | || ||
Db        336 TGTGAACTGTGCATCCCGCTCCATCTTCTCT----TCCA--CGAGTTGC-------
TTCT 290


Qy       2581
GACCCTGATCCGTGCCCGCCTCCAGGAGAAGTTGTCACCTCCCTACAGCTCCCCACAGGA 2640
               || ||            |||| ||      || | ||||| | ||||
Db        289 GATACT------------CCTC--------GT--ACTCCTCC---
CGGCTC--------- 264


Qy       2641
GTTTGCCCAGGATGTGGGCCGCATGTTCAAGCAATTCAACAAGTTAACTGAGGACAAGGC 2700
                       ||||||        || ||              |||
Db        263 --ATGCCC------TGAGC---------------TTC--------------------
GGC 247


Qy       2701
AGACAGTGCAGTCCATCATCGGCCTGCAGCGCGCTTCTTCGAGACGCGCATGAACGAGGCCTT 2760
               | ||     |||| |||| ||| |||        || |||     ||| |  | ||||
Db        246 TGCCGACTTGTCCC-CATCTCCCT------TATCCTCGC----CGCCT--
CCCAGGCTCC 200
```

```
Qy      2761 CGGTGACACCAAGTTC-TCTGCTGTGCTGGTGGAGCC-
CCCGCCGATGAGCCTGCCTGGT 2818
             | |||    |  | |||| ||  ||||         ||| ||| ||
Db       199 CAGTG-----AGGTTCTTCAGCTG----------
GCCGCCCACC--------------- 171

Qy      2819
GCTGGCCTGAGTTCCCAGGAGCTGTCTGGTGGCCCTGGTGATGGCCCCTGAGGCTGGAGC 2878
             ||| ||   |  ||| || |         ||| |||| | |||    ||| ||
||
Db       170 -ATGGTCT---TCACCATGAAC---------GCCATGGTCTTCGCC-----
GGCCGGGGC 129

Qy      2879 CCCCATGGCCAGC--CCA---
GCCTGGCTCTGTTCTCTGTCCTGTCACCCCATCCCCACT 2933
             ||   ||| ||| |||   ||| |||         || | ||   | ||| |
Db       128 ACCGGGCGCCTGCTACCACGCGCCAGGC-----------ACCGGGCA---
CGTCCGC--- 86

Qy      2934
CCCCTGGTGGCCTGACTCCCACTCCCTGGTGGCCCCATCCCCCAGTTCCTCACGATATGG 2993
                       |||| ||| |  | | | ||  | ||  |    ||||   | |||
||
Db        85 ---------GCCT-ACTTCAGCACTCCAGTAGGCCAA-----CAGT---GCTCGA---
GG 47

Qy      2994 TTTTTACTTCTGTGGATTTAATAAAAAAAACTTCAC--CAGTTCAAAAAAA 3042
                     | ||| |  | ||| | |  | || |   ||| | || ||     |
Db        46 -----AATTCCGCAGCTTTTAGAGCAGAAGTAACACTTCCGTACAGGCCTA 1


RESULT 9
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match          27.7%;  Score 5415.5;  DB 1;  Length 2495;
  Best Local Similarity   40.4%;  Pred. No. 3e-302;
  Matches 1291;  Conservative   0;  Mismatches 1030;  Indels  875;
Gaps  163;
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```
Qy          11 CCGGCGGCGGAGGCCGGGCCGCG-GAGC-CAGGAGTGAC----
TAGCAGCAGTTGGCCGT 64
               |  |||||  | || || ||  |||| ||     |      || |
|
Db        2495 CTAGCGGCCGCGACC-TGCAGCTCGAGCACATGTG-
GCCTTTTTTTTTTTTTTTTTTACAT 2438

Qy          65 GCCGTAGCAGCGTCCCGCGCGCGGCGG-
GCAGCGGCCCAGGAGGCGCGTGGTGCGGGTTT 123
               |   |    |  |       |  |       | | ||| |      | || |
|||
Db        2437 GTTTAAATATATTTTATTTCAAGTTAATATAACAGCCATGAT------TTGTTC--
ATTT 2386

Qy         124 CGGCGGCG-
GCTGAGGAAGAAGCGCGGGCGGCGCCTTCGGGAGGCGAGCAGGCAGCAG-- 180
               | |   ||     ||| |  ||| || || || | | || ||      || |   |||
Db        2385 AAGTGAAATGCTTCGATAAAAACCCCGGTGTCAC--
TTGGTTAAAATATTGGAGACAGAT 2328

Qy         181 -------
TTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGGAGGC- 232
               |  ||| | | ||| || | | |            || |   ||
|
Db        2327 TAAATGTTAAGCC--ACTATAGTAGTGACTC---------------
TGGTTCTTTAGACT 2285

Qy         233 ---GCGTGGCGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCAG--
CGGCCCAGCAGTTGGC 287
               || || ||      ||| |    |    |  ||| || ||   |||
Db        2284 ATTGCATG---------TACCTTGTTAATG----AACTACAGGAATGCACA----
TTGAT 2242

Qy         288 GGCGAGCGC---GTCTGCGCCTG-
CGCGGCGGGCCCCGCGCCCCTCCTCCCCCCCTGGGC 343
               || |  ||| | | | | | | |     || |   |||| |||    | |
Db        2241 ATAATGCACAATGTCTTCACATGTCTC-----
AATCCTCATTCCTCTTCCTTTCAT---- 2191

Qy         344
GCCCCCGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCGGCAGCCTCGGCAGCAGCGGCCTCG 403
                                              ||||||  |  ||||| ||  |    |
Db        2190 ------------------------GCCTCC----CTAATGCCTCAGTATC--
CAATATAA 2161

Qy         404 GCCGCCTCTGGCAGCCCGGGCCCGGGCGAGGGCTC----
CGCTGGCGGCGAAAAGCGCTC 459
               | |   |   ||               | ||   || | | | | | |  | |
|
Db        2160 AACTACAAAAACTACT---------------
GTTCTTTTCGTTTGAGTGGTATTTAATTA 2116

Qy         460 CACCGCCCCTTCGG--------CCGCAGCCTCGGCCTCTGCCTCAGC----
CGCGGCGTC 507
                | |  |  |||          || ||| |   | | | |        |
||
Db        2115
AAACTTCAATTCTATGTTATTTCCACAGTCCAGTAATTTATTTTAAATTTGAGTAATTTC 2056
```

```
Qy          508 GTCGCCCGC----------
GGGGGGCGGCGCCGAGGCGCTGGAGCTGCTGGAGCACTGCG 557
                    || |           | | ||        | | || | ||      | ||
|
Db         2055 AAATTCCACAAACAAAACTGAAGAACAGCAATATTTTGTTTGAATTTCT----
CTCTTCT 2000

Qy          558 GCGTGTGCAGAGAGCGCCTGCGACCCGAGAGGGAGCCCCGCCT--
GCTGCCCT------ 608
                    |       |||| || |     |  | | | |      || | |    |      |||
Db         1999 GTACACTCAGTGATCTAAAACACCACAATA-----
TCCAACATACACAAACCTCAGGGAA 1945

Qy          609 --GTTTG--
CACTCGGCCTGTAGTGCCTGCTTAGGGCCCGCGGCCCCCG----------- 653
                    ||| |   || |    |   | ||      | | | || |    || || |
Db         1944
GGGTTAGTAAACACACACAAGATTGGAATCATGGTGCTCTTTGCTCCTGAATGGAATGGT 1885

Qy          654 -
CCGCCGCCAACAGCTCGGGGGACGGCGGGGCGGCGGGCGACGGCACCGTGGTGGACTGT 712
                    || | |   || ||| || || || ||      | |    | |||||| || |
|
Db         1884 CCCACAG-AAAAAGCACAGGATACAGC---ACAACATAAG--GGCACC--
TGTTACATAT 1833

Qy          713 CCCGTGTGC--AAGCAACAGTGC-
TTCTCCAAAGACATCGTGGAGAATTATTTCATGCGT- 769
                    ||| || || |  || | | |  ||| ||| ||      | |||
|
Db         1832 GAAGTGAGCAAAACATACTAGCATTTTCTATATGCATAATGGGGAA-----
ACCTGCATA 1778

Qy          770 -
GATAGTGGCAGCAAGGCTGCCACCGACGCCCAGGATGCGAACCAGTGCTGCACTAGCTG 828
                    | ||| ||             ||| |||| || | || |||           | ||
||
Db         1777 GGTTAGAGG----------GCCTTTTACGCTCA-TTTAAAAATCAG------
GCAAGTTG 1735

Qy          829 TGAGGATAATGCCCCAGCCACCAG-------
CTACTGTGTGGAGTGCTCGGAGCCTCTGT 881
                    | | | || || | || |     || | |    | ||| | || |
Db         1734
TCTGTAACATTTTCAATAATCTGGGAAGCACTGCAATCCAGTGTACGATGTGCTGATTA 1675

Qy          882 GTGAGACCTGTGTAG----
AGGCGCACCAGCGGGTGAAGTACACCAAGGACCATACTGTG 937
                    ||| || ||| |     | |   || |   || ||| |      | ||
|
Db         1674 GTGTTGTCTTTGTTGGCACTGACAGTCTTGCATG-GTCATATGCCAGTGTTTTTGCT-
TT 1617

Qy          938 CGCTCTAC--TGGGCCAGCCAAGTCTCG--
GGATGGTGAACGTACTGTCTATTGCAAC-G 992
                    ||| | | |  || | | ||  | ||  ||  ||| |||| | |   | |
|
Db         1616 AGCTTTTCTTTGAATAAAACAGATTTAAATGCATTTAGACAATAC-
GTATTTGTAAGCTG 1558
```

```
Qy         993  TACACAAGCATGAACCCCTTGTGCTGTTTTGTGAGAG---CTGTGATACTCTCA--
CCTG 1047
                |  |||  ||  ||      |  |     |  | ||||   || ||  || |
||
Db        1557  TTTACATACACTAAATTTAAGAGATTCAATATTAGAGTTTCTTTGTTTCTTTAAACACTA 1498

Qy        1048  CCGAGACTGCCAGCTCAATGCCCACAAGGACCACCAGT----------
ACCAGTTCTTAG 1097
                |  |||  || ||  |||     |   ||      || |||         |  ||||||||
Db        1497  CAGAG--TG-CAAATCAGGTTCTTCA-----
CAACAGATTGAATATTGAGCAGTTCTTTA 1446

Qy        1098
AGGATGCAGTGAGGAACCAGCGCAAGCTCCTGGCCTCACTGGTGAAGCGCCTTGGGGACA 1157
                   |  ||   || || | || |      ||| |         |  |  ||||
Db        1445  AAGA--AAGAGGGGGAAGAAAAAAAG----------
CCCAAGTGA--------------- 1413

Qy        1158
AACATGCAACATTGCAGAAGAGCACCAAGGAGGTTCGCAGCTCAATCCGCCAGGTGTCTG 1217
                        ||  ||||||| |      | ||     |||| |  | |||
Db        1412  ---ATAAAACATTGAAACTATTCCCC-------TTCGAAAATAAAT----------
TCTA 1373

Qy        1218  ACGTACAGAAGCGTGTGCAAGTGGATGTCAAGAT-GGCCATCCTGCAGATCATG--
AAGG 1274
                 |   |    |   | |  |||| |  | || ||| || |  ||  || || | ||
||
Db        1372  AAATGATGTGGAATGTGAAATAAGGTTTTAACATAGGTGATCC--
AAGTTTATAGTTAGA 1315

Qy        1275  AGCTGAATAAGCGGGGC--CGTGTGCTGGTCAATGATGCCCAGAA---
GGTGACTGAGGG 1329
                 | |  || ||| |  | || | |  | ||     || | |  ||||    |  || |||
Db        1314  AAC--AAAAAGAAGTCCTTCATGAAAT----
AAAGGTTACAAGAACACGTTGCCTGTTTT 1261

Qy        1330  GCAGCAGGAGCGCCTGGAGCGGCAGCACTGGACCATGACCAAGATCCAGAA--
GCACCAG 1387
                 |  || |   |||        || | |||   | ||| | | | ||| |     |
||
Db        1260  CCCCCATTATAAACTG-------
AGAAGTGGGTAAAGACGATGTTTCAGTACGAAAATAG 1208

Qy        1388  GAG----
CACATTCTGCGCTTTGCCTCTTTGGGCTCTGGAGAGTGACAACAACACAGCC-- 1441
                 | |     ||    || || |||||   |||   |||      || |     || ||||
Db        1207  GTGACTACAGGATCAGCGCTTCATCTCACATGCT-------GTACC-----
CAAAGCCAG 1160

Qy        1442  -
CTTTTGCTTTCTAAGAAGTTGATCTACTTCCAGCTGCACCGGGCCCTCAAGATGATTGT 1500
                 ||  ||| | |  |             | | |   ||| |   || | ||| ||
Db        1159  GCTGTGGCTGTCCATACGGTGG-------
TGCGGTATAACCATAACCAAAAGGTG----- 1112

Qy        1501
GGATCCCGTGGGAGCCACATGGCGAGATGAAGTTTCAGTGGGACCTCAATGCCTGGACCAA 1560
```

```
                    || | |||| | ||  ||| |           || |||| |||   || | | |
                    |||
Db    1111 ----CCTGGGGAGGGAC--GGCAA----------CACTGGGTCCT-
GCTGTCAGCATCAA 1069

Qy    1561 GAGTGCCGAGGCCTTTGGCAA--
GATTGTGGCAGAGCGTCCTGGCACTAACTCAACAGGC 1618
                    | | | ||| | |||| | || | |||||| |      |||   ||   || |
Db    1068 CTGGGGC-TGACCATAAACAATGGGTTGTGTCT-------
CTGTAGCTTGTTCTTCT--- 1020

Qy    1619 CCTGCACCCA-------
TGGCCCCTCCAAGAGCCCCAGGGCCCCTGAGCAAGCAGGGCTC 1671
                    || | || |      || |  | || |       |||    || |  |||| |
                    |||
Db    1019 TCTTTTCTCAGTGATTCTGAAGCATCTAATTTATCCA----CCTTTGTCAAGTA---
CTC 967

Qy    1672
TGGCAGCAGCCAGCCCATGGAGGTGCAGGAAGGCTATGGCTTTGGGTCAGGAGATGATCC 1731
                    | | | || |||| || | ||| ||||||              |
                    ||||
Db     966 ------CTTCATGACC-TGGA--TGAAATAGGGC-ATGGC-------------
AAAATCC 930

Qy    1732
CTACTCAAGTGCAGAGCCCCATGTGTCAGGTGTGAAACGGTCCCGCTCAGGTGAGGGCGA 1791
                    | | |  |||| | ||||| |||  |               ||    |||
                    |||
Db     929 ATGATATTGTGC----CTCCATG---CAGTT---------------TCT----
AGGACGA 896

Qy    1792
GGTGAGCGGCCTTATGCGCAAGGTGCCACGAGTGAGCCTTGAACGCCTGGACCTGGACCT 1851
                    | | | |                    |||||| | | |
                    |
Db     895 ----------CATCTG-------------------GCCTTAAAAG-------------
AT 878

Qy    1852
CACAGCTGACAGCCAGCCACCCGTCTTCAAGGTCTTCCCAGGCAGTACCACTGAGGACTA 1911
                    | | | | |  ||| ||  |            ||| |||| |   | ||
Db     877 CGTAACAGGTAAACAGACAAGC-------------TCCAAAGCA----
CTCT-------- 843

Qy    1912
CAACCTTATTGTTATTGAACGTGGCGCTGCCGCTGCAGCTACCGGCCAGCCAGGGACTGC 1971
                    | | ||| || || | |  |  | | |||| | |   || | | | |  |||    ||
Db     842 ---CTTTTTCTTCCTGCAAAAACCACTGCAGGAGTT-
CTTCAGCCAATTCAGTATCTTT 787

Qy    1972
GCCTGCAGGAACCCCTGGTGCCCCACCCCTGGCTGGCATGGCCATTGTCAAGGAGGAGGA 2031
                    | | ||| | |            ||| | |||| | |||| |
Db     786 AGATTCAGAAGC-------------ATACTGCATTGCAT---
CCTTGTAA---------- 753

Qy    2032 GACGGAGGCTGCCATTGGAGCCCCTC-
CTACTGCCACTGAGGGCCCTGAGACCAAACCTG 2090
                    |||||| | || | | | |||        | |||   |||
```

```
                |
Db        752 -----AGGCTGTCTTTCTTGCACAGCTCTAC-----------
ACTCTGTTTCCA-----G 714

Qy       2091
TGCTTATGGCTCTTGCGGAGGGTCCTGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAG-- 2148
               | || | || |||  |||         || |    ||    |||| ||||   ||
Db        713 CGATTGTTGCCTTTGAAGAG-----ATAAGCAGCAATTCT---
CCTGAACTCAATGAGTT 662

Qy       2149 --
TGGCAGCACCAGCTCAGGGCTGGAGGTGGTGGCTCCTGAGGGTACCTCAGCCCCAGGT 2206
                   ||      | | | | | | | | |     | ||   | | ||| |
                |
Db        661 CATGTTTTTCCAAACGCTGAGCAAGC-
GAGATATTGTCAAAGTTGTCATAAGCATCTATT 603

Qy       2207
GGTGGCCCGGGAACCCTGGATGACAGTGCCACCATTTGCCGTGTCTGCCAGAAGCCAGGC 2266
               | || |    || | | |   || |  | | | | ||        |||
Db        602 GATGTTCGCAGAGCC-----TGATAAT-----
CTTCTTCTGTAATAAAAAGA-------- 561

Qy       2267 GATCTGGTTATGTGCAACCAGTGTGAGTTTTGTTTCCACCTGG-
ACTGTCACCTGCCGGC 2325
                   | |||    || | || |   || |||||    |  ||| |||   | |||
             ||
Db        560 ----TTGTTCAATG-ATTCATTCACAGATTTGTTGTTA--TGGTTCTG--
AACTGAACGC 510

Qy       2326
CCTGCAGGATGTACCAGGGGAGGAGTGGAGCTGCTCACTCTGCCATGTGCTCCCTGACCT 2385
                   || | |||| ||       ||||| |  | || | |   |  ||       |||
             ||
Db        509 AAATACGGTTTCACCAGTGGT-------AGCTGTTTAACCTTGC-TGAAATAATTGA-
CT 459

Qy       2386
GAAGGAGGAGGGATGGCAGCCTCAGCCTGGATGGTGCAGACAGCACTGGCGTGGTGGCCAA 2445
               | | |||  |||       || ||    ||| |||||||||||
Db        458 GCACGAGTGTGAT-------CCAACC------
GTGGAGACAGCAC-------------- 427

Qy       2446
GCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTCACGA 2505
                   || |||| || ||    | |   |||       ||| |    |||||
             ||
Db        426 -----CATCAGCAAATCATTTAACAACAGAG--------GCTTG---
AATTCTAAGTAGA 383

Qy       2506
ACCCTGCCGCCCCCTGCATCAGCTGGCTACCGACTCCACCTTCTCCCTGGACCAGCCCGG 2565
               || |  ||||      || |  |  ||  ||     ||||| |
Db        382 ACTGTATTGC--------TCTGTAGTATA---
GTTCCACAT------------------ 353

Qy       2566 TGGCACCC-
TGGATCTGACCCTGATCCGTGCCCGCCTCCAGGAGAAGTTGTCACCTCCCT 2624
               ||||| || |||   |||       ||| ||                   | |||
             ||||
```

```
Db        352 TGGCAACCTTGGTAATGAT----ATCTTTG--------------AATTG------
CCCT 318

Qy       2625
ACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCCGCATGTTCAAGCAATTCAACAAGT 2684
              |   |||  ||  ||||    |||||               |||||  ||
|
Db        317 TCT--TTCCAGGCATCAGTT------GGATG--------------------
ATTCATCATGG 284

Qy       2685
TAACTGAGGACAAGGCAGACGTGCAGTCCATCATCGGCCTGCAGCGCTTCTTCGAGACGC 2744
              ||| || | ||                  ||| |||            ||||||
Db        283 TAATTATGG------------------CATTATC---------
ATATTCTTC------- 259

Qy       2745
GCATGAACGAGGCCTTCGGTGACACCAAGTTCTCTGCTGTGCTGGTGGAGCCCCCGCCGA 2804
                      ||  |  |  |   ||||||        ||  |||        |||
||
Db        258 ----ATACTTGTCATACAAAAACACCA-----------GTTCTG--------
CCCAAAGA 222

Qy       2805 TGAGCCTG-CCTGGTGCTGGCCTGAGTTCCCAGGAGCTGT---
CTGGTGGCCCTGGTGAT 2860
                    ||||| ||  |||  |||  || ||  || ||   | |   ||  | ||| |
|
Db        221 TGAGCTTGTTCTGCAGCT---CTTAGCACCTTGGGAATATTCACT-CTAGACCAG--
AAC 168

Qy       2861 GGCCCCTGAGGCTGGAGCCCCCAT-------GGCC---------
AGCCCAGCCTGGC--- 2901
                    || || | |||   ||| |||        |||          ||   ||  | ||
Db        167 AGCTCCAGGTGCT----
CCCTCATTTTCTGAGGCTTAAATTTAGAGTATAGAATAGCTAA 112

Qy       2902 -TCTGTTCTCTGTCC--
TGTCACCCCATCCCCACTCCCCTGGTGGCCTGACTCCCACTCC 2958
                    || ||   |  ||| ||| | | | |||   ||| ||| ||| |
|
Db        111 TTCAGTAAACATTCCCATGTGAGCTCG-CTCAAGTCCC--AGTG--
CTGCTTCCAA---C 60

Qy       2959 CTGGTGGCCCCATCCCCCAGTTCCTCACGAT-
ATGGTTTTTACTTCTGTGGATTTAATAA 3017
                    |||||  |  || ||  | ||||||| || | |  | | | ||
Db         59 ATGGTGATCAGCTCTTCAAAATAGCCACGATCCTGATAGTAGC--
CAGTAGG-------- 10

Qy       3018 AAAAAACTTCACCAGT 3033
                          || ||||
Db          9 --------CCAACAGT 2


RESULT 10
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
```

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  Query Match              27.3%;  Score 5339;  DB 1;  Length 2198;
  Best Local Similarity    41.5%;  Pred. No. 5.6e-298;
  Matches 1274;  Conservative    0;  Mismatches  814;  Indels  982;
Gaps  180;


Qy        6 GCGGGCCGGCGGCG-GAGGCCG---GGCC-------------------------
GCGGAG 36
             || | || || ||  ||| |    ||||                          ||
|
Db     2198 GC-
GACCTGCAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTATGGTG 2140


Qy       37 CCAGGAGTGACTAGCAGCAGTTGGCCGTGCCGTAGCAGCGTCC-
CGCGCGCGGCGGGCAG 95
             |||      | | |||    | ||       | | ||  ||| |   |    | |
Db     2139 CCAATTTTAAATAGTTTTATTT----
AAGACATTGCATTTTCCACTTACAATACAG---- 2088


Qy       96
CGGCCCAGGAGGCGCGTGGTGCGGGTTTCGGCGGCGGCTGAGGAAGAAGCGCGGGCGGCG 155
             |  | | | || | | ||  ||    |||| |  |  ||| | | |  |
|
Db     2087 -TGTTTATAAAGTGCAATGT---TATTTC--CTTCCCCTGT-GCATATGTTC------
CA 2041


Qy      156
CCTTCGGGAGGCGAGCAGGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGG 215
              ||| |    ||| | ||  |||| |    | | ||||||| | |
Db     2040 TATTCAAGTATTGAGAATGCC-CAGT--AACTTACTATAGCAGCTTAACTT------
TTT 1990


Qy      216 GCAGCGGCC-
CAGGAGGCGCGTGGCGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCAGCGG 274
              | | ||| ||| |             | || ||
||
Db     1989 AAAACTGCCACAGAA--------------------TTTGCTACG--------
AATTTAGG 1958


Qy      275 CCCAGCAGTTG--------GCGGCGAGCGCGTCTGCGCCTGCGC--
GGCGGGCCCCGCGC 324
             || || ||        | | || |   || | || | | | ||  ||| |||
Db     1957
```

```
TCCTTCAAATGTTTTAAATGTGTGGAACAATGCTACATCTACACTTGGTTGGCTTAATCA 1898


Qy         325 CCCTCCTCCCC------CCCTG----
GGCGCCCCCGGCGGCGTGTGAATGGCGGCCTCCG 374
                   |||| ||      |||||     || || || | ||     ||    || ||
                                                                            ||
Db        1897 ACCTCTTCAATGGTGGGCCCTGAGGAAGCACCACCAGAGG-----GAGGAGC-
TCCACCA 1844


Qy         375 CGGCGGCAGCCTCGGCAGCAGCG-GCCTC--GGCC-
GCCTCTGGCAGCCCGGGCCCGGGC 430
                 |   | | ||| |  ||| || |||| ||| ||| ||||| ||| | ||  | |
Db        1843 CCAGGAAATCCCC--CAG--GCATTCCTCCTGGCATGCCTCCTGCA-
CTCTGGTACAGCT 1789


Qy         431 
GAGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCCTTCGGCCGCAGCCTCGGCCTCT 490
                   | |  ||| | | |||| |  ||  | | || ||| |  |  ||
                                                                            |||
Db        1788 TGGTGAT--GATGGGGTTGCAAA-CTTTCTCCAGCTCTTTCTGTTGATG-
TTCAAATTCT 1733


Qy         491 GC---CTCAGCCG-
CGGCGTCGTCGCCCGCGGGGGCGGCGCCGAGGCGCTGGAGCTGCT 546
                 |   |||||| |   || |  || |  ||                  | |   | |
                                                                              |
Db        1732 TCCTTCTCAGCAGTCTGATTCTTATCAAGC-------------------
CAGTTGATAAT 1692


Qy         547 GGAGCACTGCGGCGTGTGCAGAGAGCGCCTG--
CGACCCGAGAGGGAGCCCCGCCTGCTG 604
                   || | |  | | ||| |  | | |||     || | |  | |  |  |  ||||
Db        1691 --TTCATTAC-ACTTGTCCAGA-ATCTTCTGTTTGTCCTCATCGTTAATCTTGCCT--
TG 1638


Qy         605 CCCTGTTTGCACTCGGC--
CTGTAGTGCCTGCTTAGGGCCCGCGGCCCCCGCCGCCGCCA 662
                   |||| ||| || | |              | |   | |
                                                                            ||
Db        1637 --AAGTTT---CTCATCTTCAACAGT---TGCTTT-----------
CATGTTGAAGGCA 1598


Qy         663 ACAG-CTCGGGGGACGGCGGGGCGGCGGGCGACGGCACCGTGGTGGACTG--
TCCCGTGT 719
                   | ||| | ||  | |        || | ||||| ||     ||| || | |
                                                                              |
Db        1597 TAGGACTCAAGTGAATTCTTG---------
GATGACACCTTGTCCCTCTGCTTCTCATCT 1547


Qy         720 
GCAAGCAACAGTGCTTCTCCAAAGACATCGTGGAGAATTATTTCATGCGTGATAGTGGCA 779
                   | |||   || | |||||   | || ||||     ||| ||| |||
                                                                             ||
Db        1546 TC-AGCTT-TGTACTTCTC----AGCTTCCTGGA--------CCATACGT-
TCAATGTCT 1502


Qy         780 
GCAAGGCTGCCACCGACGCCCAGGATGCGAACCAGTGCTGCACTAGCTGTGAGGATAATG 839
                   |  ||| | || |||| | |    | || |||      | ||||
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|
Db      1501  TCCTTGCT-CAAACG--GCCCTTGT---------------CATTAGT------
GATAGTA 1466

Qy       840  CCCCAGCCACCAGCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACC-
TGTGTAGAG 898
                |  |    |   | |         || |||   || | |   ||||| || |||
Db      1465  ATCTTGTTCTCTTTTCC-------CGTACTCTTGTCCACAGC-
AGAGACATTGAGTA--- 1417

Qy       899  GCGCACCAGCGGGTGAAGTACACCAAGGACCATACTGTGCGCTCTA-
CTGGGCCAGCCAA 957
                ||||  ||         || ||| | | |  |||   || | ||| |    |  |
Db      1416  ---TACCATTGG--------CATCAATGTCAAAA--
GTGACTTCAATCTGAGGAACAC-- 1372

Qy       958  GTCTCGGGATGGTGAACGTA---
CTGTCTATTGCAACGTACACAAGCATGAACCCCTTGT 1014
                ||||||| | | |||   |||    ||  ||| | | |||||| |
||||
Db      1371  --CTCGGGGTGCAGGAGGTATGCCTGTGAGTTCAAACTTGC-CAAGCAGG------
TTGT 1321

Qy      1015
GCTGTTTTGTGAGAGCTGTGATACTCTCACCTGCCGAGACTGCCAGCTCAATGCCCACAA 1074
                |  ||||| |  ||       || || ||| |  | ||       || |||
|
Db      1320  TATCCTTTGTCATGGC------ACGCTCGCCTTCATAAAC------
CTGAAT-------A 1280

Qy      1075
GGACCACCAGTACCAGTTCTTAGAGGATGCAGTGAGGAACCAGCGCAAGCTCCTGGCCTC 1134
                |  ||||||| |  ||   |||   | | |||    | | |   || |||
Db      1279  AGCACCACAG-GCTGGTTGTCAGAATAGGTAGTGAAGGT-CTGTGTCTGCT--
TGGTAGG 1224

Qy      1135  ACTGGTG---AAGCGCCT--
TGGGGACAAACATGCAACATTGCAGAAGAGCACCAAGGAG 1189
                | |||||   ||| | |||| |||| |           |||||
Db      1223  AATGGTGGTATTACGCTTGATGAGGACAGTCATGACTC------------
CACCA----- 1181

Qy      1190  GTTCGCAG-CTCAATCCGCCAGGTGTCTGACGTACAGAAGCGTG---
TGCAAGTGGATGT 1245
                ||||  |||||   ||| |     | | ||| | |||   | |||| |
Db      1180  ----GCAGTTTCAAT--ACCAAG--------
GGAAAGAGGAGTGACATCCAAGAG----- 1140

Qy      1246
CAAGATGGCCATCCTGCAGATCATGAAGGAGCTGAATAAGCGGGGCCGTGTGCTGGTCAA 1305
                | ||| ||| |||| ||   ||            | |    || |||
Db      1139  -------------CAGCAAATCTTGAACATTCT------------CAG---
ACTTGTCT- 1109

Qy      1306  TGATGCCCAG--
AAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGCGGCAGCACTGGACC 1363
                ||||  ||| || ||               ||||||| | || ||
                ||||
Db      1108  ------CCAGACAAGATGGCT----------------GCCTGGA-CAGCTGC-----
ACC 1077
```

```
Qy        1364
ATGACCAAGATCCAGAAGCACCAGGAGCACATTCTGCGCTTTGCCTCTTGGGCTCTGGAG 1423
          || | |||    ||| || |||      |  ||| |||
Db        1076 ATAAGCAA----CAGCTTCATCAGGG----
TTGATGCTCTT------------------- 1044

Qy        1424
AGTGACAACAACACAGCCCTTTTGCTTTCTAAGAAGTTGATCTACTTCCAGCTGCACCGG 1483
                        |  |||  ||||| ||||  ||||        ||| || || |
                                                                    |
Db        1043 ----------ATTCAGTTCTTTTCCATT-GAAGAAGT-------
CTTGGAGAAGCTTCTG 1002

Qy        1484 GCCCTCAAGATGATTGTGGATCC-
CGTGGAGCCACATGGCGAGATGAAGTTTCAGTGGGA 1542
                          |        ||| |||| |  || || ||||
Db        1001 AATC---------
TTGGGGATACGAGTAGAACCAC------------------------ 976

Qy        1543
CCTCAATGCCTGGACCAAGAGTGCCGAGGCCTTTGGCAAGATTGTGGCAGAGCGTCCTGG 1602
                 | | || |   | || ||| | | |  ||| | ||| ||        || |
Db        975 CAACCAGGACAATATCATGAAT-CTGTGAC--TTGTCTAGTTTG-------
GCAT----- 931

Qy        1603
CACTAACTCAACAGGCCCTGCACCCATGGCCCCTCCAAGAGCCCCAGGGCCCCTGAGCAA 1662
              ||| ||| |                |  || |  ||   | ||| | ||
              ||
Db        930 ------CTCGAAGGGCTTT-----------
CTCTACTGGGTCCAGGGTGCCACGGAACAG 888

Qy        1663 GCAGGGCTCTGGCAGCAGCCAGCCCATGGAG--
GTGCAGGAAGGCTATGGCTTTGGGTCA 1720
                 |        ||||| ||| | | |  | ||| | || |||| ||
                |
Db        887 GT----------CAGCATTCAGTTCTTCAAATCGGGCACG--GGTAATGG---
AGGTATA 843

Qy        1721
GGAGATGATCCCTACTCAAGTGCAGAGCCCCATGTGTCAGGTGTGAAACGGTCCCGCTCA 1780
              | || ||| ||| |                    | | ||| || | |  |
Db        842 GAAGTCGATTCCTTCATA-----------------------
GAGAGAATCGATCTCAAT-- 807

Qy        1781
GGTGAGGGCGAGGTGAGCGGCCTTATGCGCAAGGTGCCACGAGTGAGCCTTGAACGCCTG 1840
              |        ||||| ||| |    ||||||     |   | ||  | |||| |
              |
Db        806 ---------------ACTGGCCT--------GGGTGCTGGAAGAGAG---
GGTACGCTTA 773

Qy        1841
GACCTGGACCTCACAGCTGACAGCCAGCCACCCGTCTTCAAGGTCTTCCCAGGCAGTACC 1900
              |                                | ||            ||| ||
              |||||||
Db        772 G----------------------------CACG-----------
TTCACAAGCAGTACG 753
```

```
Qy        1901
ACTGAGGACTACAACCTTATTGTTATTGAACGTGGCGCTGCCGCTGCAGCTACCGGCCAG 1960
               | |    |||| |  |  | |||||  |            |   | ||| |          ||
Db       752 GAGGCGTCTTACAGCTCTCTTGTTCT--------------CACTGATGT------
CCTT 714


Qy        1961
CCAGGGACTGCGCCTGCAGGAACCCCTGGTGCCCCACCCCTGGCTGGCATGGCCATTGTC 2020
                |   |  | |||| |  |||   || ||  |       | |       ||| || |    |
|||||
Db       713 CTTATGCTTGCGCTT-----AAACTCAG----
CAATAAAATGGTTGACCATTCGGTTGTC 663


Qy        2021
AAGGAGGAGGAGACGGAGGCTGCCATTGGAGCCCCTCCTACTGCCACTGAGGGCCCTGAG 2080
                   ||                     | |  |||| || | ||||  ||
Db       662 AA-------------------------AATCTTCTCC----ACCCAAGTGGG---
TGTC 636


Qy        2081
ACCAAACCTGTGCTTATGGCTCTTGCGGAGGGTCCTGGTGCTGAGGGTCCCCGCCTGGCC 2140
                 |||       ||| | ||            | |||     | ||  |||
Db       635 TCCA-------GCTGTAGACTT---------GACCT----CAAAGATTCCAT------
CC 602


Qy        2141
TCACCTAGTGGCAGCACCAGCTCAGGGCTGGAGGTGGTGGCTCCT-
GAGGGTACCTCAGC 2199
                 |||  |||||            ||  |        || | | |  |  || || |
Db       601 TCA-ATAGTG--------------AGGAT--------
TGACACATCAAAAGTGCCACC-T 566


Qy        2200
CCCAGGTGGTGGCCCGGGAACCCTGGATGACAGTGCCACCATTTGCCGTGTCTGCCAGAA 2259
                |||||||               |  |||   |  |||| ||   |  | |  |||||
Db       565 CCCAGGT--------------CAAAGATGA----GC--ACGTTT--C-
TTTCTGC----- 534


Qy        2260
GCCAGGCGATCTGGTTATGTGCAACCAGTGTGAGTTTTGTTTCCACCTGGACTGTCACCT 2319
                         ||          |||||      ||||||      || |  || |
|
Db       533 ---------TC----------CAACCT-------TTTTGT------
CTAAGCCGTAAGCA 506


Qy        2320 GCCGGCCCTGCAGGATGTACCAGGGGAGGAGTGGAGCTGCTCACT----
CTGCCATGTGC 2375
                 |  | ||||        ||| |            ||||| |    |  | | ||
|
Db       505 ATAG---CAGCAG-------CAGTTG------------
GCTCATTAATAATTCTAAGTAC 468


Qy        2376 TCCCTGACCTGAAGGAGGAGGATGGCAGCCTCAGCCTGGATGGTGCAGACAGCA-
CTGGC 2434
                 |||| |             |                    ||||   |  ||||| ||
Db       467 ATTGAGACCAGCA--------------------------ATAGTTC---
CAGCATCT--- 440


Qy        2435
GTGGTGGCCAAGCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCCCTA 2494
```

```
                   ||||  |||   |  || |   ||  ||           ||  ||  |||   |  ||||  || ||
Db       439 TTGGTAGCCTGACGCTGA-GAGTCAT-------TAAAGTAAGCTGGCACTG-
TGACC--- 392

Qy      2495
TTCTGTCACGAACCCTGCCGCCCCCTGCATCAGCTGGCTACCGACTCCACCTTCTCCCTG 2554
                  | |    |   | | |  ||| |   | | |||| | |    |||||  |
|
Db       391 -ACAGCATTGGTAACAGTCTTCCCAAG-----
GTAGGCTTCTGCAATTTCCTTCATCTTT 338

Qy      2555 GACCAGCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCTCCAGG-
AGAAGTT 2613
                  | |          |  ||| | ||   |||          ||  ||||  |  |||||
|
Db       337 GTC---------AGAACCATAGA--AGAC-----------
ACCTCCTCTGGATAGAAGCT 300

Qy      2614 ----
GTCACCTCCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCCGCATGTTCA 2669
                   |||  ||||||    || |      || ||    ||||||    |
Db       299 TTTGGTCT-CTCCCTTGTATTCTAC-------TTGGACCT-----TGGGCC-----
TGCC 258

Qy      2670 AGCA--
ATTCAACAAGTTAACTGAGGACAAGGCAGACGTGCAGTCCATCATCGGCCTG-- 2725
                   ||||  |||||  |  |||      |  ||| | ||    | ||| ||| | |||
Db       257 AGCATCATTCACCACCATAA--------AGGGCCAATGT----TTCAT-
ATCAGACTGGA 211

Qy      2726 CAGC-GCTTCTTCGAGAC-
GCGCATGAACGAGGCCTTCGGTGACACCAAGTTCTCTGCTG 2783
                   || | || || | |   ||    |  |  || |  ||   || ||
|||
Db       210 CAACAGCATCATCAAATCTGCGTCCAATC-AGACGTTTGGCATCAAAAA--------
CTG 160

Qy      2784 TGCTGGTGGAGCCCCCGCCGATGAGCCTGCCTGGTGCT----
GGCCTGAGTTCCCAGGAG 2839
                   || |||||| |     | || |    ||| ||   ||| | ||   || |
|
Db       159 TGTTGGTGGGGT-----TCATTG---CAACTTGATTCTTTGCGGCATCA---
CCGATCAA 111

Qy      2840
CTGTCTGGTGGCCCTGGTGATGGCCCCTGAGGCTGGAGCCCCCATGGCCAGCCCAGCCTG 2899
                   | ||   ||| || |  || | |||  | || |||||        ||  |  |  |
|
Db       110 CCGTTCAGTGTCC---GTAAAGGCGACATAGCTTGGAG------TG----
GTTCGGTTT- 65

Qy      2900
GCTCTGTTCTCTGTCCTGTCACCCCATCCCCACTCCCCTGGTGGCCTGACTCCCACTC-- 2957
                   | ||| ||  || |   |  |    | | | | || |||    || ||||| |
Db        64 -CCCTGATCATTGGCAATTATC----TCGACTTTTCCGTGCTGG-
AAAACACCCACACAA 11

Qy      2958 --CCTGGTGG 2965
                   || |  ||
```

RESULT 11
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match   27.0%; Score 5283.5; DB 1; Length 2495;
  Best Local Similarity   42.1%; Pred. No. 1.5e-294;
  Matches 1324; Conservative   0; Mismatches 1002; Indels 817;
Gaps 189;

Qy   51
CAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGGAGGCGC 110
             || | ||||||| || | ||| | | |||
 |
Db   1 CA-CTGTTGGCC------TA-------------------CTGGCTACTATC----
AGGATC 31

Qy   111
GTGGTGCGGGTTTCGGCGGCGGCTGAGGAAGAAGCGCGGGCGGCGCCTTCGGGAGGCGAG 170
             ||| || ||| |||| || | | || | ||
Db   32 GTG--GCTATTTT-----------------GAAGAGCTGAT--CACCAT--
GTTGG---- 64

Qy   171
CAGGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGGAG 230
             | |||||| | || || | || |||| || | ||| | | |
 |
Db   65 -AAGCAGCACTGGGACTTG-------AGCG---AGCTCAC-
ATGGGAATGTTTACTGAAT 112

Qy   231
GCGCGTGGCGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCGCAGCGGCCCAGCAGTTGGCGGC 290
                || | ||| | | || | ||| | ||
 |
Db   113 TAGCTATTCTATACTCTAAATTTAAGC-----------------CTCAGAAAATG--
AGG 153

Qy   291 GAGCGCGTCTGCGCCTGCGCGG--

```
       CGGGCCCCGCGCCCCTCCTCCCCCCCTGGGCGCCCC 348
          | | | |  | | |      | | |  | | | |  | |     |  |     ||| ||  ||
Db        154 GAGCAC--CTG-----GAGCTGTTCTGGTCTAGAGTGAATATT----
       CCCAAGGTGCTAA 202

Qy        349
       CGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCAGCCTCGGCAGCAGCGGCCTCGGCCGC 408
                  | | ||    ||| |   ||| |      |       ||||| |       | |
       |
Db        203 GAGCTGC---AGAA---CAAGCTCATCTTTG--------GGCAGAA-------
       CTGGTGT 241

Qy        409
       CTCTGGCAGCCCGGGCCCGGGCGAGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCC 468
                  | ||        | |   || | |  | |    | |     | |    |    |
       |
Db        242 TTTTGTAT-----
       GACAAGTATGAAGAATATGATAATGCCATAATTACCATGATGAATCA 296

Qy        469 TTCGGCCGCAGCCTCGGCC-
       TCTGCCTCAGCCGCGGCGTCGTCGCCCGCGGGGGGCGGCG 527
                  | | | | |||| |      | |    |   | || |  ||    || ||
       |
Db        297 TCCAACTGATGCCTGGAAAGAAGGGCAATTCAAAGATATCATTACC--AAGGTTGC--
       CA 352

Qy        528
       CCGAGGCGCTGGAGCTGCTGGAGCACTGCGGCGTGTGCAGAGAGCGCCTGCGACCCGAGA 587
                  | || || | |||  | ||||| | |  ||      |||   |
       Db        353 ATGTGGAACTATA-CTAC-AGAGCAATACAGT-
       TCTACTTAGAATTC------------ 396

Qy        588 GGGGAGCCCCGCCTGCTGCCCTGTTTGCACTCGGCCTG-
       TAGTGCCTGCTTAGGGCCCGCG 646
                  |||| |   ||||      ||||    ||| | |||| ||         ||
       ||
Db        397 --AAGCCTCTGTTGTTAAATGATTTG--------CTGATGGTGCTGTCT------
       CCACG 440

Qy        647 G------CCCCCGC-CGCCGCCAA------CAGCTCGG-
       GGGACGGCGGGGCGGCGGGCG 692
                  |        | | | |  || |||         |||| ||    || ||    |  | ||
       |
Db        441 GTTGGATCACACTCGTGCAGTCAATTATTTCAGCAAGGTTAAACAGC--
       TACCACTGGTG 498

Qy        693 ACGGCACCGTG---
       GTGGACTGTCCCGTGTGCAAGCAACAGTGCTTCTCCAAAGACATCG 749
                  |   ||||| | | | | |      | |||||       ||| ||
       |||
Db        499 A---AACCGTATTTGCGTTCAGTTCAGAACCATAACAACA---
       AATCTGTGAATGAATCA 552

Qy        750
       TGGAGAATTATTTCATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGCCCAGGATGCGA 809
                  | || | | |||      | ||   | ||||  | || ||  | | ||
       |||||
Db        553 TTGAACAATCTTT------TTATTACAGAAG-AAGATTATCA--GGCTC------
       TGCGA 597
```

```
Qy         810 ACCAGTGCTGCACTAGCTGTGAGGATAATGCCCCAGCCACC--
AGCTACTGTGTGGAGTG 867
               ||        ||  |||         ||||    |  | |  |  |  |  | | | |
||
Db         598 ACAT------CAATAG-----------
ATGCTTATGACAACTTTGACAATATCTCGCTTG 640


Qy         868 CTCGGAGCCTCTGTGTGAGACCTGTGTAGAGGCGCAC-
CAGCGGGTGAAGTACACCAAGG 926
               |||  ||| ||| | |  |||             |  || |  | ||          ||
|
Db         641 CTC--AGCGTTTG-GAAAAACAT----------GAACTCATTGAGT--------
TCAGGA 679


Qy         927 ACCATACTG-
TGCGCTCTACTGGGCCAGCCAAGTCTCGGGATGGTGAACGTACTGTCTAT 985
                   |  |||| |   ||||| |  | || |  || |   ||   ||  |  ||
||
Db         680 GAATTGCTGCTTATCTCTTCAAAGGCAAC--AATCGCTGGA-----AACAGA--
GTGTAG 730


Qy         986 TGCAACGTACACAAGCATGAACCCCTTGTGCTGTTTTGTGAGAGCTGTGATACTCT-
CAC 1044
                   ||   |    |||| || ||  |||| | |      || |  || ||     |||
|
Db         731 AGCTGTG----CAAGAAAGACAGCCTT-TACAAGGATGC-
AATGCAGTATGCTTCTGAAT 784


Qy         1045 
CTGCCGAGACTGCCAGCTCAATGCCCACAAGGACCACCAGTACCAGTTCTTAGAGGATGC 1104
                    ||   ||  |||||     | | |   ||| | |      ||||  |   ||||  |
|||
Db         785 CTAAAGATACTG------AATTGGC--TGAAGAACTCCTG---CAGTGGTTT----
TTGC 829


Qy         1105 AGTGAGGAACCAGCGCAAGCTCCTG-
GCCTCACTGGTGAAGCGCCTTGGGGACAAACATG 1163
                   ||  || || ||    |   |     |  | ||  |  |||  |    |||  |  || |
|
Db         830 AGGAAGAAAAAAGAGAGTGCTTTGGAGCTTGTCTGTTTA----CCT--
GTTACGATCTTT 883


Qy         1164 CAA--
CATTGCAGAAGAGCACCAAGGAGGTTCGCAGCTCAATCCGCCAGGTGTCTGACGT 1221
                   || |    |||| |   || |      || | ||  || |
Db         884 TAAGGC----CAGATGTCGTCCTAG--------------
AAACTGCATGGAGGC------ 919


Qy         1222 ACAGAAGCGTGTGCAAGTGGATGTCAAGATGGCC---
ATCCTGCAGATCATGAAGGAGCT 1278
                   |||   | |      |||| |   ||| ||   || | ||| | ||||||||||
Db         920 ACAATATC--------
ATGGATTTTGCCATGCCCTATTTCATCCAGGTCATGAAGGA--- 968


Qy         1279 
GAATAAGCGGGGCCGTGTGCTGGTCAATGATGCCCAGAAGGTGACTGAGGGGCAGCAGGA 1338
                    || ||  |||  | ||        | | |  ||  || |  ||  ||  |||
|
Db         969 ----------------GTACTTGACAAAGGTG-------
GATAAATTAGATGCTTCAGAA 1005
```

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Qy        1339
GCGCCTGGAGCGGCAGCACTGGACCATGACCAAGATCCAGAAGCACCAGGAGCACATTCT 1398
          |  |    ||  |  ||          |  | || |||| | ||| |||    |  | ||||
Db        1006 TCACTGAGAAAAGAAG---------AAGAACAAGCTACAGAGACAC----
AACCCATT-- 1050


Qy        1399 GCGCTTTGCCTCTTGGGCTCTGGAGAGTGACAACAACACAGCCC--
TTTTGCTTTCTAAG 1456
          | ||   |||    ||     || |  |      ||    ||| |  ||| |  | ||||
Db        1051 --GTTTATGGTC---
AGCCCCAGTTGATGCTGACAGCAGGACCCAGTGTTGC-------- 1097


Qy        1457 AAGTTGATCTACTTCCAGCTGCACCGGGC-CCTCAAGATGATTGTGG--
ATCCCGTGGAG 1513
                           |  |||  || || |||| ||||  ||  ||    || ||  ||  || ||
Db        1098 -----------CGTCC--CT-CCCCAGGCACCTT---TTGGTTATGGTTATACC---
GCA 1137


Qy        1514
CCACATGGCGAGATGAAGTTTCAGTGGGACCTCAATGCCTGGACCAAGAGTGCCGAGGCC 1573
                  ||||    ||  || |||  |   |||     || ||  ||||||  |    | ||| |
          ||
Db        1138 CCAC----CGT-ATGGA----CAG-----CCACA--GCCTGG-CTTTGGGTAC---
AGCA 1177


Qy        1574 TTTGGCAAGATTGTGGCAGAGC--GTCCT---GGCACTAA--CTC-
AACAGGCCCTGCAC 1625
                   |  ||   ||||    | || ||   |||| |  ||  || | ||   |   |
Db        1178 TGTG---AGAT----
GAAGCGCTGATCCTGTAGTCACCTATTTTCGTACTGAAACATCGT 1230


Qy        1626 CCATGGCCCC-TCCAAGAGCCCCAGGGCCCCTGAGCAAGCAGG------
GCTCTGGCAGC 1678
                  |  |  ||||   |  |   ||       | || |  | | |||| |    | ||| | |
          |
Db        1231 CTTTACCCACTTCTCAGTTTATAATGG-----
GGGAAAACAGGCAACGTGTTCTTGTAAC 1285


Qy        1679 AGCCAGCCCATGGAGG--TGCAGGAAG------
GCTATGGCTTTGGGTCAGGAGATGATC 1730
                            | | |||| ||| | | |     | |        |||| |||| |||
Db        1286 CTTTATTTCATGAAGGACTTCTTTTTGTTTCTAACTATAAACTTGGATCA---------- 1335


Qy        1731 CCTACTCAAGTGCAGAGCCCCATGTGTCAGGTGTGAAACGGTCCCGCTCAGGTGAGGGCG 1790
                            |||    | | |  ||||  | | |     ||   |||      ||  ||  | |
          |
Db        1336 CCT----ATGTTAAAA---CCTTATTTC----------
ACATTCCACATCATTTTA----G 1375


Qy        1791 AGGTGAGCGGCCTTATGCGCAAGGTGCCACGAGTGA--
GCCTTGAACGCCTGGACCTGGA 1848
                   | | |         | || ||| ||||||    |   |  |     | ||| | |
Db        1376 AATTTA------TTTTCG-
AAGGGGAATAGTTTCAATGTTTTATTCACTTGGGCTT--- 1424


Qy        1849 CCTCACAGCTGACAGCCAGCCACCCGTC-TTCAAGGTCTTCCCAGGCAGTACCA-
CTGAG 1906
```

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                          |   |   ||   ||   |  || || |||  || | ||       |  |  |||
Db      1425  -------TTTTTCTTCC--CCCTCTTTCTTTAAAGAACTGCTCA--
ATATTCAATCTGTT 1473

Qy      1907 GACTACAACCTTATTGTTATTGAACGTGGCGCTGCCGCTGCA--
GCTACCGGCCAGCCAG 1964
                          |   |  ||||| ||             |  || ||    ||| |  | |       |  |
||
Db      1474 GTGAAGAACCTGAT------------TTGCACT----
CTGTAGTGTTTAAAGAAACAAAG 1517

Qy      1965 GGACTGCGCCTGCAGGAACCC------CTGGTGCCCCACCCCTGGCTGGCATGGCC--
AT 2016
                          ||| |  | |    | | | |          | |||          |  ||| || |     |
||
Db      1518 AAACT-CTAATATTGAATCTCTTAAATTTAGTGTATGTAAAC-
AGCTTACAAATACGTAT 1575

Qy      2017
TGTCAAGGAGGAGGAGACGGAGGCTGCCATTGGAGCCCCTCCTACTGCCACTGAGGGCCC 2076
                          |||| |  |                  |||| |  | | | |        |  | || || ||
|
Db      1576 TGTCTAAATG-----------------CATTTAAATCTGTTTTATT--
CAAAGAAAAGCT 1616

Qy      2077 TGAGACCAAAC-
CTGTGCTTATGGCTCTTGCGGAGGGTCCTGGTGCTGAGGGTCCCCGCC 2135
                          ||   |||| ||| ||  |||| |  | ||   | |            |||    || ||
|
Db      1617 AAAGCAAAAACACTG-GCATATGAC-CATGC--AAG--------
ACTGTCAGTGCCAACA 1664

Qy      2136 TGGCCTCACCTAGTGGCAGCACC-
AGCTCAGGGCTGGAGGTGGTGGCTCCTGAGGGTACC 2194
                          |  |    ||| |  ||||| |  | ||   |||     | ||          ||
|
Db      1665 AAGACAACACTAAT--CAGCACATCGTACA---CTGGA-----TTGC-------
AGTGCT 1707

Qy      2195 TCAGCCCCAGGTGGTGGCCCGGGAACCCTGGATGACAGTGCCACCATTTGCC-
GTGTCTG 2253
                          |   ||||| |  |       ||| ||   |  | ||||    || | ||||| |  |
|
Db      1708 T----CCCAGATTAT------TGAAAAATG--TTACAG----
ACAACTTGCCTGATTTTT 1751

Qy      2254 CCAGAAGC----CAGGCGATCTGGTTATGTGCA------
ACCAGTGTGAGTTTTGTTTCC 2303
                          |  |||   |||| |||| |||       |       ||| | ||   | | |
Db      1752 AAATGAGCGTAAAAGGCCCTCT-
AACCTATGCAGGTTTCCCCATTATGCATATAGAAAAT 1810

Qy      2304 ACCTGGACTGTCACCTGCCGGCCCTGCAGGATGTACCAGGGG---
AGGAGTGGAGCTGCT 2360
                          || |  ||   |||    ||| |  | ||  | |||| |||| |        || | ||||
Db      1811 G-CTAGTATGTTT--TGCT--CACTTCA-
TATGTAACAGGTGCCCTTATGTTGTGCTG-- 1862

Qy      2361
CACTCTGCCATGTGCTCCCTGACCTGAAGGAGGAGGATGGCAGCCTCAGCCTGGATGGTG 2420
```

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                  |   |  ||||||   |    |||   |||                ||    ||      ||
                  |
Db      1863 -----TATCCTGTGCT---TTTTCTGTGGGA------------CCATT-
CCATTCAGGAG 1901

Qy      2421
CAGACAGCACTGGCGTGGTGGCCAAGCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTG 2480
               || | |||||  | || |  |||| ||                     |||| |
                ||
Db      1902 CAAAGAGCAC---CATGAT-TCCAATCT----------------------
TGTGTGTGTT 1935

Qy      2481
TACTGCTGGCCCTATTCTGTCACGAACCCTGCCGCCCCCTGCATCAGCTGGCTACCGACT 2540
               || || ||||              |||||  |     || |  | ||| ||
Db      1936 TA---CTAACCCT------------TCCCTGAGG---
TTTGTGTATGTTGGATA------ 1971

Qy      2541
CCACCTTCTCCCTGGACCAGCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCC 2600
                   ||                    ||||    | |||   | |||| ||||   |||
Db      1972 -----TT-----------------GTGGTGTTTTAGAT----CACTGA---
GTG------ 1996

Qy      2601 TCCAG----GAGAAGTT--
GTCACCTCCCTACAGCTCCCCACAGGAGTTTGCCCAGGATG 2654
               | |||    ||||| ||   |   | | || |     ||||| |
                ||
Db      1997 TACAGAAGAGAGAAATTCAAACAAAATATTGCTGTTCTTC-----AGTTT----
TGTTTG 2047

Qy      2655 TGGGC--
CGCATGTTCAAGCAATTCAACAAGTTAACTGAGGACAAGGCAGACGTGCAGTC 2712
               |||     | | | |  | |||| |  ||| |||| |   | || |
Db      2048 TGGAATTTGAAATTACTCAAATTTAAAATAAATTACT--GGACT--
GTGGAAAT------ 2097

Qy      2713
CATCATCGGCCTGCAGCGCTTCTTCGAGACGCGCATGAACGAGGCCTTCGGTGACACC-- 2770
               | |||  | | |   || |  || |  || |   ||  | |||||       | ||
Db      2098 -AACATAGAATTGAAGTTTTAATTAAATAC-
CACTCAAACGAAAAGAACAGTAGTTTTTG 2155

Qy      2771
AAGTTCTCTGCTGTGCTGGTGGAGCCCCCGCCGATGAGCCTGCCTGGTGCTGGCCTGAGT 2830
               |||| |  || |  || | || |       | || ||| |  ||     ||    ||
                ||||
Db      2156 TAGTTTTATATTG-GATACTGAGGCATTAG--GGAG-
GCATGAAAGGAAGAGGAATGAG- 2210

Qy      2831 TCCCAGGAGCTGTCTGGTG--GCCCTGGTGATGGCCCCTGAGGCTG-
GAGCCCCCATGGC 2887
               |         | | |||  | | | |||   |      |  | ||    | ||
Db      2211 -----GATTGAGACATGTGAAGACATTGTG-----
CATTATATCAATGTGCATTCCTGTA 2260

Qy      2888
CAGCCCAGCCTGGCTCTGTTCTCTGTCCTGTCACCCCATCCCCACTCCCCTGGTGGC--- 2944
               |       |  |  ||   |  | | ||     |||    |||| |  | |||||
Db      2261
```

```
GTTCATTAACAAGGTACATGCAATAGTCTAAAGAACCAGAGTCACTACTATAGTGGCTTA 2320

Qy      2945 ---------CTGACTCCCA-----CTCCCTGGTGGCCCC-------
ATCCCCCAGTTCCT 2983
                        ||| |||| |        || ||| | ||        |  |  ||
|
Db      2321
ACATTTAATCTGTCTCCAATATTTTAACCAAGTGACACCGGGGTTTTATCGAAGCATTT 2380

Qy      2984 CAC-GATATGGTTTTTACTT--CTGTGGATTT-------
AATAAAAAAAACTTCACCAGT 3033
                        ||| | |||        | | |||| || ||        ||||||| | | || | ||
Db      2381
CACTTAAATGAACAAATCATGGCTGTTATATTAACTTGAAATAAAATATATTTAAACATG 2440

Qy      3034 TCAAAAAAAAAAAAAAAAAAAAA 3056
                        | ||||||||||||||||    |
Db      2441 TAAAAAAAAAAAAAAAAAGGCCA 2463


RESULT 12
US-10-478-914-57/c
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match             27.0%;  Score 5269.5;  DB 1;  Length 2336;
  Best Local Similarity   42.6%;  Pred. No. 7.9e-294;
  Matches 1254;  Conservative    0;  Mismatches  897;  Indels  793;
Gaps  177;

Qy       277
CAGCAGTTGGCGGCGAGCGCGTCTGCGCCTGCGCGGCGGGCCCCGCGCCCCTCCTCCCCC 336
                ||||            ||||| | | || ||||                  |  |
Db      2336 CAGCT--------CGAGCACATGTG-GCCT--------------------
TTTTTTTTT 2307

Qy       337
CCTGGGCGCCCCCGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCAGCCTCGGCAGCAGC 396
                    |                     | |  | |    ||| |    || ||| |    |||
|
Db      2306 TTT-----------------TTTTTTTTGTATTCTCAG---- 
```

```
AGCTGCCAGGAGTGCATC 2268


Qy        397 GGCCTCGGCCGCCTCTGGCAGCCCGGGCCCGGGCGAGGGCTCCG-
CTGGCGGCGAAAAGC 455
              |          ||||  |    || |  | |    ||   | ||  || | ||
Db       2267 G--------AGCCTGTAATTTCCTGTTCTC---
TGAATCCCCCATCTTTCTGC------A 2225


Qy        456 GCTCCACCGCCCCTTCGGCCGCAGCCTCGGCCTCTGCCTCAGCCGCGGCGTCGTCGCCCG 515
              ||||||  ||     |    || |||||| | ||||| |   |     ||     | |
                                                                      | |
Db       2224 GCTCCA-AGCTTTGTGTCCCACAGCCTGTGACTCTG-
TGCTAACAAATCGCTATTGTCC- 2168


Qy        516 CGGGGGGCGGCGCCGAGGCGCTGGAGCTGCTGGAGCACTGCGGCGTGTGCAGAGAGCGCC 575
              | | ||||| | || |||| |  | |   ||  ||| | |||      ||| | |    |
Db       2167 ---AGTGGGGCGAATGGTGGCTGGA---ACTAAAGAATTGC----TGT-
CTGGTTTCTAT 2119


Qy        576 TGCGACCCGAGAGGGAGCCCCGCCT---GCTGCCCTGTTTGCACTCGGCCTG----
TAGT 628
              |    | ||   ||| |||  | | |         ||   ||| ||| | ||     ||
Db       2118 TCAAATCC---AGGTAGCGAGATATATGAATGGACTTTTCG-
AATCGTCATGTGAATAAC 2063


Qy        629 GCCTGCTTAGGGCCCGCGGCCCCCGCCGCCGCCGCCAACAGCTCGG--
GGGACGGCGGGGCGG 686
              |  ||||||  ||| |  | | | |      ||||   ||| ||  ||      | |
Db       2062 GTCTGCTC--GGCATGAAGGCTCAG----AGCCA--
TGCTAGGAAGGATTAACTCGTAGG 2011


Qy        687 CGGGCGAC-GGCA-
CCGTGGTGGACTGTCCCGTGTGCAAGCAACAGTGCTTCTCCAAAGA 744
              | | || | || |    || |   | |    || | |  || |||        |||
                                                                      |||
Db       2010 CTGACCACTAACATCCTTTGTGGT-----ACGAGGG--AGAAACA------
TTCCCAAGT 1964


Qy        745 CATCGTGGAGAATTATTTCATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGCCCAGGA 804
                     ||| |       || |||| | | ||  |         ||   |  || ||||
              |
Db       1963 -ATCAT------TTTATTCACACTTAATTTT----------
CTATCCCATACCCCCAAAA 1921


Qy        805 TGCGAACCAGTGCTGCACTAGCTGTGAGGATAATGCCCCAGCCAC----
CAGCTACTGTG 860
              | |       ||  |||||| |    |||   || |    |   | || |
              |
Db       1920 TAAG------------GCTAGCTAT----
TTAATTAGTTGGCCGCTTTTCTCTTAATTTT 1877


Qy        861 TGGAGTGCTCGGAGCCTCTGTGTGAGACCTGTGTAGAGGCGCACCAGCGGGTGAAGTACA 920
              | | ||    |       |   ||| |||||||| | | ||| |   | |   ||
                                                                      |
Db       1876 TAGTGTTTCTGTTGATAATGTGTGAGT-TTGGGAAAATGCTAAGTAGC------
```

```
TTTTCA 1824

Qy        921 CCAAGGACCATACTGTGCGCTCTACTGGG-------CCAGCCAAGTCT--
CGGGATGGTG 971
                  |  || ||   |   | |    ||||      |        ||   || ||    | ||
||
Db       1823
CTTAGAACACTGTTATTTTCTCTTTAAAGTTTTCTACCTTACATTTATTATAGCATAGTT 1764

Qy        972 AACGTACTGTCTATTGCAACG-TACA-CAAGCATGA-
ACCCCTTGTGCTGTTTTGTGAGA 1028
                  | |       |  | ||| ||| | |||  |  | |      |||| | |||    ||
|
Db       1763 ATC------TTTATAGCATAGATGCAGAAAGTAAGAGAGAGCTTGT--
TTTTTCAAGAAA 1712

Qy       1029 G-----CTGTGATACTCTCACCTGCC--------
GAGACTGCCAGCTCAATGCCCACAAG 1075
                  || || |     || ||  ||        || |    ||   ||     | |||
||||
Db       1711
ACAACCCTTTAAAATACTTTCCAACCCATGAAGGGAAAAATCCTCCTTTTTTCCCCCAAG 1652

Qy       1076 GACCACCAGTACCAGTT-CTTAGAGGATGCAGTGAGGAACCAGCGCAAGCTCC---
TGGC 1131
                  |    |   |||   || | |||     ||||  |                   ||||
|
Db       1651 TGCATTC--TACTTATTACTT------TGCATT-------------
TTTCTCCCAAAGTC 1613

Qy       1132 CTCACTGGTGAAGCG-CCTTGGGGACAA----
ACATGCAACATTGCAGAAGAGCACCAAG 1186
                  |  |  |  | |  |   | |||     | ||||||   |||| |
|||||
Db       1612 CAAATTTATGCAAAGAAAATAGAAACAAGTTCAAATGCAA---TGCATTA----
ACCAAA 1560

Qy       1187 GAGGTTCGCAGCTCAATCCGCCAGGTGTCTGACGTACAGAAGCGTGTG-
CAAGTGGATGT 1245
                  |        ||   ||   |||  || ||        ||   ||   ||||  |  || |||||| |
Db       1559 TA---AAACAAGTC--TCCTTCAAATTAGGAACCAACCTAAGCATTTGTAAAGTG--
TAG 1507

Qy       1246 CAAGATGGCCATCCTGCAGA--
TCATGAAGGAGCTGAATAAGCGGGGCCGTGTGC----T 1299
                  ||   ||   ||||   | |   |  |  ||      || || || ||   |
|
Db       1506 CAGAAT----------CAGAATTCTTTTAAAAATTAGATTT--GGAACC-
TGAACTATAT 1460

Qy       1300
GGTCAATGATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGCGGCAGCACTG 1359
                  |  || | ||   |  |  ||| ||   |  |    | |    || | |||
|||
Db       1459 AATTCATAATTCTCATT---
TTTCTGTGGAAAATTATTTTATCTTTCTCCTGTATACCTG 1403

Qy       1360 -GACCATGACCAAGATCCAGAAGCACCAGGAGC----ACATTCTGCGCTT---
TGCCTCT 1411
                  |  ||| |||    |  |||   ||   ||      ||||||   |||    |  |
```

```
|
Db      1402 AAAAAATGTCCATAGGCTTAAAGGGTCA--TGCTTTTACATTC----
CTTCCATATCACA 1349

Qy      1412
TGGGCTCTGGAGAGTGACAACAACACAGCCCTTTTGCTTTCTAAGAAGTTGATCTACTTC 1471
              |  || ||  ||    |        || | ||| | |||||     || ||||
|
Db      1348 GGTACTATGAAGTAAGG---------AGACTTTTAGGTTTCTT-----
TTTGTCTTAAAC 1303

Qy      1472 -CAG-CTGCACCGGGCCCTCAAGATGATTGTGGATCCCGTGG---AGCCACA---
TGGCG 1523
                 ||| | ||  |    |   ||  |  ||| |||  |   |     || || |
||||
Db      1302 TCAGACAGCTTTGTAAGC---
AGTAGTGTGTAGATTACAAGAGTTAGACAAAAGCAGGCG 1246

Qy      1524 AGA---
TGAAGTTTCAGTGGGACCTCAATGCCTGGACCAAGAGTGCCGAGGCCTTTGGCA 1580
                 ||    |||| | |||||         |||            || ||
Db      1245 CGACTGAGAAGAGTTGGTGGG------------GGA-----------
GAAGC-------- 1217

Qy      1581
AGATTGTGGCAGAGCGTCCTGGCACTAACTCAACAGGCCCTGCACCCATGGCCCCTCCAA 1640
              ||| |||| | ||||| |     ||||||||   || | | | | ||
||
Db      1216 ---TTGGGGCA---CTTCCTGTC----ACTCAACA-------
CATTCCAGATCACTAAAA 1174

Qy      1641 GA--
GCCCCAGGGCCCCTGAGCAAGCAGGGCTCTGGCAGCAGCCAGCCCATGGAGGTGCA 1698
              |  || ||   |||| |||  |   || ||     ||| ||    || |
|
Db      1173 AATTTCCACA----CCCTCTGCATTCC---CCCTTGC-----CCACTCC----
AGTTCCC 1130

Qy      1699
GGAAGGCTATGGCTTTGGGTCAGGAGATGATCCCTACTCAAGTGCAGAGCCCCATGTGTC 1758
              || |        || |  |    |||| ||  |   |||         ||||
||
Db      1129 GGTA---------TTT---TC------
TGATTCCATATGTTGTGGTATTTACCATACTTC 1088

Qy      1759 AGGTGTGAAACGGTCCCGCTC-AGGTGAGGGCGAGGTGAGCGGC--
CTTATGCGCAAGGT 1815
                | ||||| | |||    |||  || || | | | | | |
|
Db      1087 ---------TC--TCCCTCACTAGGCTCTGGCAAG----
ACTGCTTCAGAGGGGATGCAT 1043

Qy      1816 GCCACGAGTGAGCCTTGAACGCCTGGACCTGGACCTCACAGCTGACAG--
CCAGCCACCC 1873
              || ||   ||  ||  || || ||| |||       |  |||| |||    ||| |
Db      1042 TCCTTTAGATTGCAC--AAAGC--GGAGCTGGG-
AAAATGGCTGGCAGTTTCAGAATCTA 988

Qy      1874 GTCTTCAAGGTCTTCCCAGGC---
AGTACCACTGAGGACTACAACCTTATTGTTATTGAA 1930
```

```
                   |||   | |     ||  || ||    ||  ||| |     ||  ||| || | |
Db       987 GTC-ACGA-----TCGCACGCATGAGCACCTC-----AC-
ACATCCATGT---------- 950

Qy      1931
CGTGGCGCTGCCGCTGCAGCTACCGGCCAGCCAGGGACTGCGCCTGCAGGAACCCCTGGT 1990
                        ||     |||||         ||||      |||| |
|
Db       949 ----------CC-------CTACC----------------CGCC--------
CCCCCGCT 931

Qy      1991 GCCCCACCCCTG--
GCTGGCATGGCCATTGTCAAGGAGGAGGGAGACGGAGGCTGCCATTG 2048
                      ||| |||||| ||||||  || ||  ||||
Db       930 --CCCGCCCCTGCAGCTGGC-TGACC--
TGTCT------------------------- 903

Qy      2049 GAGCCCCTCCTACTGCCACTGAGGGCCCTGAGACCAAACCTG--
TGCTTATGGCTCTTGC 2106
              | ||  || ||| | ||    |  |      |  ||    ||| || || |||||
|||
Db       902 ---CACCCACTGCTGGC-CTATCGAAC----
GGCCAGGACTGTCTGGTTTTGGCTCGTGC 851

Qy      2107
GGAGGGTCCTGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAGTGGCAGCACCAGCTCAGG 2166
                         ||   |||| | ||||| |        ||  ||  |||
|
Db       850 --------------CTTT--GTCCATGTCTGGCTT-----------AGTTCCT-
CTCTG- 820

Qy      2167
GCTGGAGGTGGTGGCTCCTGAGGGTACCTCAGCCCCAGGTGGTGGCCCGGGAACCCTGGA 2226
                          || | | |||| ||| |           |||    |||
||
Db       819 ----------------TCTATGCTTGCCTCTACCCCC--------ACCG---
CCCCAGG- 788

Qy      2227 TGACAGTGCCACCATTTGCCGTGTCTGCCAGAAGCCAGGC-
GATCTGGTTATGTGCAACC 2285
              | |  |||| | |  |||| || |   |||| | |||| || |
Db       787 ---CGG---CACAA------GTGTTTG------GCCACACAAAACTAGAGAT----
AGAA 750

Qy      2286
AGTGTGAGTTTTGTTTCCACCTGGACTGTCACCTGCCGGCCCTGCAGGATGTACCAGGGG 2345
              |  |||    ||| | ||  ||| ||    ||   || ||| | | |
Db       749 AAGGTGGTAAAAACTTCAAACTTTTCTAAATTCT------
CCAACAGTTTATTTCT---- 700

Qy      2346 AGGAGTGGAGCTGCTCACTCTGCCATGTGCTCCCT--------
GAC-------------- 2383
              ||| | ||| |  |  | |||| | | |||| |        ||
Db       699 ---TGTGAATTTCTTCCTTCT-
TTAAATACTCCATTTTAAGAAAACAAAAAAATTAATTA 644

Qy      2384 -CTGAAGGAGGAGGATGGCAGCCTCAGCCTGGATGGTGCAGACAG-
CACTGGCGTGGTGG 2441
              || |||| || ||||   || |||   |||| | | | |   |||| ||| |
Db       643 TCTAAAGGCAAAGAATGGAA--
```

```
AGCAACCTTTGTGTTCCTTATAATAACTGACTT----- 591


Qy       2442 CCAAGCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGC-
CCTATTCTGT 2500
              |  |  ||||| |||      |  | |  ||| ||  |||||      ||  ||
|||||
Db        590 CATAACTCTCTCCAG-----CTGC-GTTATGGGA-
TGTGTATAAAAAGCTTCTGTTCTG- 539


Qy       2501 CACGAACCCTGCCGCCCCCTGCATCAGC-TGGCTACCGACTCCACCTTC----
TCCCTGG 2555
              ||||  |  | | |||| |||||  |   |  | |  | ||||| |    | ||
Db        538 --AGAACAAAGGAG-
CACGTGCAGAAATGAGACGAAAAAATCCACTGACAGTATTCCATT 482


Qy       2556 CACCT-CCCTACAGCTCCCCA----------
ACCAGCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCTCCAGGAGAAGTTGT 2615
              ||       ||  |  ||   |||  |       |  | | |||| |  |||      | ||
                                                                     |
Db        481 AC---ACAAATTACTTAAAAGATTT-----TAGT-
CAAGCCCCTCAACAGATTCAATTTT 431


Qy       2616 CACCT-CCCTACAGCTCCCCA----------
CAGGAGTTTGCCCAGGATGTGGGCCG--- 2661
              |  |  |||| |  | ||  |        |  | | |  || ||||| |   |  |||
Db        430 
AAAATGGCTTTTAGTTAAAAAAAAAAAAATTGAAAGTGCTTACCCAGTAAAAGAACCGAAG 371


Qy       2662 ----CATGTTC--------AAGCAATTCAACA----------
AGTTAACTGAGGACAAGG 2699
              | || |      |||  || |||          || || | |||
||
Db        370 
TAGTCCTGAACTGTTACGTAAGACTTTTTACAGTTGGATCTTTGTCAAAAGGGGATGGGG 311


Qy       2700 CAGACGTGC-AGTCCATCATCGGCCTGCAGCGCTTCTTCGAGACGC----
GCATGAACGA 2754
              || |  |   ||  || || |   ||        |||||| ||    || || ||
||
Db        310 GTGATGGGAGAAAGCAGCAACGACAATCAAAAAAG-TTCGAGCTGCTGTGGCTAGAG-
GA 253


Qy       2755 GGCCTTCGGTGACACCA-----AGTTCTCTGCTGTGCTGGTGGAGC-
CCCCGCCGATGAG 2808
              |||| |||   |||        |||| |||||  ||||  | || |||
||
Db        252 CAACTTCTGTGTTTCCAGATAGGATTCT-TGCTGTAGAAATGGAACTTCCAGCC----
AG 198


Qy       2809 C-CTGCCTGGTGCTGGCCTGAGTTCCCAGGAGC----------
TGTCTGGTGGCCCTGGT 2857
              | | || |      ||||   |||||| ||         ||||  |  |
Db        197 CACAGCAT--------CCTG---TCCCAGTAGAGAAATGAGTTTGTCAGTTAAAAC-
AAA 150


Qy       2858 
GATGGCCCCTGAGGCTGGAGCCCCCATGGCCAGCCCAGCCTGGCTCTGTTCTCTGTCCTG 2917
              |          ||  |||||| |||   ||| || |  | |   ||    || |
Db        149 AAAAAAATTAGATACTGGAACCC---AGGCTAGACGA----
GGTATTGAAC--------- 106
```

```
Qy      2918 TCACCCCA----
TCCCCACTCCCCTGGTGGCCTGACTCCCACTCCCTGGTGGCCCCATCC 2973
              | | ||| |  ||| | ||||| || |||||  ||||  ||| || |  ||| |
Db       105 -CGCGCCAGATTTCCTTGCAGCCCTGTCTGCTCAGCTCGCATTCC--
AGTAGGCCAA--- 52


Qy      2974 CCCAGTTCCTCACGATATGGTTTTTACTTCTGTGGATTTAATAAAAAAAACTTCAC--
CA 3031
              ||||   |  |||  ||  |  |||| |  | ||| | |  | ||   |||
|
Db        51 --CAGT---GCTCGA---GG-----
AATTCCGCAGCTTTTAGAGCAGAAGTAACACTTCC 5


Qy      3032 GTTC 3035
              || |
Db         4 GTAC 1



RESULT 13
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;  LENGTH: 2198
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match             26.6%;  Score 5207.5;  DB 1;  Length 2198;
  Best Local Similarity   42.2%;  Pred. No. 2.6e-290;
  Matches 1241;  Conservative    0;  Mismatches 824;  Indels 873;
Gaps  170;

Qy       223
CCCAGGAGGCGCGTGGCGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCAGCGGCCCAGCAG 282
              || |                 || || || | | || |    |    | || | |
|
Db         1 CCTA-----------------CT-GGTCTTGTGTGGGTGTTTTC-----
CAGCACGGAA- 36

Qy       283
TTGGCGGCGAGCGCGTCTGCGCCTGCGCGGCGGGCCCCGCGCCCCTCCTCCCCCCCTGGG 342
                | ||||   | |||  || | | || |||  ||| || |||| |
Db        37 ---AAGTCGAGATAAT-TGCCAATGATCAG-
GGAAACCGAACCACTCCAAGC-------- 83
```

```
Qy          343
CGCCCCCGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCGGCAGCCTCGGCAGCAGCGGCCTC 402
                                  ||| | |||| |||  ||   ||| | ||| |
     ||
Db           84 ------------------TATGTC-GCCTTTACGGACACTG-AACGGTTG-------
ATC 116


Qy          403
GGCCGCCTCTGGCAGCCCGGGCCCGGGCGAGGGCTCCGCTGGCGGCGAAAAGCGCTCCAC 462
                ||         |  |||        || |  || |  |||     || |  |
||||
Db          117 GGT--------GATGCC---------GCAAAGAATCAAGTTGC-----
AATGAACCCCAC 154


Qy          463
CGCCCCTTCGGCCGCAGCCTCGGCCTCTGCCTCAGCCGCGGCGTCGTCGCCCGCGGGGGG 522
                 |         |  ||||  |  |  |    |||| |         || | |    |
Db          155 C---------AACACAGTTTTTG---ATGCCAAA-------------
CGTCTGATTG--- 186


Qy          523
CGGCGCCGAGGCGCTGGAGCTGCTGGAGCACTGCGGCGTGTGCAGAGAGCGCCTGCGACC 582
                  | |||| ||   | ||  |||| ||                            || |
     |
Db          187 -GACGCAGATTTGATGATGCTGTTG------------------------TCCAG---
TC 217


Qy          583
CGAGAGGGAGCCCCGCCTGCTGCCCTGTTTGCACTCGGCCTGTAGTGCCTGCTTAGGGCC 642
                | | | | |        |  |||| |       |  ||| | | | || | ||  |
||||
Db          218 TGATATGAAACATTG------GCCCTTTATG---GTGGTGAATGATGCTGGC---
AGGCC 265


Qy          643
CGCGGCCCCCGCCGCCGCCAACAGCTCGGGGGACGGCGGGGCGGCGGGGCGACGGCACCGT 702
                | | || ||  | ||| | |  | |  |||    |||| ||  ||  | ||  |
     |
Db          266 CAAGGTCCAAGTAGAATACAA--------GGGA----
GAGACCAAAAGCTTCTATCCAGA 313


Qy          703 GGTGGACTGTCCCGTGTGCAAGCAACAGTGCTTCT-
CCAAAGACATCGTGGAGAATTATT 761
                || |        |||| |      |  | || ||||  ||||||   || || |
Db          314 GGAG---------GTGT-----CTTCTATGGTTCTGACAAAGA-----
TGAAGGA----- 349


Qy          762
TCATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGCCCAGGATGCGAACCAGTGCTGCA 821
                            | | |||| |   ||| |   |    |||| |||  ||   || |
     |
Db          350 -----------AATTGCAGAA-----GCCTAC---CTTGGGAAG---AC---
TGTTACC 383


Qy          822 CTAGCTGTGAGGATAATGCCCCAGCCACCAGC-
TACTGTGTGGAGTGCTGGAGCCTCTG 880
                ||||||        |  ||| |||| |||||  ||| | | |  ||   ||   ||| ||
Db          384 AATGCTGTG--------GTCACAG-TGCCAGCTTACTTTAATGA---
CTCTCAGCGTC-- 429
```

```
Qy        881
TGTGAGACCTGTGTAGAGGCGCACCAGCGGGTGAAGTACACCAAGGACCATACTGTGCGC 940
                    ||||              |||||  |  || |||
|
Db        430 ----------------AGGC------------------TACCAAAG---ATGCTG---
GA 449


Qy        941
TCTACTGGGCCAGCCAAGTCTCGGGATGGTGAACGTACTGTCTATTGCAACGTACACAAG 1000
              ||| ||        |  |||||        || |||||     | |  | |
||
Db        450 ACTATTG-------CTGGTCTC---------AATGTACT-----
TAGAATTATTAATGAG 488


Qy        1001
CATGAACCCCTTGTGCTGTTTTGTGAGAGCTGTGATACTCTCACCTGCCGAGACTGCCAG 1060
                |    |  ||        ||||        ||||      ||  |
|
Db        489 C-----CAACT------------------GCTG------------
CTGCTATTGCTTACGG 514


Qy        1061
CTCAATGCCCACAAGGACCACCAGTACCAGTTCTTAGAGGATGCAGTGAGGAACCAGCGC 1120
              || |  | | |||              || ||   |||| || |||  ||
|
Db        515 CTTA--GACAAAAAGG-----------------TTGGA----
GCAGAAAGAAACGTGCTC 551


Qy        1121 AAGCTCCTGGCCTCACTGGTGAAGCGCCTTGGG---
GACAAACATGCAACATTGCAGAAG 1177
                |  || || |||   |||| || | |  |   | ||| | | || |||| ||
|
Db        552 AT-CT-TTGACCTGGGAGGTG--GCACTTTTGATGTGTCAATCCT-
CACTATTGAGGATG 606


Qy        1178 AGCACCAAGGAGGT----TC-
GCAGCTCAATCCGCCAGGTGTCTGACGTACAGAAGCGTG 1232
                | | |  ||||| |  | ||||| | ||||| |  | | || ||  |||  || |||||
|
Db        607 -GAATCTTTGAGGTCAAGTCTACAGCTGGAGACACCC----
ACTTGGGTGGAGAAGATTT 661


Qy        1233 TG-CAAGTGGATGTCAAGATGGCCATCCTGCAGATCATGAAGGAGCTGA--
ATAAGCGGG 1289
                || |||        |  |||| || |        |||       |||||  ||||||
Db        662 TGACAA--------CCGAATGGTCAAC---------
CATTTTATTGCTGAGTTTAAGCGCA 705


Qy        1290
GCCGTGTGCTGGTCAATGATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGC 1349
                | |  | || ||            ||| |  || | ||| | || | ||||||
Db        706 AGCATAAGAAGGACAT-------CAGTGAG-AACAAGAGAGCTGTGAAGA-
CGCCT----- 751


Qy        1350
GGCAGCACTGGACCATGACCAAGATCCAGAAGCACCAGGAGCACATTCTGCGCTTTGCCT 1409
                | | ||||             | | || || || || |
|||
Db        752 --CCGTACTG-------------------------
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CTTGTGAACGTGCTAAGCGTACCCT 784


Qy        1410 CTTGGGCTCTGGAGAGTGACAACAACACAGCCC-TTTTG---------
CTTTCTAAGAAG 1459
               ||    ||         || || |   ||| | |||         || ||||
||||
Db         785 CT----CTT---------
CCAGCACCCAGGCCAGTATTGAGATCGATTCTCTCTATGAAG 831


Qy        1460 TTGATCTACTTCCAG--CTGCA----
CCGGGCCCTCAAGATGATTGTGGATCCCGTGGAG 1513
                    ||| ||||| |   || ||    ||| |||| ||||           |
                 ||
Db         832 -GAATCGACTTCTATACCTCCATTACCCGTGCCC-------GATT--------
TGAAGAA 875


Qy        1514 CCACATGGCGAGATGAAGTTTCAGTGGGACCTCAATGCCTGGACCAAG-
AGTGCCGAGGC 1572
                |  ||| || ||    ||| |||| |        ||||||| ||| || |    |
                ||
Db         876 CTGAATGCTGACCTG----TTCCGTGGCAC-------CCTGGACCCAGTAGAG--
AAAGC 922


Qy        1573 CTTTGGCAAGATTGTGGCAGAGC--GTCCTGGCACTAACTCAACA---
GGCCCTG----- 1622
                | || | |||| ||   || | | | | ||| | ||| |    | ||||
Db         923 CCTT--CGAGAT----
GCCAAACTAGACAAGTCACAGATTCATGATATTGTCCTGGTTGG 976


Qy        1623 ------CACCCATGGCCCC----TCCAAGAG---
CCCCAGGGCCCCTGAGCAAGCAGGGC 1669
                    ||| | |||| | || || | ||| | | ||       | |
Db         977 TGGTTCTACTCGTATCCCCAAGATTCAGAAGCTTCTCCAAGACTTCTTCAATGGAAAAGA 1036


Qy        1670 TCTGGC----
AGCAGCCAGCCCATGGAGGTGCAGGAAGGCTATGGCTTTGGGTCAGGAGA 1725
                    |||      |||| ||| ||        || | | |||| | |||| ||| |
                ||
Db        1037 ACTGAATAAGAGCA-TCAACCC-------TGATG--AAGCTGTTGCTTATGGT--
GCAGC 1084


Qy        1726 TGATCCCTACTCAAGTGCAGAGCCCCATGTGTCAGGTGTGAAACGGTCCCGCTCAG-
GTG 1784
                ||        || || |||| ||     |||| || |         |   || | |
Db        1085 TG--------TCCAG-GCAG---CCATCTTGTCTGGAG---------
ACAAGTCTGAGAA 1123


Qy        1785 AGGGCGAGGTGAGCGGCCTTATGCGCAAGG-
TGCCACGAGTGAGCCTTGAACGCCTGGAC 1843
                | | ||| ||        ||| |  || || |||         |||     | | |||
Db        1124 TGTTCAAGATTTGC-------TGCTCTTGGATGTCAC------
TCCTCTTTCCCTTGGTA 1170


Qy        1844 CTGGACCTCACAGCTGACAGCCAGCCACCCGTCTTCAAG-
GTCTTCCCAGGCAGTACCAC 1902
                || || |  || | |    | | |   | | |||| || | ||| ||| || |
Db        1171 TTGAAACT-GCTGGTGGAGTCATGACTGTCCTCATCAAGCGTAATACCA-
```

```
CCATTCCTAC 1228

Qy       1903 TGAG--
GACTACAACCTTATTGTTATTGAACGTGGCGCTGCCGCTGCAGCTACCGGCCAG 1960
                 || ||| |  |||||                 | || || | | |    |
||||
Db       1229 CAAGCAGACACAGACCTT----------------CACTACCTATTCTG---
ACAACCAG 1268

Qy       1961 CCAGGGACTGCGCCTGCAG------GAACCCCTG-
GTGCCCACCCCTGGCTGGCATGGC 2013
                 || ||   ||| | |||     ||| | | ||||| |    | || | |A|
|
Db       1269 CCTGGTG-TGCTTATTCAGGTTTATGAAGGCGAGCGTGCCATGACAAAGGATAACA--
AC 1325

Qy       2014 C--
ATTGTCAAGGAGGAGGAGACGGAGGCTGCCATTGGAGCCCCTCCTACTGCCACTGAG 2071
                 |  ||| |||| ||       ||  || ||   |||||| |  ||   |
Db       1326 CTGCTTGGCAAGTTTGA----------ACT--
CACAGGCATACCTCCTGCACCCCGAGGT 1373

Qy       2072 GGCCCTGAGACCAAACCTGT-
GCTTATGGCTCTTGCGGAGGGTCCTGGTGCTGAGGGTCC 2130
                 |  ||| |||  || | |||  ||  |        || ||| | ||| | |||
Db       1374 GTTCCTCAGATTGAA---GTCACTTTTGAC-------------
ATTGATGCCAATGGTAT 1417

Qy       2131
CCGCCTGGCCTCACCTAGTGGCAGCACCAGCTCAGGGCTGGAGGTGGTGGCTCCTGAGGG 2190
                 | |  ||| ||| || |||| |  ||  | ||    ||| |     | | | ||
Db       1418 ACTCAATGTCTCTGCT-GTGG--
ACAAGAGTACGGGAAAAGAGAACAAGATTACT----A 1470

Qy       2191
TACCTCAGCCCCAGGTGGTGGCCCGGGAACCCTGGATGACAGTGCCACCATTTGCCGTGT 2250
                 | || | |  ||||     ||| | | ||| |||| || | | | ||
||
Db       1471 TCACTAATGACAAG-----GGCCGTTTGAGCAAGGAAGACATTG--AACGTATG----
GT 1519

Qy       2251 CTGCCAGAAGCCAGGCGAT------
CTGGTTATGTGCAACCAGTGTGAGTTTTGTTTCCA 2304
                 | |  ||||| |  |    |        ||| ||| | || ||| | ||     || ||
Db       1520 C--CAGGAAGCTGAGAAGTACAAAGCTGAAGATGAG-AAGCAGAGGGA-
CAAGGTGTCAT 1575

Qy       2305
CCTGGACTGTCACCTGCCGGCCCTGCAGGATGTACCAGGGGAGGAGTGGAGCTGCTCACT 2364
                 || || | |||| || | |||                              |||
||
Db       1576 CCAAGAAT-TCACTTG--AGTCCT----------------------------ATGC---
CT 1602

Qy       2365
CTGCCATGTGCTCCCTGACCTGAAGGAGGAGGATGGCAGCCTCAGCCTGGATGGTGCAGA 2424
                 |||| |   | ||| | || |    | | | |||
||
Db       1603 TCAACATGAAAGC----AACTGTTGAAGATG---AGAAACTTCA-------------
AGG 1642
```

```
Qy        2425
CAGCACTGGCGTGGTGGCCAAGCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACT 2484
          ||  |  |  || | |                     | ||| |||  ||
|
Db        1643 CAAGATTAACGATGAG---------------
GACAAACAGAAGA--------------T 1672

Qy        2485 GCTGGCCCTATTCTGTCACGAACCCTGCCGCCCCCTGCATCAGCTGGCT---
ACCGACTC 2541
               ||||  |       ||| | |||                 |||| ||||||       ||
||
Db        1673 TCTGGACAAG---TGTAATGAAAT-------------
TATCAACTGGCTTGATAAGAATC 1716

Qy        2542
CACCTTCTCCCTGGACCAGCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCT 2601
          ||  ||     || |       |   | | || |  || | | | |       |
Db        1717 AGACTGCT-----GA-------GAAGGAA----
GAATTTGAACATCAACAGAAAGAG--- 1757

Qy        2602 CCAGGAG-
AAGTTGTCACCTCCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCC 2660
          | |||| ||||| |||| || | ||| | || |      |||| || ||
Db        1758 -CTGGAGAAAGTTTGCAAC-CCCATCATCACCAAGCTGTA------
CCAGAGTGCAGGAG 1809

Qy        2661 GCATGTTCAAGCAATTCAACAAGTTAACTGAGG----
ACAAGGCAGACGTGCAGTCCATC 2716
               ||||| | || |     |         ||| ||     | ||   | | ||  |||
|
Db        1810 GCATG--CCAGGAGGAATGC-------CTGGGGGATTTCCTGGTGGTGGAGC--
TCCTCC 1858

Qy        2717 ATCGGCCTGCAGCGCTTCTTCGAGACGCG-
CATGAACGAGGCCTTCGGTGACACCAAGTT 2775
               || |  | |    | ||||| || | ||   | |||| | |||||  | | | |   ||||
Db        1859 CTCTG---GTGGTGCTTCCTCAGGGCCCACCATTGAAGAGG---
TTGATTAAGCCAA--- 1909

Qy        2776 CTCTGCTGTGCTGGTGGAGC------
CCCCGCCGATGAGCCTGCCTGGTGCTGGCCTGAG 2829
               |  ||| | || ||    || | |   | | |     || | |||
|
Db        1910 --CC-AAGTGTAGATGTAGCATTGTTCCACACATTTAAAAC-ATTTGAAG--
GACCTAAA 1963

Qy        2830
TTCCCAGGAGCTGTCTGGTGGCCCTGGTGATGGCCCCTGAGGCTGGAGCCCCCATGGCCA 2889
          ||| || | ||| ||||| ||     || |   || | ||||        | || |
Db        1964 TTCGTAGCAAAT-TCT-GTGGC---AGTTTTAAAAAGTTAAGCTG------
CTATAGTAA 2012

Qy        2890
GCCCAGCCTGGCTCTGTTCTCTGTCCTGTCACCCCATCCCCACTCCCCTGGTGGCCTGAC 2949
          |    |  |||   ||||| |||| | |  |          |   | | | ||| |
Db        2013 G--TTACTGGGC---ATTCTCAATACT-
TGAATATGGAACATATGCACAGGGGAAGGAAA 2066
```

```
Qy      2950 TCCCACTCCCTGGTGGCCCCATCCCCCAGTTCCTCACGATATGGTTTTT----
ACTTCTG 3005
             |  || |        || |  |      |    ||| ||| ||   |    | | |
Db      2067 TAACATT--------GCACTTT-------
ATAAACACTGTATTGTAAGTGGAAAATGCAA 2111

Qy      3006 TGGATTTAATAAAA-----AAAACTT--CACCAGTTCAAAAAAAAAAAAAAAAAAAAAA
3056
             ||  || || |||||||     ||| ||  |||||    |||||||||||||||||||||
Db      2112 TGTCTTAAATAAAACTATTTAAAATTGGCACCATAAAAAAAAAAAAAAAAAAAAAAAAAA
2169


RESULT 14
US-10-478-914-57
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match            25.9%;  Score 5054;  DB 1;  Length 2336;
  Best Local Similarity  41.2%;  Pred. No. 2.9e-281;
  Matches 1262;  Conservative   0;  Mismatches  933;  Indels  868;
Gaps  185;

Qy       114 GTGCGG----GTTTCGGCGGCGGCTGAGGAAGAAGC-
GCGGGCGGCGGCCTTCGGGAGGCG 168
             || |||   ||| |  | || ||     | |||| ||||     |||
||
Db         1 GTACGGAAGTGTTACTTCTGC-TCT-----AAAAGCTGCGG--AATTCCT--------
CG 44

Qy       169
AGCAGGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGCGGGCAGCGGCCCAGG 228
             ||||      | ||||||| | | | |   ||| | | ||  | | || || ||
|
Db        45 AGCA-----CTGTTGGCC-TACTGGA-ATGCGAGCTGAGC-AGACAGG--
GCTGCAAGGA 94

Qy       229
AGGCGCGTGGCGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCAGCGGCCCAGCAGTTGGCG 288
             |  |   ||||                              |||| || |
```

```
Db          95 AATC---TGGC-----------------------------
GCGGTTCAATA------- 113


Qy         289
GCGAGCGCGTCTGCGCCTGCGCGGCGGGCCCCGCGCCCCTCCTCCCCCCCTGGGCGCCCC 348
             |  | |||||  ||||    ||  |    ||  |       | |
Db         114 -C---CTCGTCT-AGCCT-------GGGTTCC-
AGTATCTAATTTTTTTTTTG------- 153


Qy         349
CGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCAGCCTCGGCAGCAGCGGCCTCGGCCGC 408
                          | | | | |  |||
Db         154 -------TTTTAACTGACAAACTC----------------------------
ATTT 174


Qy         409
CTCTGGCAGCCCGGGCCCGGGCGAGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCC 468
               ||||      |  | ||| |||    |||  |||||| | |||    | ||||
Db         175 CTCT-----ACTGGGACAGGAT----GCTGTGCTGGCTG-GAA---- 
GTTCCA------T 214


Qy         469 TTCGGCCGC-
AGCCTCGGCCTCTGCCTCAGCCGCGGCGTCGTCGCCCGCGGGGGGCGGCG 527
                     ||| | || ||  ||     || || |   |  | || ||| |
Db         215 TTCTACAGCAAGAATC-----CTATCT-GGAAACACAGAAGTTGTCCTC--------
TAG 260


Qy         528 CCGAGGC-GCTGGAGCTGCTGGAGCACTGC--
GGCGTGTGCAGAGAGCGCCTGCGACCCG 584
                 ||   || ||| || |         ||   | ||| ||| |     | ||  |  |
Db         261 CCACAGCAGCTCGAACTTTT------TTGATTGTCGT-TGCTGCTTTCTCC--
CATCAC- 310


Qy         585
AGAGGGAGCCCCGCCTGCTGCCCTGTTTGCACTCGGCCTGTAGTGCCTGCTTAGGGCCCG 644
                       ||||      |||| |  ||     || || ||  |
Db         311 -------CCCCATC-----CCCTTTTGACA---------AAGATCCAACT---
GTAAAA 345


Qy         645 CGGCCCCCGCCGCCGCCAACAGCTCGGGG-GACGGCGGGGC---
GGCGGCGACGGCAC- 699
                   | |   ||     ||||| || ||   ||  |||  |    | || |
||||
Db         346 AGTCTTACG-------TAACAGTTCAGGACTACTTCGGTTCTTTTACTGG-
GTAAGCACT 397


Qy         700 --CG--------TGGTGGACTGT---CCCGTGTGCAA--GCAACAGT------
GCTTCTC 738
                     |           | | |||    || | || | | | || |   ||||
Db         398
TTCAATTTTTTTTTTTTTAACTAAAAGCCATTTTAAAATTGAATCTGTTGAGGGGCTTGAC 457


Qy         739
CAAAGACATCGTGGAGAATTATTTCATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGC 798
                  ||| | |    |  ||| |  |   |  | ||| |  || ||     || |
|| |
Db         458 TAAAATCTTTTAAGTAATTTGTGTAAT--GGAATACTGTCAG--
```

```
TGGATTTTTTCGTCTC 513


Qy         799 C---CAGGATGCGAACCAGTG----CTGCAC--
TAGCTGTGAGGATAATGCCCCAGCCAC 849
                   | | | | |  || ||    | | ||  |||| |    | || | |
|||
Db         514 ATTTCTGCACGTGCTCCTTTGTTCTCAGAACAGAAGCTTT-----
TTATACACATCCCAT 568


Qy         850 CA-
GCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACCTGTGTGAGGCGCACCAGC 908
                   |  || ||| ||||| | ||| ||  ||| |         | |   ||| || ||
Db         569 AACGCAGCTGGAGAGAGTTAT-GAAG--TCAGT--------TATTATAAGGAACA-
CAAA 616


Qy         909
GGGTGAAGTACACCAAGGACCATACTGTGCGCTCTACTGGGCCAGCCAA----------G 958
                   || ||  |        ||||| | || | |      | |    ||
Db         617 GGTTGCTTT----------CCATTCTTTGC-CTTTA----
GATAATTAATTTTTTTGTTT 661


Qy         959
TCTCGGGATGGTGAACGTACTGTCTATTGCAACGTACACAAGCATGAACCCCTTGTGCTG 1018
                   |||   ||||| | |  || |   | || | |||||| |  || |  |||
|
Db         662 TCTTAAAATGGAGTATTTAAAGAAGGAAGAAA--TTCACAAGAAATAAACTGTTGG--
AG 717


Qy        1019 TTTTGTGAGAGCTGTGATACTCTCACCTGCCGAGACTGCCAGCTCAA--------
TGCCC 1070
                   ||  || | |||  | | ||| |    | | ||| |        ||
||
Db         718 AATTTAGAAAAGTTTGAAGTTTTTACC-ACC--- 
TTTTCTATCTCTAGTTTTGTGTGGCC 773


Qy        1071
ACAAGGACCACCAGTACCAGTTCTTAGAGGATGCAGTGAGGAACCAGCGCAAGCTCCTGG 1130
                   |     | ||| || ||     | | |    || ||| |   || ||||| | |
|
Db         774 A-----AACACTTGTGCCG---CCTGGG----GCGGTGGGGGTAGAG-GCAAG--
CATAG 818


Qy        1131 CCTCACTGGTGAAGCGCCTTGGGGACAAACATGCAACATTGCAGAAGAGC---
ACCAAGG 1187
                   |      | ||| |     | | ||||| |  || | | |||| | |
||
Db         819 AC-----AGAGAGGAACT---AAGCCAGACATGGACAAAGGC--
ACGAGCCAAAACCAGA 868


Qy        1188 AGGTTC--
GCAGCTCAATCCGCCAGGTGTCTGACGTACAGAAGCGTGTGCAAGTGGATGT 1245
                   || |  || | ||  || || ||  |||||                   |||||
||
Db         869 CAGTCCTGGCCGTTCGATAGGCCAG------------------------- 
CAGTGGGTG- 902


Qy        1246 CAAGATGGCCATCCTGCAGATCATGAAGGAGCTGAATAAGCGGGGCCGTGTGCTGGTCAA 1305
                   |     || || || ||      || | ||| |  ||||||| | || |||
Db         903 -AGACAGGTCAGCCAGC------TGCAGGGGCGG---GAGCGGGG----
```

```
GGGCGGGTAGG 948


Qy        1306
TGATGCCCAGAAGGTGACTGAGGGGCAGCAGGAGCGCCTGGAGCGGCAGCACTGGACCAT 1365
               | |   | | |||  ||||| ||  || | | ||              || |
|
Db         949 ----GACATGGATGTG--TGAGGTGCT-CATGCGTGC-----------------
GATCGT 984


Qy        1366 GACCAAGATCCAGAAGC-
ACCAGGAGCACATTCTGCGCTTTGCCTCTTGGGCTCTGGAGA 1424
               || | |||| | ||| |  ||||    ||  ||   ||| ||  | | ||   |||
||
Db         985 GA-CTAGATTCTGAAACTGCCAG--
CCATTTTCCCAGCTCCGCTTTGTGCAATCTAAAGG 1041


Qy        1425
GTGACAACAACACAGCCCTTTTGCTTTCTAAGAAGTTGATCTACTTCCAGCTGCACCGGG 1484
                    ||  || |||         || ||||  | ||| | |||| | |||| ||   |
|
Db        1042 --------AATGCATCCC---------CTCTGAAGCAG-TCT--TGCCAG-
AGCCTAGTG 1080


Qy        1485 CCCTCAAGATG-
ATTGTGGATCCCGTGGAGCCACATGGCGAGATGAAGTTTCAGTGGGAC 1543
                     ||| | ||| || | ||        | |||       ||| | |||||
Db        1081 AGGGAGGAGAAGTATGGTAAATACC-----ACAACAT------ATG--
GAATCAG------ 1121


Qy        1544 CTCAATGCCTGGACCAAGAGT--GCCGAGGCCTTTGGCAAGATTGTGGCAG------
AGC 1595
                     ||| || ||| |  |||| ||   ||     ||   ||  ||||| |
||
Db        1122 -
AAAATACCGGGAACTGGAGTGGGCAAGGGGGAATGCAGAGGGTGTGGAAATTTTTTAGT 1180


Qy        1596 GTCCTGGCACTAACTCA---ACAGGCCCTGCACC---CATGGCCCCTCCAAGAGC--
CCC 1647
               |  |||| |        | |  ||||| ||| ||  | | |||| | |  | |
|
Db        1181
GATCTGGAATGTGTTGAGTGACAGGAAGTGCCCCAAGCTTCTCCCCCACCAACTCTTCTC 1240


Qy        1648 AGG-GCCCCTGAGCAAGCAGGGCTCTGG----
CAGCAGCCAGCCCATGGAGGTGCAGGAA 1702
               || | || ||||        |||| |    | || | |   |           || |
Db        1241 AGTCGCGCCTGCTTTTGTCTAACTCTTGTAATCTACACACTACTGCTTACAAAGCTG--- 1297


Qy        1703 GGCTATGGCTTTGGGTCAGGAGATGATCCCTACTCAAGTGCAGAGCCCCATGTGTCAGGT 1762
                 | || ||| |  | |  ||| ||| |||| |  ||||  | | |     | || |    ||
Db        1298 ---TCTGAGTTTAAGACA--AAAAGAAACCTA--AAAGT------
CTCCTTACTTC---- 1340


Qy        1763
GTGAAACGGTCCCGCTCAGGTGAGGGCGAGGTGAGCGGCCTTATGCGCAAGGTGCCACGA 1822
                  |   ||| || ||  | | || |  | ||           || |||
Db        1341 -----ATAGTAC--CTGTGATATGGAAGGAATG--------
TAAAAGCA----------- 1374
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Qy        1823
GTGAGCCTTGAACGCCTGGACCTGGACCTCACAGCTGACAGCCAGCCACCCGTCTTCAAG 1882
          ||| |||| || |||| |||||    |||||| |   |   |   |||        |      |
Db        1375 -TGACCCTTTAA-GCCT----
ATGGACATTTTTCAGGTATACAGGAGAAAGATAAAATA 1428


Qy        1883 GTCTTCCCAGGCAGTACCACTGAGGACTACAACCT-
TATTGTTATTGAACGTGGCGCTGC 1941
               | |||| ||| |  | |||| | ||   |   | ||| |||
Db        1429 ATTTTCC---ACAG-
AAAAATGAGAATTATGAATTATATAGTT---------------- 1467


Qy        1942
CGCTGCAGCTACCGGCCAGCCAGGGACTGCGCCTGCAGGAACCCCTGGTGCCCCACCCCT 2001
                  ||| ||        ||    ||      |   |   |   ||| | |   |   |
          ||
Db        1468 -----CAGGTTCC---------
AAATCTAATTTTTAAAAGAATTCTGATTCTGCTACACT 1513


Qy        2002
GGCTGGCATGGCCATTGTCAAGGAGGAGGAGACGGAGGCTGCCATTGGAGCCCCTCCTAC 2061
                   |  | ||  |||    ||                     ||||
          |||||
Db        1514 --------TTACAAATGCTTAGG--------------------TTGGT-----
TCCTAA 1539


Qy        2062 TGCCACTGAGGGCCCTGAGACCAAACCTG--
TGCTTATGGCTCTTGCGGAGGGTCCTGGT 2119
                  |   |||  |      ||||         |   || |||  || ||||     |  | ||
          |
Db        1540 T----TTGAAG-----GAGACTTGTTTTATTTGGTTAATGC-
ATTGCATTTGAACTTGTT 1589


Qy        2120 GCTGAGGGTCCCCGCCTGGCCTC--
ACCTAGTGGCAGCACCAGCTCAGGGCTGGAGGTGG 2177
                  ||| ||  || | |  | | |||   |  || ||  |  |
          |
Db        1590 TCT-ATTTTCTTTGCATAAATTTGGACTTTG-GGAGAAAAATGCAAAGTAAT-
AAGTAGA 1646


Qy        2178 TGGCTCCTGAGGGTACCTCAGCCCCAGGTGGTGGCCCGGGAACCCTGGAT--
GACAGTGC 2235
                  || |  || ||| |      |    ||| |  |||      | ||| | | || |||
Db        1647 ATGCACTTGGGGGAAAAAAGG----AGGATTTTTCCC----
TTCATGGGTTGGAAAGT-- 1696


Qy        2236 CACCATTTGCCG---TGTCTGCCAG--
AAGCCAGGCGATCTGGTTATGTGCAACCAGTGT 2290
                  |||   |   ||| |  |  || | | || || ||  |||                |   |
Db        1697 ---ATTTTAAAGGGTTGTTTTCTTGAAAAAACAAGCTCTCT---------
CTTAC----- 1739


Qy        2291 GAGTTTTGTTTC--
CACCTGGACTGTCACCTGCCGGCCCTGCAGGATGTACCAGGGGAGG 2348
                  ||||  || ||  ||| |  |     |   |  | |||    | || |   |
Db        1740 --------TTTCTGCATCTATGCTATAA--AGATAACTATGC----
TATAATAAATGTAA 1785


Qy        2349 AGTGGAGCTGCTCACTCTGCCATGTGCTCCCTGACCTGAAGGAGGAGGATGGCAG---
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CC 2405
                    || ||                      || | || || ||   ||  |||
       |
Db      1786 GGTAGA------------------------AAACTTTAAAGA-
GAAAATAACAGTGTTC 1819

Qy      2406 TCAGCCTGGATGG-
TGCAGACAGCACTGGCGTGGTGGCCAAGCTCTCACCAGCCAACCAG 2464
             | || || | | |   |||| | |       |||| ||| |||      |
||
Db      1820 TAAG--TGAAAAGCTAC--TTAGCATTTTC-------CCAAACTCACACAT---
TATCAA 1865

Qy      2465
CGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTCACGAACCCTGCCGCCCCCTGCAT 2524
             | |||| |                | |||   | | ||    || ||| ||
||
Db      1866 CAGAAA-------------------CACTA-AAAATTAAGAGAAAAGCGGCCAACT-
AAT 1904

Qy      2525 CAGCTGGCTACCGACTCCACCTTCTCCCTGGACCAGCCCGG--
TGGCACCCTGGATCTG- 2581
             |  | |||||        |||| |   ||    | || | | |   |  |
||
Db      1905 TAAATAGCTA--------GCCTTATTTTGGG---
GGTATGGGATAGAAAATTAAGTGTGA 1953

Qy      2582 --ACCCTGATCCGTG-----------CCCGC---CTCCAGGAGAAGTT----GTCA-
CCT 2620
               |   |||| | ||        ||| |   | ||   || |||    ||||
|||
Db      1954
ATAAAATGATACTTGGGAATGTTTCTCCCTCGTACCACAAAGGATGTTAGTGGTCAGCCT 2013

Qy      2621
CCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCCGCATGTTCAAGCAATTCAAC 2680
             |    ||| |  |         | | ||| | | |   |||| ||    ||
Db      2014 ACGAGTTAATCCTTCCTAG-------CATGGCTCTGAGCC-----
TTCATGCCGAGCAG- 2060

Qy      2681 AAGTTAACTGAGGACAAGGC-AGACGTGCAGTCCA-
TCATCGGCCTGCAGCGCTTCTTCG 2738
             | ||||       ||| | | ||  ||||| ||||     ||    |||| | |
|
Db      2061 ACGTTATTC----ACATGACGATTCGAAAAGTCCATTCATATATCT----
CGCTACCTGG 2112

Qy      2739
AGACGCGCATGAACGAGGCCTTCGGTGACACCAAGTTCTCTGCTGTGCTGGTGGAGCCCC 2798
             |    |       |  ||  |   ||||  ||| |||  |   | | |
|
Db      2113 ATTTG-----AATAGAAACC-----AGACAGCAA-TTCTTT--AGTTCC-----
AGCCAC 2154

Qy      2799
CGCCGATGAGCCTGCCTGGTGCTGGCCTGAGTTCCCAGGAGCTGTCTGGTGGCCCTGGTG 2858
             |    || ||| |    |||             ||  |||  | || | || | |
Db      2155 C----ATTCGCC--CC----ACTGG---------
ACAATAGCGATTTGTTAGCACAG--- 2192
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Qy      2859
ATGGCCCCTGAGGCTGGAGCCCCCATGGCCAGCCCAGCCTGGCTCTGTTCTCTGTCCTGT 2918
                  | | |  ||||||          |||    |  ||| |||  |||
Db      2193 --AGTCAC--AGGCTG---------
TGGGACACAAAGCTTGGAGCTG------------ 2226


Qy      2919 CACCCCATCCCCACTCCCCTGGTGGC--
CTGACTCCCACTCCCTGGTGGCCCCATCCCCC 2976
                            ||      ||| ||   | ||   |        |  ||| | || |
|
Db      2227 -----------
CAGAAAGATGGGGGATTCAGAGAACAGGAAATTACAGGCTCGATGCAC- 2274


Qy      2977
AGTTCCTCACGATATGGTTTTTACTTCTGTGTGGATTTAATAAAAAAAACTTCACCAGTTCA 3036
                  ||||  |       |   |||        |  || ||||||  |  ||| ||
Db      2275 ---TCCTGGCAGCTCTGAGAATACAAAAAAAAAAAAAAAAAAAAAAGGC--
CACATGTGCT 2329


Qy      3037 AAA 3039
                  |
Db      2330 CGA 2332



RESULT 15
US-10-478-914-3/c
; Sequence 3, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 2083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-3

  Query Match            24.2%;  Score 4731.5;  DB 1;  Length 2083;
  Best Local Similarity  38.9%;  Pred. No. 1.3e-262;
  Matches 1192;  Conservative   0;  Mismatches  810;  Indels 1065;
Gaps  173;

Qy       47 CTAGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGC-
GCGCGGCGGGCAGCGGCCCAGGA 105
               |||||       ||||          ||| || || || ||        || ||
|
Db     2083 CTAGC-------GGCC-----------GCGACCTGCAGCTCG---------
AGCACATGT 2051
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Qy        106 GGCGCGTGGTGCGGGT-------
TTCGGCGGCGGCTGAGGAAGAAGCGCGGGCGG----- 153
              | | | | |  | |   |  ||   |  ||    || | || ||
Db       2050 GGC-CTTTTTTTTTTTTTTTTTTATTTTGC--CTTCT--------
TGCTCTGGTGGTTAGT 2002


Qy        154
CGCCTTCGGGAGGCGAGCAGGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGC 213
              | ||| |  | | |        || | ||  | ||||
Db       2001 CTCCTACTATAAACATG---------ATTTTCCTT----------
CTTCCCTT------- 1968


Qy        214
GGGCAGCGGCCCAGGAGGCGCGTGGCGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCAGCG 273
              ||| | ||  |  ||  | |      ||    || |                | | ||
Db       1967 ---CAGAGTCC----TGTC---AATCTTTACTTTTTTTCTCATTAAT--
ATACAGAAGTT 1920


Qy        274
GCCCAGCAGTTGGCGGCGAGCGCGTCTGCGCCTGCGCGGCGGGCCCGCGCCCCTCCTCC 333
              |  ||| |  | ||| ||        |  |||| |      || |       |||
Db       1919 ATACTACAGATACATTCAAGCTCAT----
GACTGCTAAAAACTTCCTGAAATGAGCCTTA 1864


Qy        334 CCCCCTGGGCGCC-
CCCGGCGGCGTGTGAATGGCGGCCTCCGCGGCGGCAGCCTCGGCAG 392
              |  |  || | |   |    |   ||| |    |      | | ||| ||
Db       1863 ATTCAT--ACGAATCATTTCTATTTGT-----
TCTTTTTTTTTTGAGACAGACT------ 1817


Qy        393
CAGCGGCCTCGGCCGCCTCTGGCAGCCCGGGCCCGGGCGAGGGCTCCGCTGGCGGCGAAA 452
              |  ||| | |||| |||| | ||  | || |  | | || | ||| ||  | ||| |
Db       1816 ---CTTACTCTGTCGCC-CAGGCTG-
GAGTGCACTGGCATGATCTCGGCTCACTGCAA-- 1764


Qy        453 AGCGCTCCACCGCCCC-----
TTCGGCCGCAGCCTCGGCCTCTGCCTCAGCCGCGGCGTC 507
              || | |||| | |  |     || ||   |   | ||||||||||| |
Db       1763 ------CCTCTGCCTCACGAGTTAGGT--
CAAGCAATTCTTCTGCCTCAGCCTC------ 1718


Qy        508
GTCGCCCGCGGGGGGCGGCGCCGAGGCGCTGGAGCTGCTGGAGCACTGCGGCGTGTGCAG 567
                               ||||| ||| |   | | | ||| |  |||| |
||
Db       1717 --------------------CCGAGGAGCTAGGATTACAGGT-CCCTGCCAC-----
CA- 1685


Qy        568 AGAGCGCCTGCG---------------ACCCGAGAGGGAGCCCCGCC-
TGCTGCCCTGT 610
                     ||||| |   |    |||| || |  || ||   | ||
Db       1684 ----
TGCCTGAGTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTAGCCAAG 1629


Qy        611 TTGCACTCGGCCTGTAGTGCCTG--CTTAG--
GGCCCGCGGCCCCCGCCGCCGCCAACAG 666
                 || |||| |     | | |||| || || | |||| || || || ||| || |
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Db        1628 CTGGTCTCG------AATTCCTGACCTCAGGTGATCCGC--
CCACCTCAGCCTCCCAAAG 1577

Qy         667 CTCGGGGG--
ACGGCGGGGCGGCGGGCGACGGCACCGTGGTGGACTGTCCCGTGTGCAAG 724
              | ||| ||   |||| | || | ||||  ||   ||||  || | |  |
Db        1576 TGCTGGGATTAC----GGGC-GTGAGCCACGGTGCC----TGGCC--
TCTATTTTTTATT 1528

Qy         725
CAACAGTGCTTCTCCAAAGACATCGTGGAGAATTATTTCATGCGTGATAGTGGCAGCAAG 784
               | |   ||| | |  ||||  |        ||| || ||||  |
Db        1527 TTAAATACCTTTTGCCCTGAAATC---------TATGTCCT-C-
TGATTAT--------- 1488

Qy         785 GCTGCCACCGACGCCCAGGATGCGAACCAGTGCTGCACTAGCTGTGAGGATAATGCC-
CC 843
              | ||| |     ||| ||||||  |   | ||| |    || | |
                                                                        |
Db        1487 --------CAACAC------TGCTTACCAGTTTTATTTTTGTTG-
GTATTTATTTCATTC 1443

Qy         844
AGCCACCAGCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACCTGTGTAGAGGCGCA 903
              | | ||| |||||||       ||          |   | ||    ||| || ||
Db        1442 AATC-CCAGCT-------------CT----ACAACT------
TACCAGTATA-------- 1415

Qy         904 CCAGCGGGTGAAGTACACCAAGGACCA--
TACTGTGCGCTCTACTGGGCCAGCCAAGTCT 961
                            | |  ||| || |||| |   || | | |   |  || |
                                                                        |
Db        1414 --------------AAAATTTGGATCAGTTACT-TAATCT-TGCAGTTTCTTCCT--
TTT 1373

Qy         962
CGGGATGGTGAACGTACTGTCTATTGCAACGTACACAAGCATGAACCCCTTGTGCTGTTT 1021
                        ||||  |   || |||| |||||    | | | ||| ||  ||| |   |
Db        1372 AAAAATGG-AATAATATTATCTAT-----CATATAAA---ATG--
CCCAGTTAACAAATA 1324

Qy        1022
TGTGAGAGCTGTGATACTCTCACCTGCCGAGACTGCCAGCTCAATGCCCACAAGGACCAC 1081
                        ||              ||| ||||| |  |  ||||||
Db        1323 TG------------AACTAACACCTACAATG--TGCCAG-----------------
GCAC 1295

Qy        1082
CAGTACCAGTTCTTAGAGGATGCAGTGAGGAACCAGCGCAAGCTCCTGGCCTCACTGGTG 1141
                        ||        ||| ||| | || | ||    ||  || ||||  || || | |
Db        1294 CA-------TTC-TAGGGAATAGAATGT-
AAATAAGTTCAAGTTCTTGACCTGAATAAGT 1244

Qy        1142 AAGCGCCTTGGGGACAA-
ACATGCAACATTGCAGAAGAGCACCAAGGAGGTTCGCAGCTC 1200
                        |   || || ||  || ||| |    ||        | ||| |       ||
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Db        1243 TTACATTTTAGTGAGAAGACAGACAATAAATCAAT-----AACATG-----
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TC------C 1200

Qy        1201
AATCCGCCAGGTGTCTGACGTACAGAAGCGTGTGCAAGTGGATGTCAAGATGGCCATCCT 1260
           | |  ||||| |                        || |     |  |||||| |
Db        1199 ATTATGCCAGAT----------------AGTTT----- 
TAAATGTCACAA---------- 1171

Qy        1261 GCAGATCATGAAGGAGCTGAATAAGCGGGGCCGTGTGCTGGTCAATGATGCCC----- 
AG 1315
                   |||   | |   ||||| |||  ||       ||| |||   | | | |
||
Db        1170 --AGAAAAAGGGGGAGC--AATCAG------ATAGTGATGG--- 
AAGTTACACTCTAGAG 1124

Qy        1316 AAGGTGACTGAGGGGCAGCAGGAG---CGCCT-GGAG----CGGCAGCACTG-
GACC--- 1363
                | |||          || ||| |  ||   | | | ||||     |  | | || || |
Db        1123 AGGGT------- 
GGACAGAAAAAGTTTCTCTTAGGAGATGACATCTGAACAGAGATCTAA 1071

Qy        1364
ATGACCAAGATCCAGAAGCACCAGGAGCACATTCTGCGCTTTGCCTCTTGGGCTCTGGAG 1423
           |||||  || |   || | |||    | |    | | | |         | ||
|
Db        1070 ATGACTGAGTAC---AAACCCCAATGGAAAA----GTGATTGG----------
TGTGTTG 1028

Qy        1424
AGTGACAACAACACAGCCCTTTTGCTTTCTAAGAAGTTGATCTACTTCCAGCTGCACCGG 1483
           |  ||| ||||||||| | |||
Db        1027 
TGAAACAGCAACACAGCCAGTTTG----------------------------------- 1004

Qy        1484 GCCCTCAAGATGATTGTGGATCCCGTGGAGCCACATGGC-
GAGATGAAGTTTCAGTGGGA 1542
            | |||||        || | |   ||| | ||| ||       |  ||||
Db        1003 ----ACTAGATGA-----------GTAGATCAGAATGACTGAGGTGGG---
ACTGTGG-- 964

Qy        1543
CCTCAATGCCTGGACCAAGAGTGCCGAGGCCTTTGGCAAGATTGTGGCAGAGCGTCCTGG 1602
                ||| |        |      | ||||  | |         | | ||
|||||
Db        963 --TCA--------TCAAAGAGATCAGA----------------GAGGTAG-----
CCTGG 935

Qy        1603 CACTAACTCAACAGGCC-
CTGCACCCATGGCCCCTCCAAGAGCCCCAGGGCCCCTGAGCA 1661
            |         |       ||||| | ||| | | | ||  |              ||||| |||
Db        934 GA---------AGGCCACATCACAGAATGTCCTT------------
TGGGCCTCTGTGTAAG 896

Qy        1662
AGCAGGGCTCTGGCAGCAGCCAGCCCATGGAGGTGCAGGAAGGCTATGGCTTTGGGTCAG 1721
            |||   | | ||  |   |  ||| |       | ||| |||| ||
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Db        895 AGC---GTTTTG--AAAAAACAGTTCT-----GAGCA--AAGGTTA---------
GTCAT 857
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Qy        1722
GAGATGATCCCTACTCAAGTGCAGAGCCCCATGTGTCAGGTGTGAAACGGTCCCGCTCAG 1781
                 ||    |  |||||  | ||  | | |  | |  ||| |   |         |
|
Db        856 TTAACTTGACTTACTCTTTAGAAGGATCACTT-TGGCTATTGAGTGGCAAAC---
AACTG 801


Qy        1782
GTGAGGGCGAGGTGAGCGGCCTTATGCGCAAGGTGCCACGAGTGAGCCTTGAACGCCTGG 1841
             | ||   | ||  |   | |||  | | | ||    ||   |      | | |||
||
Db        800 GAGA---AGTGGTTAGGGG-----AGCACTGTGGGC-------AGGAATAGAA-----
GG 761


Qy        1842
ACCTGGACCTCACAGCTGACAGCCAGCCACCCGTCTTCAAGGTCTTCCCAGGCAGTACCA 1901
             | |||    | ||| |||  |  | |||| |   ||          |  ||   |||||
Db        760 A---GGA----AAAGCAGACTG-GAGCC--------------TAATC-----
CAGTACTT 728


Qy        1902
CTGAGGACTACAACCTTATTGTTATTGAACGTGGCGCTGCCGCTGCAGCTACCGGCCAGC 1961
             | || ||           | ||| ||                          | |   || |
||
Db        727 CAGATGA-----------------------------------
GAAATGACAGATTTGC 705


Qy        1962 CAGGGACTGCG---
CCTGCAGGAACCCCTGGTGCCCCACCCCTGGCTGGCATGGCCATTG 2018
             | || || |||  |   ||| |    ||||| |   |   |  ||   ||| |       |
Db        704 CTGGTACATCATTTCCT------ATCCCT--
TTACTTATAACTTATTGGTGTATTTTTAT 653


Qy        2019 TCAAGGAGGAG------
GAGACGGAGGCTGCCATTGGAGCCCCTCCTACTGCCACTGAGG 2072
             | | | | |     | || ||     ||| ||            | |||
Db        652 TTTAAGTGTAAATTTTTATAAATGAAGCATAATTTGAAG--------------
ATTGA-- 609


Qy        2073
GCCCTGAGACCAAACCTGTGCTTATGGCTCTTGCGGAGGGTCCTGGTGCTGAGGGTCCCC 2132
                  |  |   | |||| |  || ||        || ||||||          ||
||
Db        608 ----TATGTTCGGACTTGTGTTTT---CTATT-------ATCATGGTGTC-----
TCTCC 568


Qy        2133
GCCTGGCCTCACCTAGTGGCAGCACCAGCTCAGGGCTGGAGGTGGTGGCTCCTGAGGGTA 2192
             | | | | ||      | |  | || |             ||| || |
||
Db        567 ACATACCTTTTCC---------CTTTAGTTCT----------------
GCTTCTTATTGTG 532


Qy        2193
CCTCAGCCCCAGGTGGTGCCCGGGAACCCTGGATGACAGTGCCACCATTTGCCGTGTCT 2252
             |     || | ||      ||   ||  ||   || | |     | ||| ||
|||
Db        531 CT----CCTCAAGT---------------CT--ATTTTTGT----TCTTTTCCC---
TCT 500
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Qy      2253 GCCAGAAGCCAGGCGATCTG--
GTTATGTGCAACCAGTGTGAGTTTTGTTTCCACCTGGA 2310
             |           |||   ||| ||   |     ||  | || | |||    ||
|||
Db       499 AC------------TTCTACTGTTTTGAACTGTATATGCTATTTCTATTT-
TGCCAGGA 454

Qy      2311 CTGTCACCTGCCGGCCCTGCAGGATGTACCAGGGGAGGAGTGGAGCTGCTCACTCTGCCA 2370
             || |||    ||||                                      ||| |  |
Db       453 --GTTACC------CCCT------------------------------
TCAATTTTCGT 433

Qy      2371 TGTGCTCCCTGACCTGAAGGAGGAGGATGGCAGCCTCAGCCTGGATGGTGCAGACAGCAC 2430
                ||| ||| ||                    ||| ||||                |
|||
Db       432 TGTACTCTCT--------------------CAGTCTCA-----------------
AACAC 410

Qy      2431 TGGCGTGGTGGCCAAGCTCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGC 2490
               |         ||| |||||| |                       ||| || ||
Db       409 ATAC-------CCATGCTCTCTTC------------------------
TGTCCTTCTCTT 381

Qy      2491 CCTATTCTGTCACGAACCCTGCCGCCCCCTGCATCAGCTGGCTACCGACTCC-
ACCTTCT 2549
             | |||           |   |   | |||||| ||||    || |
||||
Db       380 CATAT---------------CATCTTCTAGAATTAGTT--CTACC----
CCGATTTCT 343

Qy      2550 CCCTGGACCAGCCCGGTGGCACCCTGGATCTGACCCTGATCCGTGCCCGCCTCCAGGAGA 2609
                  ||                     |  | |  | ||| || |  |  | |||
Db       342 ACC------------------            |   | |   | ||| ||  |  | |||
AATTTATTTTATTTCCAATCAGTACATTGATTCAG---- 305

Qy      2610 AGTTGTCACCTCCCTACAGCTCCCCACAGGAGTTTGCCCAGGATGTGGGCCGCATGTTCA 2669
             | || ||| ||     ||  |  | |||   | ||  |   | | || ||| || ||||
Db       304 ATTTATCA-----ATATGTTTTACCA----
ATTTTATCATTTTTTTGGAGGCTTGTT-- 256

Qy      2670 AGCAATTCAACAAGTTAACTGAGGACAAGGCAGACGTGCAGTCCATCATCGGCCTGCAGC 2729
                    ||| | ||| |  |                 | |  ||| |||      |||
Db       255 ----ATTTA--AGGTTCATT-----------TTTCTTGGAGTACAT------
CCTTCAGA 219

Qy      2730 GCTTCTTCGAGACGCGCATGAACGAGGCCTTCGGTGACACCAAGTTCTCTGCTGTGCTGG 2789
                   |||||  |   ||| |||   | | | |  | |   |||  ||
|
Db       218 AGTTCTTTCA-----GCAAGAAC----TCATGGTTGTTA-----ATCTTTG-------
AG 180

Qy      2790
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```
TGGAGCCCCCGCCGATGAGCCTGCCTGGTGCTGGCCTGAGTTCCCAGGAGCTGTCTGGTG 2849
            |                || ||     |  |||||| |       |||||     ||  ||
Db       179 T----------CCTTTG----TTTCTGGTGTTTTAACTTTTTCCC-----
CTCACT---- 143

Qy       2850 GCCCTG-
GTGATGGCCCCTGAGGCTGGAGCCCCCATGGCCAGCCCAGCCTGGCTCTGTTC 2908
             | || || || |     |   | |||||     |||    |   ||| |||| | |
|
Db       142 --CTTGAGTAATAG----TTTAGCTGGG-----CAT-AAAATTTCAGATTGGCAGT-
TAC 96

Qy       2909
TCTGTCCTGTCACCCCATCCCCACTCCCCTGGTGGCCTGACTCCCACTCCCTGGTGGCCC 2968
             | |   | ||        |||| |   | ||        || |||| ||
|
Db        95 TTTTCCTTGG-----------CACTACGAAGATG---------CCGCTCC---
GTTATCT 59

Qy       2969 CATCCC--
CCAGTTCCTCACGATATGGTTTTTACTTCTGTGGATTTAATAAAAAAAACTT 3026
             || |  ||| |  ||| |   ||  ||| ||| | | ||| | |   |  | | |
Db        58 TATTACAGCCAAT--ATTAC--TATTGTT----
CCTTTGTAGGTAATCTCCAGTAGGC-- 9

Qy       3027 CACCAGT 3033
             || ||||
Db          8 CAACAGT 2


Search completed: March  9, 2010, 15:52:07
Job time : 13.4292 secs

                        GenCore version 6.3
              Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:        March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                          (without alignments)
                                          1134.946 Million cell
updates/sec

Title:         US-10-572-905-10
Perfect score: 3243
Sequence:      1 cttttttttttttttttttta.........ttcttaaaagcatgtgtaat 580

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:      834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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                    Listing first 45 summaries

Database :        7335755.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being
printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

                      %
Result              Query
   No.    Score   Match Length DB  ID                       Description

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 c   3    1375    42.4   2120  1  US-10-478-914-64         Sequence 64,
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 c   4    1374    42.4   2437  1  US-10-478-914-61         Sequence 61,
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 c   5   1373.5   42.4   3589  1  US-10-478-914-21         Sequence 21,
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 c   9    1360    41.9   1813  1  US-10-478-914-63         Sequence 63,
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    10   1359.5   41.9   1946  1  US-10-478-914-62         Sequence 62,
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    11    1357    41.8   2120  1  US-10-478-914-64         Sequence 64,
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 c  13    1347    41.5   3210  1  US-10-478-914-4          Sequence 4,
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 c  14   1345.5   41.5   2022  1  US-10-478-914-60         Sequence 60,
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    16   1342.5   41.4   3210  1  US-10-478-914-4          Sequence 4,
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    17   1340.5   41.3   2437  1  US-10-478-914-61         Sequence 61,
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 c  18    1339    41.3    814  1  US-10-478-914-36         Sequence 36,
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 c  20   1335.5   41.2   2083  1  US-10-478-914-3          Sequence 3,
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 c  21    1326    40.9   1946  1  US-10-478-914-62         Sequence 62,
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Appli
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    27   1309   40.4    891  1  US-10-478-914-10       Sequence 10,
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    28   1306   40.3   2336  1  US-10-478-914-57       Sequence 57,
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    32   1296   40.0    781  1  US-10-478-914-55       Sequence 55,
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    33   1295   39.9    779  1  US-10-478-914-53       Sequence 53,
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    35   1293.5 39.9    868  1  US-10-478-914-19       Sequence 19,
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 c  38   1286.5 39.7    839  1  US-10-478-914-16       Sequence 16,
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 c  39   1285.5 39.6    811  1  US-10-478-914-37       Sequence 37,
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 c  40   1281   39.5    909  1  US-10-478-914-66       Sequence 66,
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    41   1278.5 39.4    855  1  US-10-478-914-11       Sequence 11,
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 c  42   1277.5 39.4    749  1  US-10-478-914-29       Sequence 29,
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    43   1277.5 39.4    772  1  US-10-478-914-52       Sequence 52,
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    44   1275.5 39.3    726  1  US-10-478-914-43       Sequence 43,
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    45   1275   39.3    860  1  US-10-478-914-12       Sequence 12,
Appl


                             ALIGNMENTS


RESULT 1
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
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  Query Match            43.2%;  Score 1402.5;  DB 1;  Length 2198;
  Best Local Similarity   39.3%;  Pred. No. 8e-84;
  Matches  398;  Conservative   0;  Mismatches  172;  Indels  443;
Gaps   59;

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TCTTTAGTATATTTATTTG------------ 42
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Db     2163
TTTTTTTTTTTTTTTTTTTATGGTGCCAATTTTAAATAGTTTTATTTAAGACATTGCATTT 2104

Qy       43 --------------------TATAAAGAGTAA------------
ACAAAGTGCATAT--- 67
                            ||||||| | ||            |  ||||||||
Db     2103
TCCACTTACAATACAGTGTTTATAAAGTGCAATGTTATTTCCTTCCCCTGTGCATATGTT 2044

Qy       68 ----------------AGAGTGGCCA--------------
CAGGTT-------------T 84
                             ||| || |||            ||| ||
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Db     2043
CCATATTCAAGTATTGAGAATGCCCAGTAACTTACTATAGCAGCTTAACTTTTTAAAACT 1984

Qy       85 GACACAGA-----------------GACCTT--GGTGATGTA-------GG--
CTATG-A 115
            | ||||||                 | ||||    || | ||       || | |||
Db     1983
GCCACAGAATTTGCTACGAATTTAGGTCCTTCAAATGTTTTAAATGTGTGGAACAATGCT 1924

Qy      116 ACAAATTTAAATGG-------------CAACTTCATTG-------
CTG-----------C 144
              ||| |  |  |||          |  ||||| ||       |||
|
Db     1923
ACATCTACACTTGGTTGGCTTAATCAACCTCTTCAATGGTGGGCCCTGAGGAAGCACCAC 1864

Qy      145 CA----------CTGAACCA----------------------------------
ATCCTG 160
              ||          ||  ||||
|||||
Db     1863
CAGAGGGAGGAGCTCCACCACCAGGAAATCCCCCAGGCATTCCTCCTGGCATGCCTCCTG 1804

Qy      161 AATTTGGGCTCAAC-AGGTGAAAA----GT----
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Qy       AACAATATCAAACGAATACT------ 205
                     |  |   ||  || |  |||||  |     ||     |||  | || | |    | ||
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Qy       206  ----AAA------CAGCATAACAAAAAGATT----TTCAGACTCTTGG-----
         TCATAA- 245
                        |||       |  | | ||    ||||    |  || |  |||      ||||
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Db       1743
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Qy       246  ---AGACCGTAATC--------GTTCACATTG--
         AATCAATGACTAAACATTTTTGATTA 292
                      |  || ||||        || | ||| |  ||||  || ||   |  ||| | ||
Db       1683  ACTTGTCCAGAATCTTCTGTTTGTCCTCATCGTTAATC-
         TTGCCTTGAAGTTTCTCATCT 1625

Qy       293  CC--CAGCTACCTCCA---AGCAAACTGAAAACTGTCTAGTGGATCCT--GAAGTC-
         CAT 344
                      |  ||| | | ||     |  |  |  || ||||| || || || |  || | | |
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Db       1624  TCAACAGTTGCTTTCATGTTGAAGGCATAGGAC--
         TCAAGTGAATTCTTGGATGACACCT 1567

Qy       345  AGTGCCTCT---------------------------AG---CCGGGTCT-----
         TTCAA 368
                      || |||||                          ||    || || |
         |||||
Db       1566
         TGTCCCTCTGCTTCTCATCTTCAGCTTTGTACTTCTCAGCTTCCTGGACCATACGTTCAA 1507

Qy       369  GTG------TTGCACCACAGG-----
         GTGATGATTGATGGTA------------------ 399
                      ||    |||| | |  ||   || | |||| |||
Db       1506  -
         TGTCTTCCTTGCTCAAACGGCCCTTGTCATTAGTGATAGTAATCTTGTTCTCTTTTCCC 1448

Qy       400  ------------AAAACAGGGA-------
         TCAACCCTTGTAGATCGGTGGTAAGTATGGA 440
                      |  | |||| ||          |  ||| |||   ||| ||  ||    ||
Db       1447  GTACTCTTGTCCACAGCAGAGACATTGAGTATACCATTGGC-
         ATCAATGTCAAAAGTGAC 1389

Qy       441  AACCCTCT-AAGAACA-------GTGCAG--CGTATG--TG-
         GTATTCAGACT------- 480
                      |  ||| | |||||        ||||||  ||||| || | |||| |||
Db       1388
         TTCAATCTGAGGAACACCTCGGGGTGCAGGAGGTATGCCTGTGAGTTCAAACTTGCCAAG 1329

Qy       481  --GGTT---------------GCATAC-AGCATTCA-
         AAACCAGT-------------G 507
                      ||||               ||| |   || |||| ||||| |
Db       1328
         CAGGTTGTTATCCTTTGTCATGGCACGCTCGCCTTCATAAACCTGAATAAGCACACCAGG 1269

Qy       508  CTG-------GAATAG-----------CT-----TGCCCCAAAG---
         TGGTAGAGTTAT- 540
                      |||       ||||||            ||      |||     ||  |||| |  |||
```

```
Db      1268
CTGGTTGTCAGAATAGGTAGTGAAGGTCTGTGTCTGCTTGGTAGGAATGGTGGTATTACG 1209

Qy       541 ----AAAAGGATATACATTGAC---------GTTTCTTAAAAGCATGTGTAA 579
             |  |||| |  || ||||        ||||| || | || | | ||
Db      1208 CTTGATGAGGACAGTCA-TGACTCCACCAGCAGTTTC--AATACCAAGGGAAA 1159


RESULT 2
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match             43.1%;  Score 1397;  DB 1;  Length 2198;
  Best Local Similarity   41.7%;  Pred. No. 2e-83;
  Matches  379;  Conservative   0;  Mismatches  191;  Indels  338;
Gaps   55;

Qy         1 CTTTTTTTTTTTTTTTTTTAA--
AGTCTTTAGTATATTTATTTGTATAAAGAGTAAACAA 58
             | | | ||  || |||| || |   |    |    ||| || | ||
||||
Db       464
CAATGTACTTAGAATTATTAATGAGCCAACTGCTGCTGCTATTGCTTACGGCTTAGACAA 523

Qy        59 A-------GTGCATATAGA---
GTGGCCACAGGTTTGACACAGAGA--------------- 94
             |     | ||| | ||| ||| | ||  |||||| | | ||
Db       524 AAAGGTTGGAGCAGAAAGAAACGTG--CTCATCTTTGAC-
CTGGGAGGTGGCACTTTTGA 580

Qy        95 ---------CC------TTGGTGATGTAGGCTATGA--ACAAATTTAAA--TGG---
CAA 132
                         ||       ||| |||| |  || |||   ||| | || |   |||
 ||
Db       581
TGTGTCAATCCTCACTATTGAGGATGGAATCTTTGAGGTCAAGTCTACAGCTGGAGACAC 640

Qy       133 CTTCATTGCTG-------------CCACTG-------AACCAATC-----
CTGAATTTGG 167
             |  | | | ||            | || |      ||||| |     |||| |||
```

```
Db        641
CCACTTGGGTGGAGAAGATTTTGACAACCGAATGGTCAACCATTTTATTGCTGAGTTTAA 700

Qy        168 GCTCAA-------CAGGTGAAAAGT---AACAA------
TATCAAACGAATACTAAACAG 211
              || |||        ||| | ||| |||||     | | ||| | |  ||
|
Db        701 GCGCAAGCATAAGAAGGACATCAGTGAGAACAAGAGAGCTGTAAGACGCCTCC-
GTACTG 759

Qy        212 CATAACAAAAAGATTTTCAGACTCTTGGT-----CATAAAGACC------GTAATCG-
TT 259
                | |  ||   | |  | | | | || |  |    ||   || ||       |  ||||
||
Db        760 CTTGTGAACGTGCTAAGCGTACCCTCTCTTCCAGCACCCAGGCCAGTATTGAGATCGATT 819

Qy        260 CACATT------GAATCAATGACTAAACATTTTTGATTACCC-
AGCTACCTCCAAGCA-A 311
              | | |      ||||| |  ||| || |  |||||||  || ||      | |
|
Db        820 CTCTCTATGAAGGAATCGACTTCTATACCTCC---ATTACCCGTGC--
CCGATTTGAAGA 874

Qy        312 ACTGAAAACTGTCTAG-------------TGGATCCTG------AAGTCCATAG---
TGC 349
              |||||| ||| | |              |||| |  | |    ||| || |
|||
Db        875
ACTGAATGCTGACCTGTTCCGTGGCACCCTGGACCCAGTAGAGAAAGCCCTTCGAGATGC 934

Qy        350 C--TCTAGCCGGGTC----TTTCAAGT----------GTTG--------------
CACCA 379
              |  |||| |  |||     |||| |           ||||
||
Db        935 CAAACTAGACAAGTCACAGATTCATGATATTGTCCTGGTTGGTGGTTCTACTCGTATCCC 994

Qy        380 CAGGGT---GATGATT---------------GATGGTAAA-AACAG-------
GGATCAA 413
              || | |   || ||  ||              |||| ||| ||| |         |
|||||
Db        995 CAAGATTCAGAAGCTTCTCCAAGACTTCTTCAATGGAAAAGAACTGAATAAGAGCATCAA 1054

Qy        414 CCCT--------TGTAGAT-------CGGTGGT-------------
AAGTATGGAAACCC 445
              ||||        ||| | |       | | ||              || |||| ||
Db        1055 CCCTGATGAAGCTGTTGCTTATGGTGCAGCTGTCCAGGCAGCCATCTTGTCTGGAGACAA 1114

Qy        446 -TCTAAGAA----CAG----TGCAGC----GTATG----------------
TGGTATTCA 476
               ||| ||||     ||      ||| ||   | |||              ||||||
|
Db        1115 GTCTGAGAATGTTCAAGATTTGCTGCTCTTGGATGTCACTCCTCTTTCCCTTGGTATTGA 1174

Qy        477 GACTGGT-------------------------TGCATA----
CAGCATTCAAAAC----- 502
```

```
                ||||  |                           || ||    || ||||  | |
Db       1175
AACTGCTGGTGGAGTCATGACTGTCCTCATCAAGCGTAATACCACCATTCCTACCAAGCA 1234


Qy        503 ----CAGTGCTGGAATAGCT----TGCC--CCAAAGTGGT----------
AGAGTTAT-- 540
                ||| ||  | || ||    || |  |||   ||||          || ||||
Db       1235
GACACAGACCTTCACTACCTATTCTGACAACCAGCCTGGTGTGCTTATTCAGGTTTATGA 1294


Qy        541 ----------------AAAAGGATATACA------TTGAC--GTTT---
CTTAAAAGCA 572
                         ||||||||| |||    ||| |  |||| || | |
|||
Db       1295 AGGCGAGCGTGCCATGACAAAGGATA-
ACAACCTGCTTGGCAAGTTTGAACTCACAGGCA 1353


Qy        573 TGTGTAAT 580
              |  |  |  |
Db       1354 TACCTCCT 1361



RESULT 3
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match             42.4%;  Score 1375;  DB 1;  Length 2120;
  Best Local Similarity   40.3%;  Pred. No. 6.5e-82;
  Matches  362;  Conservative   0;  Mismatches  199;  Indels  338;
Gaps   48;

Qy         1
CTTTTTTTTTTTTTTTTTAAAGTCTTTAGTATATTTATTTGTATAAAGAGTAAACAAAG 60
              | |||||||||||||||| |||| |    || ||||||| |||  | |  ||
|
Db      2083 CCTTTTTTTTTTTTTTTTAAAAGAATGAGTTACATTTATTGATAT---
GGTTTGTCATA- 2028


Qy        61 TGCATATAGAGTGGCCACAGGTTTGACACA------GAGACCTT-----
GGTGATGTAGG 109
```

```
                   ||| |    | ||| |||   ||||| |||       ||  |    || || |
|
Db      2027 TGCTTTATAAATGGTCACC-
CTTTGAAACATGTATTATTACTATTTGGGGGAGAGGGGGA 1969

Qy       110 CTAT------------GAACAAATTTAAATGG----------------------
CAACT 134
               || |           | |||| |   |                        |||
Db      1968 CTGTTCATTTTACAGGGGACAAGCAAGACAGGCTCAAGGAGGGAAAGGACAGGCTCAAAG 1909

Qy       135 TCATTGC----TGCCACTGAA---------CCAATC---
CTGAATTTGGGCTCAAC---- 174
               |||| |    ||   ||| |      ||  ||   ||  ||  ||| || ||| |
Db      1908 TCATCACAGTGTGGGGCTGGAATGCAGTTGCCCTTCCTTCTTTCTTTTTGCACATCTTCC 1849

Qy       175 -------
AGGTGAAAAGTAACAATATCAAACGAATACTAAACAGCATAACAAAAAGATTT 227
                  ||||| ||       || | |  | | |||||             |
Db      1848 GTCTCTAGGGTGAGGAGGGGTGCAGGCACAGGCACCCAAGACAGC---------
TGCGGT 1798

Qy       228 TCAGACTC----------TTGGTCATAAAGAC-----------
CGTAATCGTTCAC----A 263
               ||| | |         ||||| |  |||         |   ||| ||| |
|
Db      1797 CCAGCCCCGGCCCCACCTGTGGTCTCAGTGACGCCCCAGAGGCCCCATCTTCCCCACATA 1738

Qy       264 TTGA--------------ATCAATGACTAAACATTTTTGATTA--CCCAG---
CTACCT 303
               |||               |||| | |  || | ||| || |  ||||| |
||||
Db      1737 ATGAGGCTGCTCCATCCTCCTCAAAGCCCAGACCTATTTCATAAGCCCCAGACCCCACCT 1678

Qy       304 ----CCA-AGCAAACTGAAAACTGT-CTAGTGGATCCTGAAGTCCATAG-------
TGCC 350
               ||| ||    |||| | | ||| ||| |                |||| |||
||||
Db      1677 TCACCCAGGGCCCCAAGAGAACAGAGCTGGAGACACTTCTACTCC-
TAGCACTGGATGCC 1619

Qy       351 TCTAGCCGGGTCTTTCAAG-TGTTG---------------
CACCAC-------------- 380
               || ||    || | ||| ||| |               |||| |
Db      1618 -
CTCTCCCCTCCTGTGAAGCTGTAGGTGGGGGGTGGAGGACACCCCTTTAAGGCAGGCTC 1560

Qy       381 --AGGGTGATGA-------------TTGATG---GTAAAAACAGGGAT------CA-
ACC 415
                 ||| ||||        | | |   |||| ||  ||||      ||
|||
Db      1559 GGGGGGCTATGAACTCCAAGACTCCTGGAAGCCAGTAAGAAGTGGGAAGGTAGGCACACC 1500

Qy       416 CTTGTAGAT------------CGGTGGTAAG----------------
TATGGAAACC---- 444
```

```
                ||   |||              | | | ||||              ||||||| ||
Db     1499
ATTTGGGATTTTTATTTTTCACTGAGCTAAGAGAGGAGATTCCAGCTATGGAATCCAGAG 1440

Qy      445 ------CTCTAAGAACAGTGCAGCGTATG---------TGGTATTCAGA------
CTGGT 483
                ||  | ||||||| |||    ||         |||    ||||
||||
Db     1439 AGCGTTCTACAGGAACAGAACAGAAATTGGCTGGGCCCTGG-
GCCCAGAGGAGGCCTGGA 1381

Qy      484 --TGCATACAGCATTCAAAACCAG---------TG-----CTG----------
GAATAG 516
                || ||| |  ||||    ||||         ||     |||           | ||
|
Db     1380 GCCGCTTACTG--
TTCAGTGCCAGCTTCATCCTTGGCACTCTGCCTCTCACACAGCATCG 1323

Qy      517 CTT--GC--------CCCAAAGTGGTAG--------------------
AGTT-------- 538
                ||  ||     |||| ||||| ||                   || |
Db     1322
CTCCGGCTCCCAGAGCCCACAGTGGCAGCCGCTGGAGGCTGTGGCAGCAGCTGCTGCCCT 1263

Qy      539 ----ATAAAAGGATAT-------ACATTGACGTTTCT------
TAAAAGCATGTGTAAT 580
                |  | ||||  |        |  |||| |||       || ||| |  | |
|
Db     1262
GCCCAAGGAGGGATGTGGGCTTGGCTCTGACAGTTCAAGCCAGAAAGAGCCTTAGAAGT 1204


RESULT 4
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match          42.4%;  Score 1374;  DB 1;  Length 2437;
  Best Local Similarity   40.6%;  Pred. No. 1.6e-81;
  Matches  354;  Conservative   0;  Mismatches  216;  Indels  302;
Gaps   44;
```

```
Qy          1 CTTTTTTTTTTTTTTTTTTTAA-AGTCT-------------TTAGTA----
TATTTATTTG 42
              |||||||||||||||||||| | ||              ||||       |   |
|
Db       2415
CTTTTTTTTTTTTTTTTTTTTAAGAATCACAGCAATCCAAGCAAAGTACCTCACTGAGTAGG 2356

Qy         43 TATAAAGA----GTAAACAAAGT------------GCATATAGAGT---
GGCCACAGGTT 83
              ||| ||||      |  | ||| |          ||| ||| |   || | | ||
|
Db       2355
TATCAAGACCCTTCAGGCAGAATTCCATCATTCTCGCAATTAGTGACAGGGACGCTGG-T 2297

Qy         84 TGACACAGAGACCTTG--GTGATG-------------
TAGGCTATGAACAAATTTAAATG 128
              ||    |||   ||| ||| ||          | ||| ||    || || |
|
Db       2296 TGTGGAGGAGTATTTGGAGTGGTGGCAGAAAATTGCATCGGC-
ATTTCCAGCTTGAGTAG 2238

Qy        129 G---CAACTTCATTGCTGC--CACTGAA-CCAA-
TCCTGAATTTGGGCTCAACAGGTGAA 181
              |    | |||| ||| |    | ||| ||||   ||| ||   | |    ||| ||
|
Db       2237 GTCTTATCTTCTTAGCGGATGCTCAGAAGCCAAGGTCTGGATGCAGTCG-
GTCAGTTGCA 2179

Qy        182 AAGTAAC--------AATATCAAACGAATAC----------
TAAACAGCATAACAAAAAG 223
              || ||||      ||| | || | | |           |  |||||| |  |
|
Db       2178 AA-
TAACAGCTCAGGAATGTTAAGTGGCTTCAGGAGTCGTGTGGACAGCACGATTACCTG 2120

Qy        224 ATTTTCAGACT----CTTGGTCATAAAGACCGTAATCG--TTCACAT-
TGAATCAATGAC 276
              || | || |      |   | || ||  | |    |||||| | || |
||||
Db       2119
GGTTCCTGGCTTCAACGATGCCACAAGATCTTTGACCATTTTCACTTCAGAGACTGTGAC 2060

Qy        277 TAAACATTTT--------------------TGATTAC----------CCAGCT-
ACCTC 304
                || |                      |  | ||         || |||
||||
Db       2059
CCCACCTACCACAAAGAGGATCAGGAGGGGGTAGTCACTAGGATGAGGCCGGCTCACCTT 2000

Qy        305 CAAG--CAAACTGAAAACTGTCT----------
AGTGGATCCTGAAGTCCATAGTGC--- 349
              || |  ||  || || |  | |          ||||  ||||||| |   || |
Db       1999
CATGAACATGCTAAATCCAGTTTTAAGGAGATCAGTGAGGCCTGAAGACATGTGTTCAAT 1940

Qy        350 ---------CTCTAGC----CGGG------TCTTTC-------
AAGTGTTGCACCACAGG 383
                       ||| ||    ||||     | ||||      |  || | || ||
||
```

```
Db       1939
ATCAACGGAATCTGGCCTCTCGGGATGAAATATTTCCTCCACAACTTGCTTCAACAATGG 1880

Qy        384 GT-----GATGATTGATGG-------------------
TAAAAAC-------------- 404
                 |     |||| || ||| | || | ||
Db       1879
CTTATAAGATGCCTGGTGGGTATGATTTCCAGGAACATATACAGACTTAAACTGTTTCAG 1820

Qy        405 --------------------------------------AGGGATCAACC------
CTTGT 420
                                              || | ||| ||      ||
|
Db       1819
GAGACTCCGAGCTCCAGCAATATCCCGAAGTGAAGTAAAGAGTTCATCCACGGCAATTTT 1760

Qy        421 AGATCGGTGGTAAGTATG----------GAAACCCTCTAAGAAC---
AGTGCAGCGTATG 467
                 ||| ||| | || |         || ||| | | |     |||||| |
|
Db       1759
GGATTTGTGAAATGTCAGATTAATTGAAGAGTCCCAGTCCGTAATTTTTTGCAGCAAAGG 1700

Qy        468 TGGTATTCAGACTGGTTGCATACAGCA-
TTCAAAACCAGTGCTGGAATAGCT-------- 518
                 || | || | | || | |||| |   | | ||| ||||    | ||
Db       1699 TGACAATC---
CAGATTCCTCACAGAAGACCTGAGCCAATGCTTTCTTGACTTTTTCTTC 1643

Qy        519 TGCCCCAAAGTGGT------------AGAGTT-----ATAAAAGGATATACAT---
TGA- 557
                 ||| || | |||           ||| |     | | || ||| | ||
|||
Db       1642
TGCTTCACACAGGTCTTTGTCTACCGTGAGCTCTCCAGTGACAGAATAAATATATATGAG 1583

Qy        558 ---------CGTTTCTTAAAAGCATGTGTAAT 580
                       | ||| | | || ||||| |
Db       1582 AAGGATCAGCAGTTCCTCAGGGC---TGTAGT 1554


RESULT 5
US-10-478-914-21/c
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
```

```
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match              42.4%;  Score 1373.5;  DB 1;  Length 3589;
  Best Local Similarity    45.5%;  Pred. No. 1.4e-80;
  Matches   338;  Conservative    0;  Mismatches  230;  Indels  175;
Gaps   33;

Qy        1 CTTTTTTTTTTTTTTTTTTTAAAGTCTTTAGTATATTTATTTGTATAAAG---------
AG 51
            ||||||||||||||||||||    ||| | | |||   | || ||
|
Db     3567 CTTTTTTTTTTTTTTTTTTTT-----
TTTTTTTTTTTTGAAAGAATCCAGCAGATATTTAT 3513

Qy       52 TAAACAAAGTGCATATAGAGTGGC---CACAGG-------
TTTGACACAGAGACCT---- 97
            ||| ||| || | | | |  |  |||||||       || || |||    ||
Db     3512
TAAGCAAGATGAAAGTGAAATTACAAACACAGGTCAACTTTTAAACTCAGCACTCTGTTG 3453

Qy       98 ---TGGTGATG---------------TAGG----CTATG-----
AACAAATTTAAATGGC 130
               ||| | ||                |||||    |||||        || || |
||
Db     3452
GAGTGGAGGTGCACGGTCCTTCATCATAGGCAGCCTATGCGAGATGCATCTTAGGAAGGG 3393

Qy      131 AACTTCATTGCTGCCACTGAACCAATCCTGAATTTGGGCT---
CAACAGGTGAAAAGTAA 187
            | ||| | ||||| |  || ||| || || | | |  | || || |
|
Db     3392 AGCTT--
TCGCTGCTCAGAAATCAAAGCTCCATCGGAGGTGTCCTACTGGAGGCATCAGA 3335

Qy      188 CAA-----TATCAAACG--AATACTAAACAGCATAAC--AAAAAGAT-------
TTTCA- 230
            |||       ||    ||| |   ||| ||| || ||    |||| |
||||
Db     3334
CAACAAGCTAAATGACGTTAGGGCTACACAACACAAAGGGGAAAGTTGACAACAATTCAG 3275

Qy      231 -GACTCTTGGTCATAAAGACCGTAATCGTT-CACATTGAATCAATGA---
CTAAACATTT 285
             | || | ||  | |||||| | | |  ||| | ||   |||||| |   ||| |
||||
Db     3274 GGGCTTTGAGTAGTCAAGACAATTAGCTTAGTACTTCAGGTCAATAAATGCTACA-
ATTT 3216

Qy      286 TTGATTACCCAGCT--------ACCTCCAAGC--AAACTGAAAAC-
TGTCTAGT------ 328
            ||  |  |||| |||  |  ||| | ||| |||| | | ||||| |
Db     3215 ATGGGCAATTAGCTGTAAAATGGCCTAC-
AGCTGAAACACTATTCTTGTCTTATTTCACG 3157

Qy      329 GGATCCTGAAGTCCATAGTGCCTCTAGCCGG------------GTCTTT----
CAAGTG- 371
            || || ||  | ||  |||| | |   |||||      || |||||    ||
```

```
 |||
Db       3156
ATTTCATGGAGATTAAAGATAATCTAAACAGATTAAGGCCTTAATCTTTAATCCAGGTGA 3097

Qy       372 --------------------TTGCA-----------
CCACAGGGTGATGATTGATGGTAA 400
                                  |||           | ||| | |   | | |
 ||
Db       3096
GTAATTTTGTTTGTAGTAAAAAGCATAAGAAATAATTCTCAGCATATTATGTAAAAGAAA 3037

Qy       401 AAACAGGGATCAACCCTTG-TAGAT----CGGTGGTAAGTA----
TGGAAACCCTCTAAG 451
             || ||| ||  || |||| | |    |  | |||| ||| |   || | | | || |
Db       3036 AAGCAGTGA--
AAACCTTGTTTGGTCTTCCAGTGGCAAGGATAGTTGAACAACTTCAAGA 2979

Qy       452 AACAGTGCAGCGTATGT-----------
GGTATTCAGACTGGTTGCATACAGCATTCAA 499
             | | | |   || |||             ||||| ||| | |   |    |
 |||
Db       2978
AGCTGAGAGAAGTTTGTTCCCAATTTACAAGTATTTTGACATATAGATAAACAAAAGCAA 2919

Qy       500 AACCAGT---
GCTGGAATAGCTTGCCCCAAAGTGGTAGAGTTATAAAAGGATATACATTG 556
             |||||||   |   || ||  |  || |  | |  | |    |     | |||||
Db       2918
AACCAGTTAAACCTTAAAAGATCATCTGAATAAGATCCTGACAATTATAATTTTACATCC 2859

Qy       557 ACGTTTCTTAAAAGCATGTGTAA 579
             | ||    || |||||  ||| |
Db       2858 ATGTGAATTTCAAGCAATTGTTA 2836


RESULT 6
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match             42.3%;  Score 1371;  DB 1;  Length 2495;
```

```
  Best Local Similarity   39.1%;  Pred. No. 3e-81;
  Matches  381;  Conservative   0;  Mismatches  190;  Indels  404;
Gaps   54;

Qy         1 CTTTTT-------------TTTTTTTTTTTTTAAAGTCTTTAGTATAT----------
TT 37
             | |  ||           | |||||  | |   ||||  |  || ||||
|
Db       220
CATCTTTGGGCAGAACTGGTGTTTTTGTATGACAAGTATGAAGAATATGATAATGCCATA 279

Qy        38 ATTTGTATAAAGAGTAAACAAA---GTGCAT--ATAGAGTGGC----CACAGGT----
TT 84
             |||  || | || | | ||    |||  |  ||| |||    || || |
||
Db       280
ATTACCATGATGAATCATCCAACTGATGCCTGGAAAGAAGGGCAATTCAAAGATATCATT 339

Qy        85 GACACAGAGACCT---TGGTGATGTA------GGCTAT---
GAACAAATTTAAATGGCAA 132
             || |  ||   |||  | ||       || || | | || |||
|
Db       340
ACCAAGGTTGCCAATGTGGAACTATACTACAGAGCAATACAGTTCTACTTAGAATTCAAG 399

Qy       133 CTTC-------------ATTGCTG------------CCACTG--------AAC-----
CA 154
             | ||           ||||||       |||| |         ||
||
Db       400
CCTCTGTTGTTAAATGATTTGCTGATGGTGCTGTCTCCACGGTTGGATCACACTCGTGCA 459

Qy       155 ATCCTGAATTTGGGC--------------TCAACAGGTGAAA--------------
AGT- 185
               ||    |||| ||              | || ||||||
|||
Db       460
GTCAATTATTTCAGCAAGGTTAAACAGCTACCACTGGTGAAACCGTATTTGCGTTCAGTT 519

Qy       186 ---AACAATATCA-----------AACGAAT-ACTAAACAG------CATAAC--
AAAAA 222
                |||  ||| ||           || |||| | | ||||     || ||   ||
||
Db       520
CAGAACCATAACAACAAATCTGTGAATGAATCATTGAACAATCTTTTTATTACAGAAGAA 579

Qy       223 GATTTTCAGACTCT-TGGTCATAAAGA-------
CCGTAATCGTTCACATTGAATCAATG 274
             |||| |||| ||||  |  ||| || |         |  | | || ||| |    ||
|
Db       580
GATTATCAGGCTCTGCGAACATCAATAGATGCTTATGACAACTTTGACAATATCTCGCTT 639

Qy       275 ACTAAACATTT-----------------TTGATTACC---------CAGC-
TACCTC--C 305
             || | | |||                ||||  | |         |  || || |||
|
Db       640
GCTCAGCGTTTGGAAAAACATGAACTCATTGAGTTCAGGAGAATTGCTGCTTATCTCTTC 699
```

```
Qy         306 AA--GCAA-----ACTGAAAA------------
CTGT----------------------- 323
               || ||||     ||| |||            ||||
Db         700
AAAGGCAACAATCGCTGGAAACAGAGTGTAGAGCTGTGCAAGAAAGACAGCCTTTACAAG 759


Qy         324 ----------------CTAGTGGATC-----------------CTGAAG---TCC-
ATAG 346
                               ||  || |||              |||||| |||
||
Db         760
GATGCAATGCAGTATGCTTCTGAATCTAAAGATACTGAATGGCTGAAGAACTCCTGCAG 819


Qy         347 TGCCTCTAGCCGG--------------------------GTCT-
TTCAAGTGTTGC--- 375
               || | | ||| ||                        |||| || |  |||| |
Db         820
TGGTTTTTGCAGGAAGAAAAAAGAGAGTGCTTTGGAGCTTGTCTGTTTACCTGTTACGAT 879


Qy         376 -------ACCA---------CAGGGTGATGATTGATGG--
TAAAAACAGGGA------- 409
                      |||          |   |    || || ||   || | || |||
Db         880
CTTTTAAGGCCAGATGTCGTCCTAGAAACTGCATGGAGGCACAATATCATGGATTTTGCC 939


Qy         410 ----------TCAACC----CTTGTAG-----------
ATCGGTGGTAAGTATGGAAAC- 443
                         ||| ||   | || ||         |  ||||| |   | ||
Db         940
ATGCCCTATTTCATCCAGGTCATGAAGGAGTACTTGACAAAGGTGGATAAATTAGATGCT 999


Qy         444 ------CCTCTAAGA-----------------ACAGTG---CAGC-----
GTATGTGGT 471
                     | || |||                |||| |   || |     || |
Db         1000
TCAGAATCACTGAGAAAAGAAGAAGAACAAGCTACAGAGACACAACCCATTGTTTATGG- 1058


Qy         472 ATTCAGAC----
TGGTTGCATACAGCATTCAAAACCAGTGCTGGAATAGCTTGCCCCA-- 525
               |||| |    | | ||| ||||||   | |||||| ||   | || |||||
Db         1059 --TCAGCCCCAGTTGATGCTGACAGCA---GGACCCAGTGTTGCCGTCCCT--
CCCCAGG 1111


Qy         526 ----AAGTGG-TAGAGTTATA-----------
AAAGGATATACATTGACGTTTCTT---- 565
                   ||| ||  ||||||      | ||| |  || | | |  |||
Db         1112 CACCTTTTGGTTATGGTTATACCGCACCACCGTATGGACAGCCACAGCC-
TGGCTTTGGG 1170


Qy         566 AAAAGCATGTGTAAT 580
               | ||||||||  ||
Db         1171 TACAGCATGTGAGAT 1185


RESULT 7
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
```

  Query Match   42.2%; Score 1367; DB 1; Length 2495;
  Best Local Similarity 41.8%; Pred. No. 5.9e-81;
  Matches 365; Conservative   0; Mismatches 211; Indels 298;
Gaps   45;

Qy   1
CTTTTTTTTTTTTTTTTTTTAAAGTCTTTAGTATATTT----------------------- 37
              ||||||||||||||||| | || || | |||||||
Db   2459 CTTTTTTTTTTTTTTTTTTTTACATGT-
TTAAATATATTTTATTTCAAGTTAATATAACAGCC 2401

Qy   38 ---ATTTGT---ATAAAGAG--------------TAAACAAAGTG-
CATATAG------- 69
                ||||||| | ||| | || | ||| || | |
Db   2400
ATGATTTGTTCATTTAAGTGAAATGCTTCGATAAAAACCCCGGTGTCACTTGGTTAAAAT 2341

Qy   70 AGTGGCCACAGGTT--------TGACAC------
AGAGACCTTGGTGATGTAGGCT---- 111
              | ||| |||| || | ||| || ||| |||| | ||| ||
Db   2340
ATTGGAGACAGATTAAATGTTAAGCCACTATAGTAGTGACTCTGGTTCTTTAGACTATTG 2281

Qy   112 -ATGAACAAATTTAAATGGCAACT-------TCATTG-----CTGC----------
CAC- 147
               ||| || |||| | || ||||| |||
|||
Db   2280
CATGTACCTTGTTAATGAACTACAGGAATGCACATTGATATAATGCACAATGTCTTCACA 2221

Qy   148 TGAACCAATCCTGA----------ATTTGGGCTCAACAGGTG-AAAAGTA-
ACAATATCA 195
              || |||||||| | || || | || |||| ||||||
|
Db   2220
TGTCTCAATCCTCATTCCTCTTCCTTTCATGCCTCCCTAATGCCTCAGTATCCAATATAA 2161

Qy   196 A---ACGAATACTAAACAGCATAAC---------------
AAAAAGATTTTCAGACTCTT 237
              | || || |||| | | | || | | |||| |

```
                |||
       Db        2160 AACTACAAAAACTACTGTTCTTTTCGTTTGAGTGGTATTTAATTAAAACTTCA-
       ATTCTA 2102

       Qy         238 GGTCAT----AAAGACC-GTAAT---CGTTCACATTGAAT------------
       CAATGACT 277
                        || ||    | || || ||||||    || |  |||| |            ||
                |||
       Db        2101 TGTTATTTCCACAGTCCAGTAATTTATTTTAAATTTGAGTAATTTCAAATTCCACAAACA 2042

       Qy         278 AAAC-------------ATTTTTGATT------------------ACCCAG----
       CT-- 299
                        ||||             ||||| ||                  || |||   ||
                |||
       Db        2041 AAACTGAAGAACAGCAATATTTTGTTTGAATTTCTCTCTTCTGTACACTCAGTGATCTAA 1982

       Qy         300 ---ACCTC-----CAAGCAAACTGAAAACT--------
       GTCTAGT-------------- 328
                          ||| |   | || || ||| ||        |  ||||
       Db        1981 AACACCACAATATCCAACATACACAAACCTCAGGGAAGGGTTAGTAAACACACACAAGAT 1922

       Qy         329 --GGATCCTGAAGTCCATAGTGCCT--
       CTAGCCGGGTCTTTCAAGTGTTGCAC------- 377
                         | ||| ||   | | |  |||   | |  |||| || |     ||||
       Db        1921 TGGAATCATGGTGCTCTTTGCTCCTGAATGGAATGGTCCCACAGAAAAAGCACAGGATAC 1862

       Qy         378 --CACAGGGTGATGATTGATGGTAAAAA--CAGGGATCAACCCTTG-TAG------
       ATCG 426
                         ||||   | |    || || |  || || ||| | | |||           |
       Db        1861 AGCACAACATAAGGGCACCTGTTACATATGAAGTGAGCAAAACATACTAGCATTTTCTAT 1802

       Qy         427 GTGGTAAGTATGGAAACCCTCTAAGAACAGTG--------
       CAGCGTATGTGGTATTCAGA 478
                        || |  | ||||||| |  ||   || |         ||  || |   |
                |||||
       Db        1801 ATGCATAATGGGGAAACCTGCATAGGTTAGAGGGCCTTTTACGCTCATTTAAAAATCAGG 1742

       Qy         479 CTGGTTGCATACAGCATT------------------CA----AAACCA---------
       GTG 507
                        |  |||| |  | |||||                 ||    || |||
                |||
       Db        1741 CAAGTTGTCTGTAACATTTTTCAATAATCTGGGAAGCACTGCAATCCAGTGTACGATGTG 1682

       Qy         508 CTGGAATAG------CTT-----GCCC---CAAAGTGGTAGAGTTATA----
       AAAGGATA 549
                        || || |||      |||     || |    | ||  | | ||| ||||   | |
                |
       Db        1681 CT-
       GATTAGTGTTGTCTTTGTTGGCACTGACAGTCTTGCATGGTCATATGCCAGTGTTTT 1623

       Qy         550 TACATTGACGTTTCTT----AAAAGCATGTGTAA 579
                        | | || | |||||||    ||| || | |||
       Db        1622 TGCTTTAGCTTTTCTTTGAATAAAACAGATTTAA 1589
```

```
RESULT 8
US-10-478-914-60
; Sequence 60, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 2022
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-60

  Query Match          42.1%;  Score 1366.5;  DB 1;  Length 2022;
  Best Local Similarity   37.9%;  Pred. No. 2.1e-81;
  Matches  369;  Conservative    0;  Mismatches  191;  Indels  413;
Gaps   45;


Qy        1 CTTTTTTTTTTTT------------------------
TTTTTTAAAGTC----------- 25
            ||  || ||| ||                        ||||||||||||
Db      743
CTAATTATTTATTTATATTGAAATAATTGATTTAACATTTTTTAAAGTCAAAGTTCTGGA 802

Qy       26 ------TT------TAGTATATTTATTT------------
GTATAAAGAGTAAACAAAGT 61
                  ||      ||||| |||| ||        || ||||| |  |  |
|
Db      803
GATAATTTGCCCAGTAGTACATTTTATTGCTGCAAGCAAAGTTTAAAGTGATATAATTGA 862


Qy       62 GCATATAGAGTGGCC-ACAGGTT----------TGAC----
ACA---------------- 90
            || | || | || ||| ||| |||          || |   |||
Db      863 GCC-
AAAGTATTGCTGACAAGTTATTTCAAGCATGTCATTTACATTACTTTGTTATTTGT 921


Qy       91 --GAGACCTTGGTG------
ATGTAGGCTATGAACAAATTTAAATGGCAACTTC------ 136
              | ||| |||| ||         || |||| ||| | |||| ||||| || |
Db      922 GTGTGACGCAGGTGGAAGCTATAAAGGCCATGTGGATATTT---
TGGCACCTACTGTTCA 978


Qy      137 ----ATTGCTGCCACTGAAC---------------
CAATCCTGAATTTGGGCT------- 170
                | ||||||  ||||                |  ||||| || | ||||
Db      979
AGAGTTGGCTGCCCTTGAAAAGGAGGCGCAGACATCTTTCCTGCATCTTGGCTACCTTCC 1038
```

```
Qy        171 ----CAACAG----------------------------------------
GTGAAAAGTA 186
                  || | |                              | | || |
                                                                    |
Db       1039
TAACCAGCTGTTCAGAACCTTCTGATTTTTACATTTACTGAATAAGATTTGAGTAATGAA 1098

Qy        187 A-----------------CAATATCA----
AACGAATACTAAACAGCA----------T 214
                  |                  | | | | ||    ||   | | || |||||
                                                                    |
Db       1099
AGTCTGTAGTCTTAAAACTCTAAAACAGTTGTACTGCTTCCAAGCAGCAGTATTTATAGT 1158

Qy        215 AACAAAAAGATTTT----CAGACTCTTG---
GTCATAAAGACCGTAATCGT--------- 258
                  |||   ||| | || |    | |||||||   |||| | | || || || |
Db       1159 AAC-GTAAGCTATTAATGCTAACTCTTGCATGTCA-
AGAAACATTAGTCTTAGGAATTCT 1216

Qy        259 -------------TCACATTGAA-------
TCAATGACTAAACATTTTTGA--------- 289
                          || || ||||        |  ||||||| |  ||  |||
Db       1217
TCAAAAAATGGCATCCCAATGAAAATAAATTTGATGACTATATTTTCATGAAGGTTTGTG 1276

Qy        290 -------------TTACCCAGCTACCTCCAAGCAA-------
ACTGAAAACTGTCTAGTG 329
                          |||   | | ||    | |          | | ||| || |
Db       1277
TCTTATTTTAAAGTTATATTGATATATTTTTTCTATTTCTTTTTTAAGAACAGTATG--G 1334

Qy        330 GATCCTGAAGTCCA----------TAGTGCCTCTAGCCG-
GGTCTTTCAAGTGTTGCACC 378
                  | | |||||| |            ||| ||| | || |        || |
                                                                    |||
Db       1335 GCTTATGAAGTAGAATTTATGGGTATGTGAATCTGGCAGAGGACTTAC----
GTGGAACC 1390

Qy        379 ACAGGG----------------------------------------------------
TGA 387
                      || ||
                                                                    |||
Db       1391
ACTCGGGAATATTCTAAAAGTAGGTTTTCAGATGGCTAAGGTTGTCTATGTGTATATTGA 1450

Qy        388 TGATTGA-------TGGTAAAAACAGGGA---TC----AACCC----
TTGTAGATCGG-- 427
                  | | ||      ||| |  ||||| || |  |  ||| | ||| |
Db       1451
AGCTAGAGGAGAGTTGGAACATGAAGGGAAATTCGATGATCCCAATGTAGAAGAACTGCT 1510

Qy        428 TGGTAAGTATGGAAACC------CTCTAAG---------
AACAGTGCAGCGTATGTGGTA 472
                  |||| ||| ||||| |         | | ||          || | || | | | | ||
Db       1511
TGGTTAGTTTGGAAGCATGGAAGTTTTGAGGGAGTCAGTAAAGGTTCTGTATCTAAGGAC 1570
```

```
Qy         473 TTCAGACTGGT-------TGC--------ATACAGC----
ATTCAAAACCAGTGCT---- 509
                 |   ||||| |         |||         || | |     || |  ||| ||||
Db        1571
TGATGACTGATGTGATGGTGCCAGTGAAGATGTATCTTCTTTTTATGACCCTTGCTTTCC 1630


Qy         510 -GGAATAGCTTGCCCC--
AAAGTGGTAGAGTTATAAAAGGATATACATTGACGTTTCTTA 566
                 |     || | |||   ||||||    ||    |||   | | | | |  ||
|||||
Db        1631 AGATGATGCATACCCATTAAAGT-----AGAACTAATCTGCTGTCCCT--
ACAGGTCTTA 1683


Qy         567 AAAGCATGTGTAA 579
                 ||| ||   |||
Db        1684 AAATCAAACTTAA 1696


RESULT 9
US-10-478-914-63/c
; Sequence 63, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 1813
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-63

  Query Match             41.9%;  Score 1360;  DB 1;  Length 1813;
  Best Local Similarity   36.6%;  Pred. No. 3.4e-81;
  Matches   389;  Conservative    0;  Mismatches  187;  Indels  486;
Gaps   53;

Qy           1
CTTTTTTTTTTTTTTTTT----------------------------------------- 18
                 |||||||||||||||||||
Db        1791
CTTTTTTTTTTTTTTTTTTGGGGAGAACACTTTGCTTTGGCTATAAAAAAGGAGTTTCTGA 1732


Qy          19 ---------------------TAAAGTCT-------TTAGT---------ATATT-
TATT 40
                                     |  || ||     |||||         |||| |
||
Db        1731
AAATATACAATATGAGTACTATGGAGACTACTAGGATTAGTGCTGAATCCTTATTATTTT 1672
```

```
Qy         41 TGTATAAAG-----------AGTA----
AACAAAGTG---------------------- 62
              ||| || ||           |||    |||| ||||
Db     1671
TGTCTACAGTAAGGTGGGTAAGGTAATCCAACACAGTGGCAGCCAGCCAGCCATACAGTT 1612


Qy         63 --------------
CATATAGAGTGGC--------------------------------- 75
                               |||| | | || |
Db     1611
GTTAATTCTTATCACATACAAAATGTCTTTAGCATGGAATAAAACATTATACATTTCTAA 1552


Qy         76 -CACAGG--------TTTG--------------
ACACAGAGACCTTGGTGATGTAGGC-- 110
               | ||||        ||||           |||||| |  ||    || ||
Db     1551
GCTCAGGCTGAATCCTTTGCAAATCTTTTAAAAGCACAGAAAAATTAAGTATTTAAAATG 1492


Qy        111 TATGAACAAATT--------------------------TAAATGGCA-ACTTCA--
TTG 140
                | || ||||||                          | |||| || ||| ||
||
Db     1491
TTTGGACAAATATTTTCTCAAATAAGAAAATCTGAACTCTGAATGTCATACTCCAATTTA 1432


Qy        141 CTGCC---------ACTGAACCAAT---CCTG----
AATTTGGGCT------------- 170
               || ||        ||| || |||   || |    | |||  |||
Db     1431
CTACCCACAACACTAACTAAAATAATATACCAGCAGCATTTTTAGCTATATGATCAGAAT 1372


Qy        171 -----CA--ACAGGTGAAAAGTAACAATA---------
TCAAACGAATACT--------- 205
                    || ||| || || | ||| |||        || | |     ||
Db     1371
ACTTGCATTACACTTGTAATGGAACCATACACATATTCTCTATCTCTCTCTGCCATAGAT 1312


Qy        206 --AAACAGCATAACAAAAA----GATTTTCAG----------------ACTC--
TTGGTC 241
                 |  | |||||||| |||    | | ||| |                ||||    |
||
Db     1311
AAATGCTGCATAACTTAAATACTGCTCTTCTGTGCTATTAATACAGCAACTCAAATATTC 1252


Qy        242 ATAAAGACCGTAATC--------------------GTTCACATT------
GAATCAATG 274
               | |||| |  |||| |                    ||| |  |     | ||||
|
Db     1251
AAAAACATAGTAAGCTGCAACCTGTGAATCTAGTATTTTCCCTCTTTTTACAACTCAAAG 1192


Qy        275 ACTAAACAT---TTTTGATTACC---CAGC----------------
TACCTCCAAGCAAAC 313
               | |  | |||   |  ||| ||||    ||||              | ||  |||| ||
|
Db     1191 GCATCCCATAGATGATGGTTACAAATCAGCACAGGATTAAAATAGTGCCCCCAA-
CACAT 1133


Qy        314 TGAAAACTG--TCTAGTGGAT---CCTGAAGT--CCATAGTGCCT---
CTAGCCGGGTCT 363
```

```
              |  |||  |||  |||  ||| |    ||  ||||   |||   | ||   || | | |
||
Db      1132 TAAAAGCTGACTCTGCTGGGTGTGGCTTAAGTAAACATCTCGTCTCAACTGGACAG--
CT 1075

Qy       364 TTCAAGTGTTGCA-CCACAGG-----------GTGA--------------
TGATT---- 392
              |  |||    ||  ||||||           ||||             || ||
Db      1074 ACCCAGTAACACAGCCACAGAAACCGAAAATATGTGAGTACATAAGTAAAGTGCTTCTTT 1015

Qy       393 -------GATGGTAAA-------AACAGGGATCAACC---
CTTGTAGATCGGTGGTAAGT 435
                 |  |||  |||         ||  |  ||| |    ||||  |  ||   | ||
 |
Db      1014
TGGAGGGGGTGGGAAACTAAGCCTCCATGTTTCATCTATGCTTGATGCTCAATTGTTTCT 955

Qy       436 ATGGAAACCCTCTAAGA--ACAGTGC--AGCGTATGTG-------
GTATTCA-------- 476
                |         |  ||| | |  |||||||   |  ||    ||      |  ||||
Db       954
ATACTGTACTTCTGAAATGACAGTGCCTTGAGTCAATGCTGAACATTGTTCAAGAAACCA 895

Qy       477 --GACTGG----------TTG-CATACAGCAT----------------------
TCAAAA 501
                 |||  |         |||  |  ||| |  |                     || |
 |
Db       894
AGGACAGAGAAATGTTACTTGTCCTACTTCCTCTCCTTTATTTTATGCTCCCTGTCTACA 835

Qy       502 CCAGTGCTG-----------GAATAGCTTGCCCCAAAGTGGTAG--
AGTTATAAAAGG-- 546
                 ||  || |               |  ||||  |   |||| ||||   |  ||| |   | |
Db       834
ACATGGCCGTTCTTACAAACATTTTGCTTTCATAAAAGAGGTAATCATTTAAATCAAGAC 775

Qy       547 -ATATACATTG-------ACGTTTCTTAAAAG-CATGTGTAA 579
                || | || ||        ||  |  | | ||| |||    |||
Db       774 TATGTGCAATGCGAACTCACACTGCATTACAGTCATCAATAA 733
```

```
; SEQ ID NO 62
;    LENGTH: 1946
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-62

   Query Match            41.9%;  Score 1359.5;  DB 1;  Length 1946;
   Best Local Similarity  43.2%;  Pred. No. 5.4e-81;
   Matches  369;  Conservative   0;  Mismatches  195;  Indels  291;
Gaps   55;


Qy         1 CTTTT-----TTTTTTTTTTTTTTAAAGTCTTTAGT--ATATTT--------
ATTTGTAT 45
             ||||       ||| ||| | | ||  | |||||| | ||||        | |||
             |
Db       424
CTTTACACTGTTTGCTTTCTCTGGAACATTTTTAGTTAAAATTTCATAATGCAGTTGCAC 483


Qy        46 A-AAGAGTAAACAAAG-----TGCATATAGAGT---
GGCCACAGGTTT------------ 84
             | ||  | | ||| ||    ||||||     ||      || |  ||||
             |
Db       484
ACAAATGAAGACACAGATGGCTGCATCCTCCGTCTCTTCCCCTCGTTTACAGGAAGCTGC 543


Qy        85 GACACAGAG---------------ACCTTGGTGATGTAGGCTATGA------------
AC 117
             |   ||| |               |||   || |   ||||    ||
             |
Db       544
GGATCAGGGAGGGGTGTTAGGGTTACCCACATGGTAAGGGCAGAGACAAGAGGGGACCCC 603


Qy       118 AAATTTAAATG--GCAACT--TCATTGCTG----C---------CAC-
TGAACCAATCCT 159
             |   ||| |||  ||| |  | ||||||||||    |          ||| | | ||
             |||
Db       604
AGTTTTCCATGCTGCACATGGTCATTGCTGGGGGACTGAGGTTTGCACATCACCCTGCCCT 663


Qy       160 GAATTTGGGCTCAACAGGTGA-AAAGT---------
AACAATATCAAACGAATACTAAAC 209
             |  ||    ||| | || || |||||          | ||| |  | | |    | ||
             ||
Db       664 G--
TTCTCCCTCCGCTGGGGAGAAAGTCAGGGATGGAGCAAGCTGCAGCATCTTCTGAA- 720


Qy       210 AGCATAACAAAAAGATTTTC-AGACTCTTGGT----CATAAAGACC------------
GT 252
                    || ||||| |  |   |  | ||| |||     | | ||| ||
             ||
Db       721 -----
AAAGAAAAGGTGGCCTTGTCTCCAGGTCTCCCCTCAAGTCCCACCTTCCCATAGT 775


Qy       253 AATCGTTCAC----ATTGA-----ATCAATGACTAAAC-----
ATTT------------- 285
                || |||     |||| |      || |  ||     |    |||| ||
Db       776
TTTCTGCCACTTCTCTTGATTTTCCTCTCTGCCACTTCTCTTGATTTTCCTCTCTGCCAC 835


Qy       286 -----TTGA-TTACC------CAGCTAC---------------CTCC--
AAGCAAACTGA 316
```

```
                ||||  ||  ||       |||||  |                  ||||  |  |||  |||
Db       836
TTCTCTTGATTTTCCTCTCTGCAGCTGCTTTGAGGTGGGTTTTCTCCAGATGCACACTTT 895

Qy       317 AAACTG-------------TCTAGTGGA---------------
TCCTGAAG-------- 339
                ||||               |||  ||  ||               ||  |  |||
Db       896
CCCCTGCTTTGCGTCCTTATTCTGGTAGAAGCACAATCTAAAGCTCATTAAGGGAACTAA 955

Qy       340 TCCAT--AGTGC----CTCTAGC----CGGGTCT-TTCAAGTGTTGCACCA----
CAGGG 384
                ||  ||    ||||    |  |||||   |  |  |||     ||    |  ||||  |     ||
|
Db       956
TCAATTCTGTGCATGGCGCTAGCTCAGCAGATCACCACACAGGCAGCACTATTAGCAAGT 1015

Qy       385 TGATGATTG----ATGGTAAAAACAGGGATC-------AACCCTTGTAGATC--
GGT--- 428
                |  ||  ||      ||||  |     ||  |  |||       |  |||  ||||||  |   ||
Db       1016
CGGTGCTTAACACATGGCACTTCCATGAATCGATATGGAGCCCGTGTAGAACAAGGCATG 1075

Qy       429 GGTAAGTATGGAAACCCTCTAAG---AACAG-TGC-------AGCGTATGTGGTA--
TTC 475
                |||   |  |       |||  ||||    |||  |  |||       |  |  |   |  ||
|||
Db       1076
GGTTTTTTCTCTTCCCATTAAGAAAAACTGATGCCAAAAATAACTTCTCAGATATTTTC 1135

Qy       476 A-----GAC-----TGGTTGCATACAGCATT--------
CAAAACCAGTGCTGGAATAGC 517
                |       |||    ||   |  |  ||||||||         |||||  ||  ||||   |  |
||
Db       1136 AAGTATGACTTTTATGAAGGGAAAAAGCATTTTTGTTTGCAAAATCA-TGCTTCAGT-
GC 1193

Qy       518 TTGCCCCAAAGTGGTAGAGTTATAAAAGGATATA------CATTGAC-
GTTTCTTAAA-- 568
                |||     |||  ||  ||  ||  |  |   |  ||         |    |  |  ||   |||  ||
Db       1194 AGGCC----AGTTGT-
GAATTGTGATGGCTTTTATTTCTCCTGGGGCTGTAACTTTAAGG 1248

Qy       569 ----AGCATGTGTAA 579
                ||  ||  ||  ||
Db       1249 GTTTAGAATTTGGAA 1263


RESULT 11
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
```

  Query Match   41.8%; Score 1357; DB 1; Length 2120;
  Best Local Similarity   36.6%; Pred. No. 1.3e-80;
  Matches 345; Conservative   0; Mismatches 217; Indels 380;
Gaps   42;

Qy   1 CTTTTTTTTTTTT------------
TTTTTTAAAGTCTTTAGTATATTTATTTGTATAAA 48
             |||| || || || | | | || ||| | | | || ||||
||
Db   1130 CTTTATTGTTCTTGAAAGCCCCTGCTCTCTCTGAGCCTT--
ATTTCATCATCTGTAAAAT 1187

Qy   49 GAG--TAAACAAAGTG-CATATAGAGTGGCCACAGGTTTGAC---
ACAGAGACCTTGGTG 102
             | | | | | || | | || | | || |||| ||||| |
Db   1188 GGGAATGTCCTGAATGACTTCTAAGGCTCTTTCTGGCTTGAACTGTCAGAGCC------- 1240

Qy   103 ATGTAGGCTATGAACAAATTT--
AAATGGCAACTTCATTGCTGCCACTGAACCAATC--C 158
             || | | | || | || | ||||||| | | | |
|
Db   1241 ---AAGCCCACATCCCTCCTTGGGCAGGGCAGCAGC--
TGCTGCCACAGCCTCCAGCGGC 1295

Qy   159 TG--AATTTGGGCTC----AACAGGT-----------------GAAAAGTAACAA-
TATC 194
             || | | ||||||| | | || | | ||| |||
||
Db   1296 TGCCACTGTGGGCTCTGGGAGCCGGAGCGATGCTGTGTGTGAGAGGCAGAGTGCCAAGGATG 1355

Qy   195 AAACGAATACTAAACAG--------------------------
CATAACAAAAGATTT 227
             || | ||| ||||| || | | |
||
Db   1356 AAGCTGGCACTGAACAGTAAGCGGCTCCAGGCCTCCTCTGGGCCCAGGGCCCAGCCAATT 1415

Qy   228 TCAGACTCTTGGTCATAAAGACCGTAATC--GTTCACATT----GAATC-
AATGACTAAA 280
             || | || || || | ||| || || | | ||| ||||| | ||
|
Db   1416 TGTTCCTGTAGAACGCTCTCTGGATTCCATAGCTGGAATCTCCTCTCTTAG 1473

Qy   281 C-------ATTTTTGATTACCCAGC-----TACCTCCAAGCAAACTGAAAACTG---
TCT 325

```
                 |       |   |   ||||      | |||   |  |||    ||||
Db      1474
CTCAGTGAAAAATAAAAATCCCAAATGGTGTGCCTACCTTCCCACTTCTTACTGGCTTCC 1533

Qy       326 AGTGGATCCTGAAGTCCATAGTGCCTCTAGCC----------
GGGT-------------- 361
                 ||  ||  ||  ||| |||||  || | |||||       ||||
Db      1534 AG-
GAGTCTTGGAGTTCATAGCCCCCGAGCCTGCCTTAAAGGGGTGTCCTCCACCCCCC 1592

Qy       362 --------CTT--------------------TCAAGTGTT-------------------
GC 375
                      |||               || |||| |
Db      1593
ACCTACAGCTTCACAGGAGGGGAGAGGGCATCCAGTGCTAGGAGTAGAAGTGTCTCCAGC 1652

Qy       376 AC-------------CACAGGGTGATGAT------
TGATGGTAAAAACAGGGATCAACCC 416
                   |       |  | |||||| |  |      || | |||  | |  | ||
Db      1653
TCTGTTCTCTTGGGGCCCTGGGTGAAGGTGGGGTCTGGGGCTTATGAAATAGGTCTGGGC 1712

Qy       417 TTGTAGATCGGTGG-----------TAAGTATGGAA------ACC----------
CTCTA 449
                  ||  ||   | |||         || ||  ||||      ||          |
Db      1713
TTTGAGGAGGATGGAGCAGCCTCATTATGTGGGGAAGATGGGGCCTCTGGGGCGTCACTG 1772

Qy       450 AGAACA---GT----------------GCAGC----------
GTATGTG---------G 470
                 ||| ||  ||             |||||          |  ||||
Db      1773
AGACCACAGGTGGGGCCGGGGCTGGACCGGCAGCTGTCTTGGGTGCCTGTGCCTGCACCCC 1832

Qy       471 TATTCAGACTGGT-----------TGCA--------------------
TACAGCATTCAAA 500
                 |  |||  || |           ||||                    || ||||||
Db      1833
TCCTCACCCTAGAGACGGAAGATGTGCAAAAAGAAAGAAGGAAGGGCAACTGCATTCCAG 1892

Qy       501 ACCAGTGCTG------------------------------------
GAATAGCTTG--- 520
                  ||   |||                              | | |||||
Db      1893
CCCCACACTGTGATGACTTTGAGCCTGTCCTTTCCCTCCTTGAGCCTGTCTTGCTTGTCC 1952

Qy       521 -------------------------CCCCAAAGTGGTAGAGTTA------
TAAAAGGATA 549
                               |||| || | |||     ||       | |||||
Db      1953
CCTGTAAAATGAACAGTCCCCCTCTCCCCCAAATAGTAATAATACATGTTTCAAAGGGTG 2012

Qy       550 TACAT------------TGACGTTTCTTAAAAGCATGTGTAA 579
                 |||             ||||   | || |  | |||||
```

Db   2013 ACCATTTATAAAGCATATGACAAACCATATCAATAAATGTAA 2054

RESULT 12
US-10-478-914-57/c
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match   41.8%; Score 1356; DB 1; Length 2336;
  Best Local Similarity   39.3%; Pred. No. 2.6e-80;
  Matches 367; Conservative   0; Mismatches 198; Indels 368;
Gaps   46;

Qy   1 CTTTTTTTTTTTT-------------TTTTTTAAAGT-------
CTTTAGTATATTTATT 40
            ||||| || | | | | |||| | |||| | | |
||
Db   1372
CTTTTACATTCCTTCCATATCACAGGTACTATGAAGTAAGGAGACTTTTAGGTTTCTTTT 1313

Qy   41 TGTATAAAG------------AGTAAACA-AAGTGCATA------TAGAGT--
GGCCA-- 77
            ||| | || |||| || |||| || ||||| | | |
Db   1312
TGTCTTAAACTCAGACAGCTTTGTAAGCAGTAGTGTGTAGATTACAAGAGTTAGACAAAA 1253

Qy   78 -CAGGTTTGACACAGAGACCTTGGTGATGTAG--GCTATG-----------------
AAC 117
            |||| ||| ||| ||||||| | || ||| |
|||
Db   1252
GCAGGCGCGACTGAGAAGAGTTGGTGGGGGAGAAGCTTGGGGCACTTCCTGTCACTCAAC 1193

Qy   118 AAATT------------TAAATGGCAACTTCAT-TGC--
TGCCACTGAACCAATC----- 157
            | ||| |||| | || | | ||| | || || ||| ||
Db   1192
ACATTCCAGATCACTAAAAAATTTCCACACCCTCTGCATTCCCCCTTGCCCACTCCAGTT 1133

Qy   158 -----------CTGAAT-------TTGGG---------------------
CTCAACAGG- 177

```
                                 ||||  |          |||  |                               ||||
|||
Db      1132
CCCGGTATTTTCTGATTCCATATGTTGTGGTATTTACCATACTTCTCTCCCTCACTAGGC 1073

Qy       178 --TGAAAAGTAACAATATCAAACG------AATACT---------
AAACAGCATAAC--- 217
              ||  ||| ||     ||| |  |      |  |          |  | ||| | |
Db      1072 TCTGGCAAG--
ACTGCTTCAGAGGGGATGCATTCCTTTAGATTGCACAAAGCGGAGCTGG 1015

Qy       218 -AAAAAG------ATTTTCAGACTCTTGGTCATAAAGACCGTAATCGT-------
TCACA 263
                |||| |      | ||||||| ||| |    |  | || || |  | |
             |||||
Db      1014 GAAAATGGCTGGCAGTTTCAGAATCTAG----
TCACGATCGCACGCATGAGCACCTCACA 959

Qy       264 TTGAATCAATGACTAAACATTTTTGATTACCCAGCTACCTCC----
AAGCAAACTG---- 315
                |||  ||| |||  |   ||          ||| ||| || ||     |||   |||
Db       958 ---CATCCATGTCCCTACCC-----
GCCCCCCCGCTCCCGCCCCTGCAGCTGGCTGACCT 907

Qy       316 -------------------------------AAAACTGTCTAG---
TGGATCCTG----- 336
                                               |  |||||||  |    ||| || ||
Db       906
GTCTCACCCACTGCTGGCCTATCGAACGGCCAGGACTGTCTGGTTTTGGCTCGTGCCTTT 847

Qy       337 ----AAGTC---CATAG------------------TGCCTCTA----------
GCCGGGT 361
                |  ||| | |||            |||||||||              ||
||
Db       846
GTCCATGTCTGGCTTAGTTCCTCTCTGTCTATGCTTGCCTCTACCCCCACCGCCCCCAGGC 787

Qy       362 CTTTCAAGTGTT--GCACCAC------
AGGGTGATGATTGATGGTAAAAAC--------- 404
                ||||||||  || |||     || |  |  |  | |||||||||
Db       786
GGCACAAGTGTTTGGCCACACAAAACTAGAGATAGAAAAGGTGGTAAAAACTTCAAACTT 727

Qy       405 -----AGGGATCAACC---------CTTGTAGA--------------------
TCGGTGG 430
                |   || |  |       ||||| |                      ||  |
Db       726
TTCTAAATTCTCCAACAGTTTATTTCTTGTGAATTTCTTCCTTCTTTAAATACTCCATTT 667

Qy       431 TAAGTATGGAAACC--------CTCTAAGAAC---------
AGTGCAGCGTATGTG---- 469
                |||| |   |||           |||||   |       |  ||| | | ||||
Db       666
TAAGAAAACAAAAAAATTAATTATCTAAAGGCAAAGAATGGAAAGCAACCTTTGTGTTCC 607

Qy       470 GTATTCAGACTGGTTGCATACAGCATTCAAAACCAGTGCTGGAAT----------
AGCTT 519
                |||     ||||  | ||||    |  || |     ||  ||| ||
|||||
Db       606
```

```
TTATAATAACTGACTTCATAACTCTCTCCAGCTGCGTTATGGGATGTGTATAAAAAGCTT 547

Qy       520 ---------GCCCCAAAGTG---GTAGAGTTATAAAAGG---
ATATACATTGAC------ 558
                        |  | || | |   ||  ||  || | | |   | || || ||||
Db       546
CTGTTCTGAGAACAAAGGAGCACGTGCAGAAATGAGACGAAAAAATCCACTGACAGTATT 487

Qy       559 -----------GTTTCTTAAAAGCATGT-GTAA 579
                        || |||||||| | | || |
Db       486 CCATTACACAAATTACTTAAAAGATTTTAGTCA 454


RESULT 13
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match            41.5%;  Score 1347;  DB 1;  Length 3210;
  Best Local Similarity  37.3%;  Pred. No. 6.5e-79;
  Matches  384;  Conservative   0;  Mismatches  188;  Indels  458;
Gaps   56;

Qy        1 CTTTTT---------TTTTTTTTTTT----------TTAAAGTC-------
TTTAGTATA 34
            |||| |        |||| || |          ||  ||||         | |
 |
Db     2519
CTTTATGCGCTGAGGTTTTAGTTATACAAAAACCCCTTCCAGTCAAACAGAAAAAATTAA 2460

Qy       35 TTTATTTGTATAAAGAGTAAACAAA--------------GTGC--
ATATAGAGTGG---- 74
            || | | | ||||| || ||||               |||  || | |||| |
Db     2459
TTCAAATATGGAAAGAAAAATCAAACTTTCAGTATTTTCGTGACTATCTTGAGTAGTTCA 2400

Qy       75 -----CCACAGGTTTGACA--------------------------------
CAGAG--- 93
            |  || || ||||                                  |||||
Db     2399
TTTTCCAACCTCTTAGACAGCTGACAGACACCACTAACCTGATCACCTATTTCAGAGCTT 2340
```

```
Qy         94 ------ACCTTGGTG-----------------------------ATGTAGG----
CTA 112
                    ||||  |                              |||| ||     |
Db       2339 CAAAGATCCTTAATTTCCCCAAAGACTTCCTGAGCAAAAGGACTACATGTGGGAAATCAA 2280

Qy        113 TGAAC----------------AAATTTAAA---TGGCAAC-
TTCATTGCTGCCACTG--- 149
                    ||||               ||| |||||    |||    | ||  || ||| || ||
Db       2279 TGAAAACAGGAATGAGAAGAGAAAGTTAAAAATTGGTTGCTTTTGTTCCTGTCATTGGGG 2220

Qy        150 --------------AACCAATCC-TGAATTTGGGCTCAACAGGTG--
AAAAGTAACAATA 192
                              || || ||| ||| ||   ||| ||| | |    | || ||
Db       2219 ACTTTTGGTCTTCTAAACATTCCTTGAGTTC---
CTCCACATGAGTTTTTAATATCA--A 2165

Qy        193 TCAAACGAATACTAAACAGCATAACAAAAAGATTTTCAGACTCTTGGTCATAAAGAC--C 250
                 || | | || ||||   | || |||| | | | | | || | | | |  ||
Db       2164 TCTAGCAAAAATTAAAACAAACAAAAAAAGGCCTCTGAAAGTCAGGATACTGACCACCTC 2105

Qy        251 GTAATCGTTCACATT-------------GAAT--CAATGACTAAACATTT--
TTGATTAC 293
                 |  ||| || ||            ||||   ||| || ||    | || || |
Db       2104 GGCATCTCTCCCCTTCCCCACTGCTTGCGAATGCCAGTG-
CTGGCCTGTTCCTTAAACGC 2046

Qy        294 -CCAGCT--ACCTCCA-AGCAAACTGAAAACTGT-CTAGTGG---------
ATCCTGAAG 339
                |||||||   || ||| |||| |||    || | ||| |                ||||
Db       2045 ACCAGCTCATCCCCCAGAGCAGCCTGTGTGCTCTGCCAGCGACTGCTACTTCTCCTCCGG 1986

Qy        340 TC------CATAGTGCCT------CTAGCCGGGTCTTT-----------
CAAGTGTTGCA 376
                 |       ||  || |      ||| ||| || ||         ||||| |
|||
Db       1985 CCTCAGCTCAACATCCCAGCTATGCTACCCTGGGCTATGTGAGCTTGGGCAAGT-
TAGCA 1927

Qy        377 ----------------------CC------ACAG-------GGTGATG--------
ATTGA 394
                                      ||    ||||      |||||||        ||
||
Db       1926 TACATCTCTAGGCCTCTCTTTCCATGGATACAGAGAAGATGGTGATGCCTACTTCATAGA 1867

Qy        395 ----TGGTAAAAA----CAG--------------
GGATCAACCC---------------T 417
                    | ||| ||    | |             || |||  ||
|
```

```
Db       1866
GTTCTTATAAGAATTCCCTGAGGCTAGGCATGGTGGCTCACACCTGTAATCCCAGCACTT 1807

Qy        418 TGTAGATC--GGTGGTAAG---
TATGGAAACC--------------------------- 444
              || || ||  ||||| |||   || ||  ||
Db       1806
TGGAGGTCAAGGTGGGAAGATCAATTGAGCCCAGGAGTTCAAGACCAGCCTGGGCAACAT 1747

Qy        445 -------------CTCTAAGAACAGTG--------------------
CAGCGTAT----- 466
                            |||||  || ||||                    ||| || |
Db       1746
AGCGAGAGTGCATCTCTACCAAAAGTGATTTTTTTGATTTTTTGGGACAGAGTCTCGCTC 1687

Qy        467 --------------------GTGGT--------------------
ATTCAGACT----G 481
                                    |||||                    ||| | ||
                                                                    |
Db       1686
TGTCACCCAGGCTGGAGTGCAGTGGTGTGATCTCGGCTCACTGCAACTTCTGCCTCCCAG 1627

Qy        482 GTTGCATACAGCATTCAAAAC-CAG----------TGCTGGAATAGC--TTGCC--
CCAA 526
              ||| ||  ||||  |||   | |||          ||||| ||  |   ||||
|||
Db       1626 GTT-
CAAGCAGCTCTCATGTCTCAGCCTCCCGAGTAGCTGGGATTACAGATGCCTGCCAC 1568

Qy        527 AGTGGTAGAGTTATAAAAGGATATACATT----GACG-----TTTCT-
TAAAAGCA---- 572
                      || ||     ||     || | |   ||      || |      || || ||  ||||
Db       1567
CATGCCAGGCAAATTTTGGGTTGTTTTTTTTGAGATGGAGTCTTGCTCTATCAGCAGGCT 1508

Qy        573 --TGTGTAAT 580
                 ||| | |
Db       1507 GGAGTGCAGT 1498


RESULT 14
US-10-478-914-60/c
; Sequence 60, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
;   LENGTH: 2022
```

```
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-60

  Query Match            41.5%;  Score 1345.5;  DB 1;  Length 2022;
  Best Local Similarity  39.3%;  Pred. No. 6.9e-80;
  Matches  370;  Conservative   0;  Mismatches  201;  Indels  371;
Gaps   50;


Qy        1 CTTTTTTTTTTTTTTTTTT---
TAAAGTCTTTAGTATATTTATTTGTATAAAGAGTAA--- 54
            ||||||||||||||||||   |  ||| |||  | | ||     |  |  || | ||
Db     2000 CTTTTTTTTTTTTTTTTTTTAGATGGAGT-
TTTGCTCTTTTGCCCAGGCTGGAGTGCAATGG 1942


Qy       55 ----------------ACAAAGT--GCATATAGAGT-------------------
GGC 75
                            ||| |  || |   | ||
||
Db     1941
CGCGATCTCGGCTCACTGCAACTTCCGCCTCCTGGGTTCAAGCTATTCTCCTGCCTCAGC 1882


Qy       76 CAC-----------------AGGTTTGACAC-AGAG----------
ACCTTGGTGATGT 106
            | |                 ||| |||| | ||||       ||| || | |
Db     1881
CTCCTGAGTAGCTGAGGTGAGAGGACTGACGCGAGAGGATTGCTTGAGCCTAGGAGGTTG 1822


Qy      107 AG---GCTATGAACAAATTTAAATGGCAACT----TCATTGCT--------------
GCC 145
              ||   ||  ||| |   || |   || ||||    ||  |||                 |
|
Db     1821 AGGTTGCAGTGAGCTGTGTTCAC--
GCCACTGGACTCCAGGCTGGGTGACAAAGCAAGAC 1764


Qy      146 ACTG----------------------------------------AACC---------
AAT 156
                 |||                                      ||||
||
Db     1763
CCTGTCTCAAAAACAAAAACAAACAAACAAACAAACAAAAAAATAACCAACAAAAAAAAC 1704


Qy      157 CCTGAATTT-----------------------
GGGC---------------------- 169
            ||||| |||                    || |
Db     1703
CCTGAGTTTAAGTTTGATTTTAAGACCTGTAGGGACAGCAGATTAGTTCTACTTTAATGG 1644


Qy      170 -------TCAACAGG-------------TGAAAAGTA---ACAATATCA----
AACGAAT 202
                   ||| | ||             | ||||| |  ||| |||  |||   || |
Db     1643
GTATGCATCATCTGGAAAGCAAGGGTCATAAAAAGAAGATACATCTTCACTGGCACCATC 1584


Qy      203 AC-----TAAACAG-CATAACAAAAAGA---
TTTTCAGACTCTTGGTCATAAAGACCGT- 252
               ||     | | ||| | | | | | ||| |   ||| | |||||    ||| ||    ||
|
Db     1583 ACATCAGTCATCAGTCCTTAGATACAGAACCTTTACTGACTCCC--
TCAAAACTTCCATG 1526
```

```
Qy        253 -----AATC----------GTTC----ACATT-
GAATCAATGACTAAACATTTTTGAT-- 290
                  || |     ||||    ||||| | |||| || | | || || |
Db      1525
CTTCCAAACTAACCAAGCAGTTCTTCTACATTGGGATCATCGAATTTCCCTTCATGTTCC 1466

Qy        291 --------------------TACCCAGCTACCTCC-
AAGCAAACTGAAAACTGTCTAGT 328
                               ||| ||    ||  || | ||| | |||||||| ||
                                                                   |
Db      1465
AACTCTCCTCTAGCTTCAATATACACATAGACAACCTTAGCCATCTGAAAACCTACTTTT 1406

Qy        329 GGA----TCCTGA---AGTCCA--TAGTGCCTCTAGCCGGGT---CTTTC----
AAGTGT 372
                  ||    ||| |||     |||| ||  ||||| ||| | |  | | |    || |
Db      1405 AGAATATTCCCGAGTGGTTCCACGTAAGTCCTCT-
GCCAGATTCACATACCCATAAATTC 1347

Qy        373 TGCACCACAGG--------GTGATGATTGATGGTA---AAAACAGGGATCAA---
CCCTT 418
                  | |  || | |        || | ||  | | |   |||| |  |||||
|||
Db      1346
TACTTCATAAGCCCATACTGTTCTTAAAAAAGAAATAGAAAAAATATATCAATATAACTT 1287

Qy        419 GTAGATCGG------------TGGTAAGTATGGAAACC--
CTCTAAGAACAGTG------ 458
                  | || |            | || ||| | |  | ||    || ||
Db      1286
TAAAATAAGACACAAACCTTCATGAAAATATAGTCATCAAATTTATTTTCATTGGGATGC 1227

Qy        459 CAGCGTATGTGGTATTC---AGACTG--GTT-----GCATAC-------
AGCATTCAAAA 501
                  ||  | ||  | |||||   ||||| |||       ||| |       |||||| |
Db      1226
CATTTTTGAAGAATTCCTAAGACTAATGTTTCTTGACATGCAAGAGTTAGCATTAATAG 1167

Qy        502 C---CAGTGCTGGAATAGCT--TGC-----------
CCCAAAGTGGTAGAGTTATAAAAG 545
                  |  |  | || ||  ||  ||| |||          | | || ||||||| |||
Db      1166
CTTACGTTACTATAAATACTGCTGCTTGGAAGCAGTACAACTGTTTTAGAGTTTTAAGAC 1107

Qy        546 GATATACATTGACGTTTCTTAAA--------AGCATGTGTAA 579
                  | | || || | || || ||| |         || | |||||
Db      1106 TACAGACTTT--CATTACTCAAATCTTATTCAGTAAATGTAA 1067


RESULT 15
US-10-478-914-63
; Sequence 63, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
```

```
  Query Match           41.5%;  Score 1345;  DB 1;  Length 1813;
  Best Local Similarity  44.8%;  Pred. No. 4.2e-80;
  Matches  370;  Conservative   0;  Mismatches  180;  Indels  276;
Gaps   54;


Qy        1 CTTTTTTTTTTTTTTTTTTAAAGTCTTTAGTATATTTATT--------------
TGTAT- 45
            |||||  ||||| | ||||    ||| | ||| |||| ||            |||
|
Db      570 CTTTTAGTTTTTATATTTTC---
TCTGTTGTACATTTGTTGCAGCTCCTGCCAATGTCTC 626


Qy       46 -----AAAGAGTAAACA------AAGTGCATATAG----AGTGGC-CAC---------
AG 80
                        | | |   ||      ||  ||| | |     ||| || |||
||
Db      627
TTTCCCTATATTGTTCATTTTATAATAGCAGAAAACATTAGTAGCGCACTCTGTGGTGAG 686


Qy       81 GTTTG---ACACAG------
AGACCTTGGTGATGTAGGCTATGAACAAATTTAAATGGCA 131
              | ||   |  |||        |||||||    || ||| |   || |||| | ||
Db      687 ATATGGAAAATCAGTAGAATGAACCTTGG---AGTTGGCACT--
TCATATTTATTGATG 741


Qy      132 ACTTCATTGCTG--------C-CACTGAACC-AATCCTGAATT---
TGGGCTCAAC---- 174
            |||  | ||| |        | || || ||  | || ||| ||    ||     | |
Db      742
ACTGTAATGCAGTGTGAGTTCGCATTGCACATAGTCTTGATTTAAATGATTACCTCTTTT 801


Qy      175 ----AGGTGAAAAG-TAACAATATCAAACGAATACTAAAC----
AGCATAACAAAAAG-- 223
              | |  ||| | |   || | |   |    | || ||    ||||||| | ||||
Db      802
ATGAAAGCAAAATGTTTGTAAGAACGGCCATGTTGTAGACAGGGAGCATAAAATAAAGGA 861


Qy      224 ---------------------
ATTTTCAGACTCTTGGTCATAAAGACCGTAATCGTTCA- 261
                            || || | |||||  |    || |   |
|||||
Db      862 GAGGAAGTAGGACAAGTAACATTTCTCTGTC-CTTGGT-TTCTTGAAC---
AATGTTCAG 916
```

```
Qy        262 CATTGAATCAATG-ACT----------------------
AAACATTT------------ 285
              ||||||  ||||  |  |||                    |||||  ||
Db        917
CATTGACTCAAGGCACTGTCATTTCAGAAGTACAGTATAGAAACAATTGAGCATCAAGCA 976


Qy        286 ------------------TTGATTACCCAGCTACCTCC-----
AAGCA------------ 310
                                ||  ||  ||||  |  |||||     |||||
Db        977 TAGATGAAACATGGAGGCTTAGTTTCCCA-
CCCCCTCCAAAAGAAGCACTTTACTTATGT 1035


Qy        311 ----------------------------AACT-GAAAACTGTCTAGTGGATCC-
TGA 337
                                          |||  |  ||||| ||| ||  |
||
Db        1036
ACTCACATATTTTCGGTTTCTGTGGCTGTGTTACTGGGTAGCTGTCCAGTTGAGACGAGA 1095


Qy        338 AGTCCA-TAGTGCCTCT---AGCCGGGTC----TTTCAAGTGTT----
GCACCA------ 379
              ||  |  |   ||| |   ||| |  |||    ||| | |||||    |||| |
Db        1096
TGTTTACTTAAGCCACACCCAGCAGAGTCAGCTTTTAATGTGTTGGGGGCACTATTTTAA 1155


Qy        380 --CAGGGTGATGATTGATGGTAAAAACA-----
GGGATCAACCCTTGTAGATCGGTGGTA 432
                        |   |||  |||||  ||   |  |  ||       |||||    ||  ||| ||  |  ||
|
Db        1156 TCCT--GTGCTGATT--TGTAACCATCATCTATGGGAT--GCCTTTG-AGTT--
GTAAAA 1206


Qy        433 AGTATGGAAACCCTCTAAGAACAG--TGCAGCGTA-TGTGGTATTCAGACTGGTTGC-
AT 488
              ||   |  |||  ||  |   ||||  |||||| ||  |  ||  ||  ||  |
|
Db        1207 AGAGGGAAAATACTAGATTCACAGGTTGCAGCTTACTATGTTTTT--
GAATATTTGAGTT 1264


Qy        489 ACAGCATTCAAAAC----CAGTGCTGGAAT--AGCT-TGCCCCA-----
AAGTGGTAGAG 536
                |  |  ||| |  |       ||  ||  |  |   ||  |  |||    ||
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Db        1265
GCTGTATTAATAGCACAGAAGAGCAGTATTTAAGTTATGCAGCATTTATCTATGGCAGAG 1324


Qy        537 TTATA-AAAGGATATACAT-TGACGTTTCTTAAAAGCATGTGTAAT 580
              |  |  ||  ||||   |  ||   ||| | |  |   ||  ||||||||
Db        1325 AGAGATAGAGAATATGTGTATG--GTTCCATTA---CAAGTGTAAT 1365


Search completed: March  9, 2010, 15:52:08
Job time : 3.08146 secs

                        GenCore version 6.3
              Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model
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Run on:         March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                      (without alignments)
                                      1134.946 Million cell
updates/sec

Title:          US-10-572-905-22
Perfect score:  6518
Sequence:       1 gaattccctgaggaggcgaa.........taagagaacattataattgc
1044

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:      834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      7335755.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being
printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result           Query
   No.    Score   Match Length DB  ID                        Description
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 c   1    2967    45.5   2120   1  US-10-478-914-64          Sequence 64,
Appl
     2    2963.5  45.5   2120   1  US-10-478-914-64          Sequence 64,
Appl
 c   3    2953    45.3   3210   1  US-10-478-914-4           Sequence 4,
Appli
     4    2898    44.5   3210   1  US-10-478-914-4           Sequence 4,
Appli
 c   5    2818.5  43.2   2437   1  US-10-478-914-61          Sequence 61,
Appl
     6    2816    43.2   2437   1  US-10-478-914-61          Sequence 61,
Appl
 c   7    2715    41.7   2198   1  US-10-478-914-17          Sequence 17,
Appl
     8    2696    41.4   2198   1  US-10-478-914-17          Sequence 17,
Appl
     9    2635    40.4   2495   1  US-10-478-914-20          Sequence 20,
Appl
    10    2623.5  40.3   1946   1  US-10-478-914-62          Sequence 62,
Appl
 c  11    2555.5  39.2   2495   1  US-10-478-914-20          Sequence 20,
Appl
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c	12	2502	38.4	2336	1	US-10-478-914-57	Sequence 57, Appl
	13	2498	38.3	2336	1	US-10-478-914-57	Sequence 57, Appl
c	14	2489.5	38.2	1946	1	US-10-478-914-62	Sequence 62, Appl
c	15	2483.5	38.1	2083	1	US-10-478-914-3	Sequence 3, Appli
	16	2482	38.1	3589	1	US-10-478-914-21	Sequence 21, Appl
	17	2481	38.1	2083	1	US-10-478-914-3	Sequence 3, Appli
c	18	2474.5	38.0	2022	1	US-10-478-914-60	Sequence 60, Appl
c	19	2431	37.3	3589	1	US-10-478-914-21	Sequence 21, Appl
c	20	2427	37.2	1813	1	US-10-478-914-63	Sequence 63, Appl
	21	2393.5	36.7	2022	1	US-10-478-914-60	Sequence 60, Appl
	22	2368	36.3	1813	1	US-10-478-914-63	Sequence 63, Appl
	23	2200.5	33.8	889	1	US-10-478-914-5	Sequence 5, Appli
c	24	2174	33.4	816	1	US-10-478-914-15	Sequence 15, Appl
c	25	2165.5	33.2	867	1	US-10-478-914-6	Sequence 6, Appli
	26	2139.5	32.8	867	1	US-10-478-914-6	Sequence 6, Appli
	27	2103	32.3	816	1	US-10-478-914-15	Sequence 15, Appl
	28	2102	32.2	794	1	US-10-478-914-13	Sequence 13, Appl
c	29	2102	32.2	889	1	US-10-478-914-5	Sequence 5, Appli
c	30	2064	31.7	794	1	US-10-478-914-13	Sequence 13, Appl
c	31	2011	30.9	1020	1	US-10-478-914-68	Sequence 68, Appl
	32	1996.5	30.6	839	1	US-10-478-914-16	Sequence 16, Appl
	33	1981	30.4	717	1	US-10-478-914-42	Sequence 42, Appl
	34	1969.5	30.2	1020	1	US-10-478-914-68	Sequence 68, Appl
	35	1968	30.2	938	1	US-10-478-914-69	Sequence 69, Appl
c	36	1966	30.2	938	1	US-10-478-914-69	Sequence 69, Appl
c	37	1959.5	30.1	839	1	US-10-478-914-16	Sequence 16, Appl
c	38	1958	30.0	778	1	US-10-478-914-35	Sequence 35, Appl
c	39	1957.5	30.0	811	1	US-10-478-914-37	Sequence 37, Appl
	40	1951	29.9	889	1	US-10-478-914-9	Sequence 9, Appli
c	41	1947	29.9	889	1	US-10-478-914-9	Sequence 9, Appli

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  c  42     1939    29.7    816  1  US-10-478-914-38        Sequence 38,
Appl
     43     1930    29.6    816  1  US-10-478-914-38        Sequence 38,
Appl
  c  44     1914    29.4    738  1  US-10-478-914-32        Sequence 32,
Appl
  c  45    1911.5   29.3    717  1  US-10-478-914-42        Sequence 42,
Appl
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ALIGNMENTS

RESULT 1
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match   45.5%; Score 2967; DB 1; Length 2120;
  Best Local Similarity 38.7%; Pred. No. 5.6e-188;
  Matches 716; Conservative   0; Mismatches 315; Indels 820;
Gaps 109;

Qy   4 TTCC----C-----TGAGGAGGCGAATCCGG--CGGGTATCAGAGCCA--------
TCAG 44
            |||| | ||||||| | | || | || | | || ||
|||
Db   1852 TTCCGTCTCTAGGGTGAGGAGG-
GGTGCAGGCACAGGCACCCAAGACAGCTGCGGTCCAG 1794

Qy   45 AACCGCCACCATGACGGTGGGC-
AAGAGCAGCAAGATGCTGCAGCATATTGATTACAGGA 103
               ||| | ||| | |||| | || | | || | | || ||| || |||
|
Db   1793 CCCCGGCCCCA--CCTGTGGTCTCAGTGACGCCCCA-
GAGGCCCCATCTTCCCCACATAA 1737

Qy   104 TGAGG----TGCATCCTGCAGGACGGCCGGATC---TTCATTGG----------
CACCTT 146
            ||||| | |||||| | | | || || | ||||| |
||||||
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```
Db        1736
TGAGGCTGCTCCATCCTCCTCAAAGCCCAGACCTATTTCATAAGCCCCAGACCCCACCTT 1677

Qy         147 --------------------CAAGGCTTTTGACA-----------AGCAC---
ATGAATT 172
                                  ||  |||   ||||        ||||| |||
|
Db        1676
CACCCAGGGCCCCAAGAGAACAGAGCTGGAGACACTTCTACTCCTAGCACTGGATGCCCT 1617

Qy         173 TGATCCT-CTGTGA--CTGT---------GATGAGTTCA----------
GAAAGATC--A 208
                  |||  ||||||  ||||       |  |||  ||        | | | ||
Db        1616
CTCCCCTCCTGTGAAGCTGTAGGTGGGGGGTGGAGGACACCCCTTTAAGGCAGGCTCGGG 1557

Qy         209 AGCCAAAGAACTCCAA-AC------AAG-CAGAAAGGGAAGAGAAGCGAGTC-
CTCGGTC 259
                  | | | |||||||||| ||    ||| ||| ||| | |||| || | |
|
Db        1556
GGGCTATGAACTCCAAGACTCCTGGAAGCCAGTAAGAAGTGGGAAGGTAGGCACACCATT 1497

Qy         260 TGG-------------TGCT--GCTGCGAGGGGAGAATC------
TGG------------ 286
                  |||          ||  |||  ||| ||||| ||      |||
Db        1496
TGGGATTTTTATTTTTCACTGAGCTAAGAGAGGAGATTCCAGCTATGGAATCCAGAGAGC 1437

Qy         287 --TCT-CAATGACAGTAGA----------GGGACCTCCTCCCAAAGAT--
ACTGG----- 326
                  ||| ||  |||| | |        ||| |||  |||| ||    ||||
Db        1436
GTTCTACAGGAACAGAACAGAAATTGGCTGGGCCCTGGGCCCAGAGGAGGCCTGGAGCCG 1377

Qy         327 --TATTGCTCGAGTTCCA--------CTTG-----------CTGGAGCTGC------
CGG 359
                  ||  || || ||| |||        ||||          ||  | ||       |
|
Db        1376 CTTACTGTTC-
AGTGCCAGCTTCATCCTTGGCACTCTGCCTCTCACACAGCATCGCTCCG 1318

Qy         360 GGGCCCAGGGATC-----GGCAG-----GGCTGCTG-----
GCAGAGGAATCCCAGC--- 401
                  |  ||||| |  |     ||||     ||  ||||   ||||  |  ||| ||
Db        1317
GCTCCCAGAGCCCACAGTGGCAGCCGCTGGAGGCTGTGGCAGCAGCTGCTGCCCTGCCCA 1258

Qy         402 ----------TGGG-------------GTTC---CCA-----
TGC--------------- 415
                            ||||             |||  ||  ||
Db        1257
AGGAGGGATGTGGGCTTGGCTCTGACAGTTCAAGCCAGAAAGAGCCTTAGAAGTCATTCA 1198

Qy         416 -------CCC--------------------AGGCTCC-----TGCA-
GGACTT------- 435
                  |||                    ||||||      ||| ||  |||
Db        1197
GGACATTCCCATTTTACAGATGATGAAATAAGGCTCAGAGAGAGCAGGGGCTTTCAAGAA 1138
```

```
Qy        436 --------------GCTGGG---------CCAGTCCG-
TGGGGTTGGCGGGCCATCCCA 470
                          ||||           ||  |||  | ||  ||  ||  |  |  ||||  |

Db        1137
CAATAAAGGTGGAGACTGGAACTCAGGCCTCCTGTCTGCTGAGGGTGTCTGCCCATGCTC 1078


Qy        471 AC----------------AGGTGATGAC-------------
CCCACAAGGAAGAGGTAC- 500
                   |               |||| || |             |  | ||||| ||  |
|
Db        1077
TCTCTCAGAGTTTCTGAGTGGTGGTGTCTGGAGGGGCTGGACACGCAAGGGAGCTGGCCT 1018


Qy        501 ----TGTTGC------AGCCG--------CTGCAGCTGCTGCCAC------
AGCCA---G 533
                   |||  |      ||||        |||  ||| ||| | |       ||||
|
Db        1017
CGTGTGTGTCTGTCTGTGCCGGGATGTGTCTGTGGCTTCTGTCTCTGAACGTGCCAGGGG 958


Qy        534 TATTG---CC------------------GGGGCTCC----------
AAC----------- 551
                   | |||   ||                  || |||||         |||
Db        957
TTTTGTGTCCTGTGTGTGTGTCTCTCTGTGGGTGCTCCTGTGTGCAGGAACTTGGGGCCATG 898


Qy        552 -CCAGT---------ACCCA--CCT--
GGCCGTGGGGGTCCTCCCCC------------- 584
                   ||||        || |  |||   | |||| | ||||| |
Db        897
GCCAGAGAGGGATGGGCCTATTCCTACAATCTTGGGAGGCCTCCACAGGCTGAGCTGGTG 838


Qy        585 -------ACCT-ATGGGCCGA---------GGAGC---
ACCCCC---------------T 609
                   ||| | |||  ||          ||  |   || |||
Db        837
GGGAGGGTCCTGAAGGGTAGAGTGAAGATGGGGACTTTACTCCCAGCGGAGAGGAAGAAA 778


Qy        610 CCA--------------GGCAT-------------------------
GATGGG-------- 623
                   |||               |||||                       ||||||
Db        777
CCAGAAGATAGGCTTGGGGCATGGATGGGAAAGGTCTTGGAACTAGGATGGGGCAAGGGA 718


Qy        624 --------CCCACCT------------CCTGG------------
TATGAGACCTCCTATG 651
                   ||||  |            |||||           | | || |||| |
|
Db        717
AACAAAGCCCCAAATGGAGTATGGGTCCCTGGAAGTTGACACACTCTTAGCCCTCATGGG 658


Qy        652 GGTCC--CCCAATGGGGATCCC------------
CCCTGGAAGAGGGACT---------- 687
                   || ||  |||| |||| | |||            | |  || | |  |||
Db        657
GGCCCAGCCCAGTGGGTAACCCCGGGGAAGTGGTCACATGACGTGACACTTCTCAGCTGA 598


Qy        688 --------------CCAATG-GGCATG--------CC---------CCCT--------
CC 707
                          |||  ||  |||  ||           ||          |||
```

```
                    ||
Db          597
TTGCTTGAGATCCCCCAGTGTGGCCTGGGCCTTGTCCTTGAGTGAGCCCAGGTTCAAGCC 538

Qy          708  GGGAATGC-GGCCTCCTCCCCCTGGGATGCGAGGCCTTCTT--------------
TGACC 752
                     ||||  ||  ||||   ||  |||   ||   |   ||||||||||            ||
                    ||
Db          537  AGGAAGGCTGGCCAGCTGCCCAAGGACT--
GAGGCCTTCTCCTCCTCCTCCTCTGTGTCC 480

Qy          753  -----------CTTGGCCA----------
CAG---------------------------- 763
                            ||||||||           |||
Db          479
TCCTCGATCATCTTGGCCAGCTCCCGGGGCAGCTCCACGTCTCCACCTGCCATCTGGATC 420

Qy          764  -------------------------------AGTAT-------
GGAAGTAGCTCCGCAGA 785
                                                ||||     ||||||
                    |||||||||
Db          419
TGGCTCTCATCTGTCTCGTTCTTGGGTAGCCGGTATTTGTCTCGGAAGTGGCTCCGCAGT 360

Qy          786  GGCGTGGGCTCG--ATTCCTCAGGG-----------CCACGTTAC-----CACAGAC-
CT 826
                     |  |   ||||   ||||||| |      |   |||  |      ||  |
                    |
Db          359
GTGGCCGCTCTGCCTTCCTCTGTGTGAACTGTGCATCCCGCTCCATCTTCTCTTCCACG 300

Qy          827  GTTTGTTTCTTATGCT-GTTGT--TCGTGGAGTCTCATG------------------
GGA 865
                     |||  ||||  ||  ||   |  ||   ||  |    |  ||||||                |
Db          299
AGTTGCTTCTGATACTCCTCGTACTCCTCCCGGCTCATGCCCTGAGCTTCGGCTGCCGAC 240

Qy          866  TTGT-CTGGTTTCCCTTA-CAGGGCCCCCTCC------
CCCGGGAATG------------ 905
                     ||||  |   | |||||||  |   ||| |||||       ||| |  | |
Db          239
TTGTCCCCATCTCCCTTATCCTCGCCGCCTCCCAGGCTCCCAGTGAGGTTCTTCAGCTGG 180

Qy          906  -CGCCCACCAAGG------CCCTAGACTC----ATCTTGGCCCTCCTCAGCTCC---
CTG 951
                     ||||||||| ||       ||  | |  |      ||||  |||  ||   ||  ||    |
                    |
Db          179
CCGCCCACCATGGTCTTCACCATGAACGCCATGGTCTTCGCCGGCCGGGGCACCGGGC-G 121

Qy          952  CCTGTTTCC---CGTAAGGCT--GTACATAGTCC---------
TTTTATCTCCTTGTGGC 997
                     ||||  |  ||    ||  ||||     |  ||||           |       ||||
                    |||
Db          120  CCTGCTACCACGCGCCAGGCACCGGGCA-
CGTCCGCGCCTACTTCAGCACTCCAGTAGGC 62

Qy          998  CTATGAAACT---GGTTTATAATAAACTCTTA-AGAGAACATTATAATTGC 1044
                     |  |     ||    ||  |  | |     | ||  ||||||    |    | |  ||  |  |
Db           61  CAACAGTGCTCGAGGAAT-TCCGCAGCTTTTAGAGCAGAAGTAACACTTCC 12
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RESULT 2
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match           45.5%;  Score 2963.5;  DB 1;  Length 2120;
  Best Local Similarity  41.6%;  Pred. No. 9.8e-188;
  Matches  672;  Conservative   0;  Mismatches  338;  Indels  607;
Gaps   96;

Qy        1 GAATTCCCTG--AGGAGGC--------GAATC-------------------
CGGCGGGTA 31
            ||| || ||   || |||       ||| |                |||||  |
|
Db      162
GAAGACCATGGTGGGCGGCCAGCTGAAGAACCTCACTGGGAGCCTGGGAGGCGGCGAGGA 221


Qy       32 TCAGAGCCAT-----CAGAACCGCCACCATGACGGTGGGCAAGAGCAG---------
CAA 77
            | || | ||      || | || ||    |  ||||| |||| |         |
|
Db      222
TAAGGGAGATGGGGACAAGTCGGCAGCCGAAGCTCAGGGCATGAGCCGGGAGGAGTACGA 281


Qy       78 GATG---CTGCAGCATAT-----------TGAT--TACAGGATG--
AGGTGCATCCT--- 116
            | |   | | |||| |            |||    | ||||    || ||  |
Db      282
GGAGTATCAGAAGCAACTCGTGGAAGAGAAGATGGAGCGGGATGCACAGTTCACACAGAG 341


Qy      117 ----GCAGGACGGCCGGATCTTCATTGGCACCTTCAAGGCTTTTG--------
ACAAGCA 164
                |||| ||| |     || |   | ||| | || ||    |         ||||
|
Db      342
GAAGGCAGAGCGGGCCACACTGCGGAGCCACTTCCGAGACAAATACCGGCTACCCAAGAA 401


Qy      165 CATGA---ATTTGATCCT----CTG-TGACT----GTGATGAG----
TTCAGAAAGATCA 208
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                |  ||    ||  || ||      |  | || |     | ||  | |    |  |      ||
|
Db       402
CGAGACAGATGAGAGCCAGATCCAGATGGCAGGTGGAGACGTGGAGCTGCCCCGGGAGCT 461

Qy       209 AGCCAAAGAACTCCA--AACAAGCAGAAAGGGAAGAGAAGCGAGTCCTCGGT-
CTGGTGC 265
                 |||||      || |  |  ||||    ||| ||| ||  || |||| ||  || ||  |
||
Db       462 GGCCAAGATGATCGAGGAGGACACAGAGGAGGAGGAGGAG-
AAGGCCTCAGTCCTTGGGC 520

Qy       266 TGCTG---------CGAGGGGGAGAATCTGGTCTCAATGACAGTAGAGG----
GACCTC-- 310
                 ||||          |  |  ||    ||| ||||  |||| |  |    |||     | || |
Db       521
AGCTGGCCAGCCTTCCTGGCTTGAACCTGGGCTCACTCAAGGACAAGGCCCAGGCCACAC 580

Qy       311 ------CTCCCAAAGATACTG-------GTATTGC-TCGAGT-
TCCACTTGCTGGAGCTG 355
                   || |||  |  |        || | ||| ||   ||  || |||||| |
Db       581
TGGGGGATCTCAAGCAATCAGCTGAGAAGTGTCACGTCATGTGACCACTTCC-------- 632

Qy       356 CCGGGG--GCCCA--GGGATCGGC-------AGGGCT------------
GCTGGCAGAGG 392
                   ||||||   ||||   ||| ||| |      ||||||            || |||
||
Db       633 CCGGGGTTACCCACTGGGCTGGGCCCCCATGAGGGCTAAGAGTGTGTCAACTTCCAG-
GG 691

Qy       393 AATC-----CCAGCTGGGG------TTCCCATGCCCCAGGCT----------
CCTG---- 427
                 |  |      |||  |||||      ||||| ||||||| ||            |||
Db       692
ACCCATACTCCATTTGGGGCTTTGTTTCCCTTGCCCCATCCTAGTTCCAAGACCTTTCCC 751

Qy       428 ----------CAGGACT---TGCTGG-----
GCCAGTCCGTGGGG--------------- 454
                   || | ||   | ||||        ||  |||| |||
Db       752
ATCCATGCCCCAAGCCTATCTTCTGGTTTCTTCCTCTCCGCTGGGAGTAAAGTCCCCATC 811

Qy       455 TTGGC-----------GGGCCATCCCAA------CAG---
GTGATGACCCCACAAGGAAG 494
                   || |         || || |||| |       |||    ||| | | | | ||||
|
Db       812
TTCACTCTACCCTTCAGGACCCTCCCCACCAGCTCAGCCTGTGGAGGCCTCCCAAGATTG 871

Qy       495 -AGGTACTGTTGCAGCCGCTGCAGCTGCTGCCACAGCCAGTATTGCC--------
GGGGC 545
                    ||| | |    ||| | |  ||||  ||| | | ||           ||
||
Db       872 TAGGAATAG-----
GCCCATCCCTCTCTGGCCATGGCCCCAAGTTCCTGCACACAGGAGC 926

Qy       546 TCC------------AACCCAGTACCCA-----CCTGGC-CGTG-------
GGGGTCCTC 580
                   ||             ||  ||| || ||     ||||||  |||        |    ||
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Db        927
ACCCACAGAGAGACACACACAGGACACAAAACCCCTGGCACGTTCAGAGACAGAAGCCAC 986

Qy        581 --------CCC--CACCTATGGGC-----CGAGG--AGCAC--------------
CCCCT 609
                         |||   |||   |   |   |      |||||   |||  |
                   |||||
Db        987
AGACACATCCCGGCACAGACAGACACACACGAGGCCAGCTCCCTTGCGTGTCCAGCCCCT 1046

Qy        610 CCAGGCA-----------------TG---------ATGGGC---CCACCTC--
CTGGTAT 638
                         ||||  ||                    ||       ||||||    |   ||||   |  |
                   |
Db        1047
CCAGACACCACCACTCAGAAACTCTGAGAGAGAGCATGGGCAGACACCCTCAGCAGACAG 1106

Qy        639 GAGACC-----TCCTATGGGTCCCCCAATGGGGATC-------
CCCC------------- 673
                         |||  ||      |||  |   ||| ||   |    |  ||       ||||
Db        1107 GAGGCCTGAGTTCCAGT--
CTCCACCTTTATTGTTCTTGAAAGCCCCTGCTCTCTCTGAG 1164

Qy        674 --------------CTGGAA--------------GAGGGACTCCAATG---------
GGC 696
                               |||  ||                    ||  |||| | |  |
                   |||
Db        1165
CCTTATTTCATCATCTGTAAAATGGGAATGTCCTGAATGACTTCTAAGGCTCTTTCTGGC 1224

Qy        697 ATG-----------------CC----CCCTCC-------GGGAA-----
TGCGGCCTCCT 723
                            ||                  ||    ||||||       ||| |     ||| ||| |
Db        1225
TTGAACTGTCAGAGCCAAGCCCACATCCCTCCTTGGGCAGGGCAGCAGCTGCTGCCACAG 1284

Qy        724 CCCCCTG-GGATGC----GAGGCCTTCTTTGACCCTTGGCCA--------------
CAGA 764
                            ||  ||  |  || |||     |  ||| ||||  || ||    || |
                   ||||
Db        1285 CCTCCAGCGGCTGCCACTGTGGGC-
TCTGGGAGCCGGAGCGATGCTGTGTGAGAGGCAGA 1343

Qy        765 GT---ATGGAAGTAGCT-CCGCAGAGGCGTG---GGCTC---
GATTCCTCAGGGCCACGT 814
                            ||   | |||  | |||| | | ||    ||    |||||    |   ||||| |||||
                   |
Db        1344
GTGCCAAGGATGAAGCTGGCACTGAACAGTAAGCGGCTCCAGGCCTCCTCTGGGCCCAGG 1403

Qy        815 TACCACAGACCTGTTTGT-TTCTTATGCTGTTGTTCG-----
TGGAGTCTCATGGGATTG 868
                            |||       ||  ||| |  |||||   | |||| |   ||      |||| ||  ||| |
Db        1404 GCCCA---GCCAATTTCTGTTCTGTTCCTGTAGAACGCTCTCTGGATTC-
CATAG----- 1454

Qy        869 TCTGGTTTC--CCTTACAGGGCCC-------------CCTCCCCCG-GGAATGC--
GCCCA 911
                            ||||   ||  |||   |   || |                ||||     ||  |||    ||
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Db      1455 -
CTGGAATCTCCTCTCTTAGCTCAGTGAAAAATAAAAATCCCAAATGGTGTGCCTACCTT 1513

Qy       912 CCAA---------GGC--CCTAGACTC------
ATCTTGGCCC----------------- 937
               || |         ||| ||  || ||      || | ||||
Db      1514
CCCACTTCTTACTGGCTTCCAGGAGTCTTGGAGTTCATAGCCCCCCGAGCCTGCCTTAAA 1573

Qy       938 ------TCCTCAGCTCCCTGCCT---GTTTCCCGTAAGG------------
CTGTAC--- 973
                   ||||| | ||| ||| | ||| |   ||| | ||| |
Db      1574
GGGGTGTCCTCCACCCCCCACCTACAGCTTCACAGGAGGGGAGAGGGCATCCAGTGCTAG 1633

Qy       974 -------ATAGTC-------CTTTTATCT------CCT----------------
TGTGGC 997
                   |  ||| || |||   |||     || 
Db      1634
GAGTAGAAGTGTCTCCAGCTCTGTTCTCTTGGGGCCCTGGGTGAAGGTGGGGTCTGGGGC 1693

Qy       998 CTATGAAACTGGTTTATAATAAACTCTTAAGAGAA-----------CATTATAATTG
1043
               ||||||| |||     |   ||| | ||| |           |||||| |
Db      1694 TTATGAAATAGGT-----CTGGGCTTTGAGGAGGATGGAGCAGCCTCATTATGTGGG
1745


RESULT 3
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match         45.3%;  Score 2953;  DB 1;  Length 3210;
  Best Local Similarity   38.6%;  Pred. No. 1.1e-185;
  Matches  727;  Conservative   0;  Mismatches  288;  Indels  870;
Gaps  118;

Qy        1 GAATTCCCTGAGG--AGGCG-----------------
AATCC------------------ 23
```

```
                    ||||||||||||  ||||                    |||||
Db      1856
GAATTCCCTGAGGCTAGGCATGGTGGCTCACACCTGTAATCCCAGCACTTTGGAGGTCAA 1797

Qy        24 GGCGGGT--ATCA---GAGCC------ATCAGAACC-GC-----CACCATGACG-
GTGGG 65
             || |||   ||||   |||||      ||| ||| ||   || ||| || | |
|
Db      1796
GGTGGGAAGATCAATTGAGCCCAGGAGTTCAAGACCAGCCTGGGCAACATAGCGAGAGTG 1737

Qy        66 CAAGAGCAGCAAGATGCTGCAGCATATTGATT-------ACAGGAT---GAGGTG-
CATC 114
             ||    |  | | |||| |  |     | |||||    |||| |   |   || ||
|
Db      1736 CAT-CTCTACCAAAAG-TG-
ATTTTTTTGATTTTTTGGGACAGAGTCTCGCTCTGTCACC 1680

Qy       115 CT-GCAGGACGGCCG------GATCT----TCATTGGCA-------
CCTTCAAGGCTTTT 156
              |  || ||| || |      |||||   ||| | |||       ||| | ||| |
Db      1679 CAGGCTGGAGTGCAGTGGTGTGATCTCGGCTCACT-
GCAACTTCTGCCTCCCAGGTTCAA 1621

Qy       157 GACAAGCACATGAATTTGATCCTC---TGTGACTGTGATGAGTTCAGAAAGAT-----
CA 208
             |    | |||| |  | |  |||| |   || ||| |||  | |||| |      |
||
Db      1620 GCAGCTCTCATGTCTCAG--CCTCCCGAGTAGCTGGGAT---
TACAGATGCCTGCCACCA 1566

Qy       209 AGCCA-------------------------AAGAACTC-----
CAAACAAGCAGAAAG 236
                ||||                        | | ||      | | | |||||
|
Db      1565 TGCCAGGCAAATTTTGGGTTGTTTTTTTTGAGATGGAGTCTTGCTCTATC-
AGCAGGCTG 1507

Qy       237 GGAAG-AGAAGCGAGTCCTCGG---TCTGGTGCTGCTG-----CGAG-----
GGGAGAAT 282
             |   | ||  ||| | ||||||   |||   | |||      || |     | ||
|
Db      1506 GAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCTCTGACTCCCGGGTTCAAGCGATTCT 1447

Qy       283 CTGGTCTCAATGAC---AGTAG-AGGGAC----------CTCCTCC--------
CAAA-- 318
             || | ||||    |      | ||||| |||||         | || ||
| ||
Db      1446 CTTGCCTCAGCCTCTTGAGTAGCTGGGACTACAGGCGCGCACCACCATGCCTGGCTAATT 1387

Qy       319 -----GATACTGGTATTGCTCGAGTTCCAC----TTG--CTGGAG----------
CTGCC 357
                  | |   | |||  | | ||| |||      |||   | |||
||
Db      1386 TTTGTGTTTTTAGTAGAGATGGGGTTTCACCCTGTTGGCCAAGAGGACCCCCAGCCTTCC 1327

Qy       358 GGGGGCCCAGGGATC-----GGCAGGGC-------
TGCTGGCAGAGGAATCCCAG----- 400
```

```
                  | |  |||| |    |||||||||    |||| | | || | |||||
Db      1326 CAAGCCATAGGGGGCTGGTGGGCAGGGCGGCACTTAGCTGCCTGGGGCA-
CCCAGTACCT 1268

Qy       401 ---CTGGGG----TTCCCATGCC-----------CCAGG---------
CTCC-------- 425
                 || ||   | ||| |||          ||| |       ||||
Db      1267
GTCATGAGGCACTTGCCCTGGCCAAAGGTCACTGCCAAGGCACAGCCACTCCAGAGAGTC 1208

Qy       426 ------TGCAG-GACT--------------------------TGCTGGG-------
CCA- 444
                |||| ||||                            | |||||
|||
Db      1207
AAGAGGAGCAGAGACTCCAGAGCAGATGGAAGGAGAGTGGGCTTCTGGGGATTGCACCAA 1148

Qy       445 -----------------------------------------GTCCGTGGGGTT-----
GG 458
                                                    | ||| ||||||
||
Db      1147
GGAGGAAGCAGAAGGGATGTGCAGCAGCAGAAAAGGAGGAGGACCGGGGGGTTCTGAGGG 1088

Qy       459 C-----------GGGCCA----TCCCAACAGG--------------
TGATGAC------- 482
               |         ||||||    ||| ||||||          ||| |||
Db      1087
CTTGGGGTGATGAGGCCAGAGTTCCAAACAGGGTCTGGGTGCAGGATGAGGACAGAAGAA 1028

Qy       483 ---------CCCACAAGG---
AAGAGGT------------------------------ 498
               |||| |||| |||||||
Db      1027
AACAGAGAACCCAAAAGGGGCAAGAGGTTGGTCCCTTACTTTCACTCTCCTGGGAGGAGG 968

Qy       499 -------------ACTGT-------TGCA-----GCC--
GCTGCAGCTGCTGCCACA--- 528
               || ||   ||||   |||  ||||| |||| ||  ||
Db       967
ATGGGTACACCACACAGTTGGATGGTGCATCTTTGCCTGTCTGCACCTGCAGCTCCATGG 908

Qy       529 -GCCA--------------------GTATTGCCGGGGCTCCAAC-
CCAG----------- 555
               |||               || |||| | |||| | ||||
Db       907
CACCATGGACCCTGTGCTCCGAGTGGTGGTGGTGCCTGATCTCCACCACCAGGCAGCAGTAGA 848

Qy       556 ------TACCCACCTG------------------------------
GCCGTGGGGGTC-- 577
               || ||| ||                          ||| ||| ||||
Db       847
GGCCGCTATCCAGCAGGGTCAGGTTGCGCATGGTGATGGAGAAGTTGCCATGGTGGTCGG 788

Qy       578 -------CTCC--CCCAC--CTATGGGC-----CGAGG--------
AGCACCC------C 607
               |||| |||   |  || ||    || ||          ||| ||
Db       787
AGGCCGACTCCAGCCCGTGGCGCTGAGCCAGGTCGTGGCTGGTGTTGGCAGCCTGGTGGC 728
```

```
Qy        608 CTCCAGG--------------------CAT--------GATGGGCCCAC-
CTC----C 632
              ||||| |                      | |       |||||||| | |||
              |
Db        727
CTCCATGGTGCAGGTGAAGGTCCTGGAACGTGAGGTTGCGGATGGGCCGGCGCTCTGAGC 668

Qy        633 TGGTATGAGACCTCCTATGGGTCCCCCAA--TGGGGATCCCC-
CCTGGAAGAGGGAC--- 686
                  ||| ||  |||||         | ||| |  || ||  || |  || | ||| || |
Db        667 AGGTCTGC-ACCTC------
GCCCCTCGAGCTGCGGTACCACGTCTTGTAGAAGGTCACA 615

Qy        687 ------------TCCAATGG--------GCATGC--------------------
CCCCT-- 705
                          |||| ||      || |||                |||||
Db        614
TCGTGCCCTTTGTCCACAGGGCCCAAGAGCCTGCAGGTGAGGGTGACGTTCTGCCCCTCG 555

Qy        706 -----------CCGGGAATGCGGC-----------------CT-CCTCC--
CCCT------ 729
                         | |||||| ||||                 || || ||   |||
Db        554
GGACAGACATACAGGGAATACGGCGTGGCGACCTTGAAGGCTGCCACCGGACCTGCTCAG 495

Qy        730 -GGGATGCGAGGCCT-TCT-TTGAC---------------CCTTG--
GCCACAGAGTATG 769
               | || ||| ||| || |    ||||               ||| |   || |||||
               |
Db        494
AGAGAGGAGAGCCCTGTCACCTGACTGATCCAGTGCTACTCCTGGCAACCCCAGAGCGGG 435

Qy        770 GAAGTAGCT---CCGCAG---------AGGCGTGGGCTCGATTCC--TCAG--
GGCCACG 813
              |||| | ||   || |         || |  ||| |   |   |||| | ||
              |
Db        434
GAAGAACCTTAGCCTCTGCTACTTCCCAGCCACAGGCCAGGGGCATGTCAGCTGACCTCC 375

Qy        814 TTACCACAGAC--CTG--TTTGTT----------------
TCTTATGCTGTTGTTCGTGG 853
               || || | |   |||  ||||||                 || || |||||||| |
               ||
Db        374
CTAAGACTGCCTTCTGCATTTGTTCACAAACCCCACTCCATCCTAGGCTGTTGTAGGGGG 315

Qy        854 AGTCTCA--------------TGGGATTG--TCTGGTTTC------------------
CC 879
              |||| ||             | || ||   |||| ||
              |
Db        314
AGTCACAGAAGCTTCCCCAACTAGGGGTGCTCCTGGATGCTGGACAGGGCAGGGAGAGAC 255

Qy        880 TTACAGGGCC--------------------CCCTC--
CCC-------------------- 897
              || |||||                    ||||| |||
Db        254
TTGGAGGGCAGTGATGCAGTCGGGTGTGTCCCTCTTCCCAGTAGAGTATATGCAAAACCT 195
```

```
Qy        898 ------------------------CGGGAATGC----------GCC-
CACCAAGGCCC 920
                              | |||| ||            ||  | ||  |
||
Db        194
GTTGGGTGGGAGGCAGGTTGGGGAGCAGGAAGGCTGTTTCGAACAGCAGCTCCTTGTCCT 135

Qy        921 TAGACTCATCT----TGGCC-----
CTCCTCAGCTCCCTGCCTGTTTCCCGTAAGGCTGT 971
                  | | | | |||       ||||      |  | |||| || |||| ||   | | | ||| |
|||
Db        134 TGGCCGC-TCTGTAGGGGCCATCAACACCTCTGC-CCCTTCC---
TACTCCTAGGACTGA 80

Qy        972 ACAT--AGTCCTTTTATCTCCTTGTGGC-CTATGA----AACTG-GTTTATAA----
TAA 1019
                  ||||    |||  |  |  ||  |  || |||  ||    | ||| || |   ||     |
Db         79
ACATGCCTTCCCATCCTTGCCAGGGAGCACTAAGAGAGCACCTGCGTGTGCAAGGCCTGG 20

Qy       1020 ACTCTTAAGAGAACATTATAATTGC 1044
                  |  || |  |||       | |||
Db         19 GCCAGTAGGCCAAC------AGTGC 1

RESULT 4
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match            44.5%;  Score 2898;  DB 1;  Length 3210;
  Best Local Similarity  36.7%;  Pred. No. 8.7e-182;
  Matches  737;  Conservative   0;  Mismatches  290;  Indels  980;
Gaps  121;

Qy         1 GAATTCCCTGAGGAGGC---
GAATCCGGCGGGTATCAG--------------------- 35
                  |  || || |  |  ||   | ||| | | ||| |||
Db        444
GGGTTGCCAGGAGTAGCACTGGATCAGTCAGGTGACAGGGCTCTCCTCTCTCTGAGCAGG 503
```

```
Qy        36 ---------AGCCATCAGAACCGCCA---------CCATG----------
ACGGTGGGCA 67
               |||| |||   |||||       || ||            ||
|||||
Db       504
TCCGGTGGCAGCCTTCAAGGTCGCCACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCA 563

Qy        68 AGA--------------GCA-------------------------GCAAGATG----
CTG 84
                |             |||                     ||| ||||
||
Db       564
GAACGTCACCCTCACCTGCAGGCTCTTGGGCCCTGTGGACAAAGGGCACGATGTGACCTT 623

Qy        85 CAGCATAT--TGATTAC---------AGGATGAGGTGCA-TCCTGC----AG-
GACGGCC 127
                | ||    || |  |            ||  ||||||||  |||||    || |
|||||
Db       624
CTACAAGACGTGGTACCGCAGCTCGAGGGGCGAGGTGCAGACCTGCTCAGAGCGCCGGCC 683

Qy       128 ---------------------GGATCTTCATTGGCACCTT--------
CAAGGCT----- 153
                                    ||| |||||   ||||| |         | |||||
Db       684
CATCCGCAACCTCACGTTCCAGGACCTTCACCTGCACCATGGAGGCCACCAGGCTGCCAA 743

Qy       154 ---------------------------------------------
TTTGACAAGCA------ 164
                                                              |  ||| | ||
Db       744
CACCAGCCACGACCTGGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCATGGCAA 803

Qy       165 ------------CATG---AATTTGATCCT------------------CTG-TGACT-
GT 189
                         ||||    || ||| |||                    ||| || ||
Db       804
CTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCTCTACTGCTGCCTGGT 863

Qy       190 GAT-GAGTTCAG------------------AAAGATCAA----GCCAAAGAACT-
C---- 221
                | | ||| ||||                  | | |  |    |||| ||| || || |
Db       864
GGTGGAGATCAGGCACCACCACTCGGAGCACAGGGTCCATGGTGCCATGGAGCTGCAGGT 923

Qy       222 -CAAACAAGCAGA---------------------------------------
AAGGGAAG 241
                || ||| ||| |                                         |||
Db       924
GCAGACAGGCAAAGATGCACCATCCAACTGTGTGGTGTACCCATCCTCCTCCCAGGAGAG 983

Qy       242 AGAA--------------------GC-------GAGTCCTCGGT-----------
CTGGTG 264
                |||                    ||     | | ||| ||           ||
|
Db       984
TGAAAGTAAGGGACCAACCTCTTGCCCCTTTTGGGTTCTCTGTTTTCTTCTGTCCTCATC 1043
```

```
Qy        265 CTGCTGCGAGG--------GGAGAATCTGGTCTCA-------
ATGACAGTAGAG------ 303
              ||||  | ||         ||| | ||||| ||||      |  |   |||
Db       1044 CTGCACCCAGACCCTGTTTGGA-
ACTCTGGCCTCATCACCCCAAGCCCTCAGAACCCCCC 1102


Qy        304 GGACCTCCTCC-------------CAAA--------GATAC-----
TGGT---------- 327
              || ||||||||          || |        | | |    ||||
Db       1103 GGTCCTCCTCCTTTTCTGCTGCTGCACATCCCTTCTGCTTCCTCCTTGGTGCAATCCCCA 1162


Qy        328 ------------------ATTGCTC--GAGT------TCCACTTG-----
CTGGAGCTG 355
                                 ||||| ||||      ||| |||    ||||||
|
Db       1163 GAAGCCCACTCTCCTTCCATCTGCTCTGGAGTCTCTGCTCCTCTTGACTCTCTGGAGTGG 1222


Qy        356 CCGGGGGCC----CAGGGATC----GGCAGGGC---TGC----TGGCAG-----
AGGAAT 395
              |  | |||   ||| || |   | |||||| |||   || ||| ||
Db       1223 CT--
GTGCCTTGGCAGTGACCTTTGGCCAGGGCAAGTGCCTCATGACAGGTACTGGGTGC 1280


Qy        396 CC----CAGCTGGGGTTC-CCATGCC--CCAGGCTCCT-------------
GCAGG---- 431
              ||  ||||| |   | || |||| |||| | |||          || ||
Db       1281 CCCAGGCAGCTAAGTGCCGCCCTGCCCACCAGCCCCCTATGGCTTGGGAAGGCTGGGGGT 1340


Qy        432 --ACTTG-----CTGGG------CCAGTC-----------------------------
CGT 450
                 ||||     | |||      || ||                                |
Db       1341 CCTCTTGGCCAACAGGGTGAAACCCCATCTCTACTAAAAACACAAAAATTAGCCAGGCAT 1400


Qy        451 GGGGTTGGCGGGCC----ATCCCAAC--------AGG-TGA---------------
TGAC 482
              || | ||| |||      |||||| |          ||| |||
|||
Db       1401 GGTGGT-
GCGCGCCTGTAGTCCCAGCTACTCAAGAGGCTGAGGCAAGAGAATCGCTTGAA 1459


Qy        483 CCCACAAGGAAGAGG-TACTGT-TGCAGC---
CGCTGCAGCTGCTGCCACAGCCAGT--A 535
              |||   || |||||| | || | || |    ||| || |||| |  ||||| |
|
Db       1460 CCCGGGAGTCAGAGGTTGCAGTGAGCCGAGATCGC-GCCACTGC-
ACTCCAGCCTGCTGA 1517


Qy        536 TTGC-CGGGGCTCCAACCCAG-------TACCCA-------CCTGGCC--
GTGGGGGTCC 578
              | | | ||||| || ||        |||||       |||||| |||| |
|
Db       1518 TAGAGCAAGACTCCATCTCAAAAAAAAACAACCCAAAATTTGCCTGGCATGGTGGCAGGCA 1577


Qy        579 TC------
```

```
CCCCAC-------------------------------------------------- 586
          ||      |||  |
Db      1578
TCTGTAATCCCAGCTACTCGGGAGGCTGAGACATGAGAGCTGCTTGAACCTGGGAGGCAG 1637


Qy      587 ------CTATGGGCCGAGGAGCACCCC------
CTCCAGGCATGATG------------- 621
            |  || ||||| || ||| ||   |||||| |  | ||
Db      1638 AAGTTGCAGTGAGCCGA-
GATCACACCACTGCACTCCAGCCTGGGTGACAGAGCGAGACT 1696


Qy      622 --GGCCCA----------------CCTCCTGGT----ATGAGACCTC-
CTATG------- 651
              | ||||             || ||||   |||    ||| |||||
Db      1697
CTGTCCCAAAAAATCAAAAAAATCACTTTTGGTAGAGATGCACTCTCGCTATGTTGCCCA 1756


Qy      652 ----GGTC-------------
CCCCAATGGGGATCCCCCCTGGAAGAGGGACTCCAA--- 691
            ||||              | | || |||| ||| ||       ||||||
Db      1757 GGCTGGTCTTGAACTCCTGGGCTCAATTGATCTTCCCACCTTGA------
CCTCCAAAGT 1810


Qy      692 --TGGG------------------CATGCCC--
CCTCCGGGAATGC-------------- 715
              ||||                ||||||   |||| |||||| |
Db      1811
GCTGGGATTACAGGTGTGAGCCACCATGCCTAGCCTCAGGGAATTCTTATAAGAACTCTA 1870


Qy        716 -------GGCCTC--------CTC----CCCCTGGGATGCGAGGCCTT----------
CT 746
              ||| ||        |||     || ||| | ||||||||
Db      1871
TGAAGTAGGCATCACCATCTTCTCTGTATCCATGGAAAGAGAGGCCTAGAGATGTATGCT 1930


Qy      747 ---TTGACC-------CTTGGCCACAGAGTA--------TGGAAGT--AGCT----
CCGC 782
              ||| ||        | |  ||| ||| |||        ||| ||  ||||
Db      1931 AACTTGCCCAAGCTCACATAGCC-
CAGGGTAGCATAGCTGGGATGTTGAGCTGAGGCCGG 1989


Qy      783 AG----------AGGCG-TGG----GCTC---GATTCCTCAGG-------GC---
CACGT 814
              ||          || || ||    || |   |  | ||| ||        ||
Db      1990
AGGAGAAGTAGCAGTCGCTGGCAGAGCACACAGGCTGCTCTGGGGGATGAGCTGGTGCGT 2049


Qy      815 TAC---CACAGACCTG-TTTG--TTTCTTATGCTGT-TGTTCGTGGAGT-
CTCATGGGAT 866
              |    |||| || |   ||   ||| | || ||  |  | |||| |   | | |
Db      2050
TTAAGGAACAGGCCAGCACTGGCATTCGCAAGCAGTGGGGAAGGGGAGAGATGCCGAGGT 2109


Qy      867 TGTCTGGTTTCC---
CTTACAGGGCCC------------------------------- 890
              ||| || |||   ||| ||| | ||
```

```
Db      2110 GGTC-
AGTATCCTGACTTTCAGAGGCCTTTTTTTGTTTGTTTTAATTTTTGCTAGATTGA 2168

Qy       891 --------CCTC-----------CCCCGGGAATG------CGCCCA-------
CCAAGGC 918
                       |||         | |  |||||||    | |||       ||||
|
Db      2169 TATTAAAAACTCATGTGGAGGAACTCAAGGAATGTTTAGAAGACCAAAAGTCCCCAATGA 2228

Qy       919 C-----CTA----
GACTCATCTTGGCCCTCCTCAGCTCCCTGCCTGTTTCCCGTAAGGCT 969
                  |     | |    || || ||  | | ||||  |||  | |||||||| |   | |
Db      2229 CAGGAACAAAAGCAACCAATTTTTAACTTTCTCTTTCTCATT-
CCTGTTTTCATTGATTTC 2287

Qy       970 GTACA--TAGTCCTTTT-ATC------TCCTTGTGGC----------
CTATGAAACT--- 1007
                  |||  ||||||||||  ||        ||  ||| |          || |||| ||
Db      2288 CCACATGTAGTCCTTTTGCTCAGGAAGTCTTTGGGGAAATTAAGGATCTTTGAAGCTCTG 2347

Qy      1008 -------------GGTTTAT----------------------------
AATAAACT-C 1023
                       ||||  |                         |||  ||||
|
Db      2348 AAATAGGTGATCAGGTTAGTGGTGTCTGTCAGCTGTCTAAGAGGTTGGAAAATGAACTAC 2407

Qy      1024 TTAAGA-------GAACATTATAATTG 1043
                | ||||    ||| ||  ||  |  |
Db      2408 TCAAGATAGTCACGAAAATACTGAAAG 2434


RESULT 5
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;  LENGTH: 2437
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match            43.2%;  Score 2818.5;  DB 1;  Length 2437;
  Best Local Similarity  36.1%;  Pred. No. 4.9e-177;
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  Matches  710;  Conservative    0;  Mismatches  318;  Indels  937;
Gaps  116;

Qy         1 GAATTC-------CCTGAGGAGG------
CGAATCCGGCGGGTATCAGAGCCATCAGAA- 46
             ||  ||       |||||| ||       | |    |   | || ||| |   |   || |
|
Db      1972 GAGATCAGTGAGGCCTGAAGACATGTGTTCAATATCAAC-
GGAATCTGGCCTCTCGGGAT 1914

Qy        47 ---------CCGCCACC-------------------------ATGAC-
GGTGGG------ 65
                        || ||||                        ||| | ||||||
Db      1913
GAAATATTTCCTCCACAACTTGCTTCAACAATGGCTTATAAGATGCCTGGTGGGTATGAT 1854

Qy        66 -------------------------------CAAGAG-----------
CAGCAAGATGCT 83
                                               || ||||         |||||| ||
|
Db      1853
TTCCAGGAACATATACAGACTTAAACTGTTTCAGGAGACTCCGAGCTCCAGCAATATCCC 1794

Qy        84 G----------------------CAGCATATT------------------
GATTACAGG 102
             |                      | ||| ||               |||||
|
Db      1793
GAAGTGAAGTAAAGAGTTCATCCACGGCAATTTTGGATTTGTGAAATGTCAGATTAATTG 1734

Qy       103 ATGAGGTGCA-TCC---------TGCAG-------GACGG-CCGGA-
TCTTCATTGGC-A 142
             | ||| || ||         |||||       ||| | || || || ||| |
|
Db      1733
AAGAGTCCCAGTCCGTAATTTTTTGCAGCAAAGGTGACAATCCAGATTCCTCACAGAAGA 1674

Qy       143 CCT---TCAAGGCTT--TTGAC-------------
AAGCACATGAATTTGATCCTCTGTG 184
             |||    ||| |||| |||||              |||| | |||| || |
|||
Db      1673 CCTGAGCCAATGCTTTCTTGACTTTTTCTTCTGCTTCACACAGGTCTTTG-
TCTACCGTG 1615

Qy       185 A------CTGTGA-TGAGT---------TCAGAAAGATCA--AG--
CCAAAGAAC----- 219
             |        | |||| || |         | |||| ||||| || || || |
Db      1614
AGCTCTCCAGTGACAGAATAAATATATATGAGAAGGATCAGCAGTTCCTCAGGGCTGTAG 1555

Qy       220 TCC-------------------------AAACA-----AGCAG------------
AAAG 236
             |||                        || ||   |||||              ||
|
Db      1554
TCCTCGTTGGTTCTCTGGGTTACAGGCTTAATCATGGGCAGCAGCTGATTTAACACAACG 1495

Qy       237 G------------------------GAAG-AGAAGC-------------GA-----
GTCC 253
             |                        |||| || |||         ||
```

```
    ||||
Db        1494
GACATTGCTGACTCCCCAATGCTCTGAAGAAGGAGCCTTTCAAAAGCCAGAAAGTTGTCC 1435

Qy         254 T------CGGTCT---GGTGCTGCTGCG-------AGGGGAGAATC-----------
TGG 286
                 | ||||   |||| | |  ||        | ||   | ||
    ||
Db        1434
CACTTGGCAGTCTGTGGGTGTTTCAACGTTTGAGCTGTGGCCAGTCCAAGCTGGAGGAGG 1375

Qy         287 TCTCAATGA--CAGTAGAG----------------------------
GGAC------ 307
               | |||||| || |||||                          ||||
Db        1374
CCACAATGATTCATTAGAGCTTTGAGGTTGTTCTTGAAGAGCTGAATATAGGACATGAGC 1315

Qy         308 -------------CTCCTCCCAAA--------GAT--ACTGGTAT----TGCT---
CGAG 337
                            ||| |||| |        ||| | ||| |  |||| ||
Db        1314
TGTCCCGGTGTGACTCTCCCCATACTCATCTTGATTGGCAGGTTTTCTCTGCTTGCCGC- 1256

Qy         338 TTCCACTTGCTG-----GAGCTGCCG------------
GGGGCCCAGGGATCGGCAGGGC 380
               ||||||| | ||    || || ||            | ||  || | || |
Db        1255
TTCCACTAGATGTCTCCGAACTTCCATCACTGCCTCTTTGTGCTTAGTGTTCAGTAAAGC 1196

Qy         381 TGC-----------TGGCAGAGGAATCCCAG----------------
CTGGGGTTCCCAT 413
               | |          |||| | || || |                  |||| |
Db        1195
TTCCCATAGGGCTTTGGCTGTGGTGTCACTGAATTGTGAAAGACAGCCTGGTGCAACCAC 1136

Qy         414 G-------------CCCCAG-----------------GCT----------
CCTGCAGGAC 433
                            || |||             |||           || ||
Db        1135
ATTATAATTTTCCTCCTCAGTATGGAGTGCAGTGAGCGCTATCATGTTAACCATCACATC 1076

Qy         434 --TTGCTGGGCCAGTCCG-TGGGGTTG-GCGGGC-----CATCCCAAC--
AG-------- 474
                  ||| |||| |  | ||||| |||||         |  ||||| ||
Db        1075
ATTTGTGTGGCCTGGGAGCTGGGGAAGTGCTGAAATGATCTTCTCTACTAAGTTGTCTCC 1016

Qy         475 GTGATGACCC----CACAAGGAAGA-----GGTACTGT----TGCAGCCGCTGCAG--
CT 519
               ||||| ||   | | |  ||     ||| ||||        | || ||| |
Db        1015
ATGATGTCCAACTGCTCCTGTGAGATCCAGGGTTCTGTCCACAAAAACCACTGATGCCCT 956

Qy         520 G-CTGCCACAG-------CCAGT--ATTGCGGGGCTCCAAC--CCAGTACC----
C--- 560
                 | |||| |||        || ||  |||| ||||| |    |||| ||      |
```

```
Db       955
GCCTGCAGCAGTCTTCTTCCTGTTCTTTGCAGGGGCATAATTGGCCAGATCCGCAGCGAT 896

Qy       561 -ACCTGGCCGTGGGGG--------------TCCTCCC--
CCACCTA------------ 589
                ||||| |   ||         ||||||  | ||||
Db       895
GACCTGACTTAAGGAACCTACAGCAAAACACTCCTCCCGTACTCCTAAATGTTCACACAG 836

Qy       590 -----TG-GGCC-------------------------------------------
GA 597
                   || ||||
         |
Db       835
AGAACTGAGGCCTGACACTAGGCATCTGATCTGCAGCAGCAGCTCTGGGGTTAGCGTAGT 776

Qy       598 GGAG-------CACCC--------------CCTCCAGGCATGATGGGC-
C---------- 625
                ||||      |||||            ||||  | || | |||| |
Db       775
GGAGTCCACATCACCCAGGCTTCCCAGCTTCCTCTTGTCCGGTCGGGCGCTATTAAGGAG 716

Qy       626 ---CACCTCCTGGTAT--------------GAGACCTCCTATGG-GTCC---
CCCAATG 663
                ||| |||||| |            || |    ||| |||   | |
         ||
Db       715
GTGCACATCCTGGGGTAGCAGTGGGAAAAGGGATGCAAAAGCTGGAGTCAAGGCAAAGTG 656

Qy       664 GGGATCCCC--------------
CCTGGAAGAGGGACTCCAATGGGC------------- 696
                ||||  |  |              | |||  || || ||  | |||
Db       655 GGGAGCAACAGGGGCAAGCAATAACGGGACATGGAACACC--
TCGGCCGTGTAGTTCATG 598

Qy       697 ATGCCC--------------------CCTCCGG-------------
GAATGCGGCCTCCTC 724
                |||||                  ||||| |          |  ||| |||
||||
Db       597 TTGCCCATCCATTCACACAGCTTCTCCTCCAGCTGCTCGAACACCGGCTGCTGCC-
CCTC 539

Qy       725 C----------------CC-CTGGGA----------------------
TGCGAGGCCTTC 745
                |              || ||||||                | ||| |||
         |
Db       538
CATCTCGGCCGCTGCCGCCGCTGGGACATGATTAGCTGTGAGGTGGACAGCGTGGCTCAC 479

Qy       746 ---TTTGACCCTTGGCCACAGAGTA-TGGAAGTAGCT-CCGCAGAGG------
CGTGGGC 794
                | ||||||    ||||| | || |||||||| || | ||||| |     |||
         ||
Db       478 GGTTGTGACC----
ACCACACAATACTGGAAGTGACTGCGGCAGATGATGTCCCGTAGGA 423

Qy       795 TCGATTCCTCAG---GGCC------------------ACGTTACCACAGAC-----
CTGTT 829
                ||  ||| | |  ||||               |  | |||| |    |||
         |
```

```
Db        422 TC---
TCCACGGTCCGGCCTTTCAGCAGGCAGCTCAGCACAAACACTGCCTTGGGCTGCT 366

Qy        830 TGTTTCTTATGCTGTTGTTCGTGGAG---------
TCTCATGGGATTGTCTGGTTTCC-- 878
              || || |  | | ||| |       || || | ||  ||| ||   ||
Db        365 TGGCTCCACCACCAAT-
TGCGTCGGGCTCGAACTCTCGCAGGTGACAGTCAGGGCCCCCC 307

Qy        879 ----CTTACAGGG-----------CCCCCTCCCC-----------CGG----
GAATGCG 907
                  | | ||||         || |  ||||           |||    |
Db        306
ACCGCCTCCAGGAGACGGGTGGATCCGCAGCCCCAGTGCAGGCTCTCGGCGCAGGCGGCG 247

Qy        908 CCC------
ACCAAGGCCCTAGACTCATCTTGGCCCTCCTCAGCTCCCTGCCT------G 955
                    ||        |||| |||| |  ||| |||||| | | |||||| |||
|
Db        246 TCCAGGTAAACCACAGCCC--
GTTTCACTTTGGCCAGCACCTGCTCCCATCCTTGCTGGG 189

Qy        956 TTT-----------CCCGTAAGGCT-----------
GTACATAGTC-------------- 979
                |              ||||    |||          | |  || |
Db        188
TAAAGGACAGTACGCCCGAGGCGCTCATGGTTGGGGATTCGCAGACTTGGGAAACTACGG 129

Qy        980 --------CTTTTATC-------------TCC-----
TTGTGGCCTATGAAACT-----G 1008
                    ||| | ||                 |||     ||| |  |   || |||
Db        128
TGCAGGAACTTCTTTCAGAACTCACCGCTTCCGGAAATTGGGCTCCGGGAGACTTTGACA 69

Qy       1009 GTTT--ATAATAAACTCT-TAAGAGAACATTAT------AATTGC 1044
                || | | | || || | || |  ||||| |      ||||| |
Db         68 GTCTCCACAGTACACCCAGTAGGCCAACAGTGCTCGAGGAATTCC 24
```

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;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-61

   Query Match             43.2%;  Score 2816;  DB 1;  Length 2437;
   Best Local Similarity   36.2%;  Pred. No. 7.4e-177;
   Matches  706;  Conservative   0;  Mismatches  322;  Indels  924;
Gaps  110;

Qy         2 AATTCCCTGAGGAGGCGA-------------ATCCGGC-----
GGGTATCAGAGCCATCA 43
             |||| || || | || ||            ||| ||     | | | || |
|
Db        90
AATTTCCGGAAGCGGTGAGTTCTGAAAGAAGTTCCTGCACCGTAGTTTCCCAAGTCTGCG 149

Qy        44 GAACCGCCACCATGA---CGGTGGGCAAGAG----------CAGCAA-----
GATGC--- 82
             | || | ||||||| |    ||||          |||||| |   | ||
Db       150
AATCCCCAACCATGAGCGCCTCGGGCGTACTGTCCTTTACCCAGCAAGGATGGGAGCAGG 209

Qy        83 TGCAG--CATATTGATTACAGGATGAGGT----------GCATCCTGC----
AGGAC--- 123
             |||| | || | ||| || || || |||         || ||||| || |
Db       210 TGCTGGCCAAAGTGA-
AACGGGCTGTGGTTTACCTGGACGCCGCCTGCGCCGAGAGCCTG 268

Qy       124 ------GGC--CGGATCTTC----------------------------
ATTGGCACCTT 146
                   ||| |||||| |                        | ||
|||||
Db       269
CACTGGGGCTGCGGATCCACCCGTCTCCTGGAGGCGGTGGGGGGCCCTGACTGTCACCTG 328

Qy       147 CAAGGCTTTTGACAAGCAC-ATGAATTTGAT----------------CCT---
CTGTGAC 186
             | || || | ||| | | | ||| |            || | |||
Db       329 CGAGAGTT----
CGAGCCCGACGCAATTGGTGGTGGAGCCAAGCAGCCCAAGGCAGTGTT 384

Qy       187 TGTGATGAGTT-----CAGAAAGATCAAGCCAAAGAACTCCAA----ACA--------
AG 229
             |||| |||| |     | ||||| |   || || ||| ||    |||
|
Db       385
TGTGCTGAGCTGCCTGCTGAAAGGCCGGACCGTGGAGATCCTACGGGACATCATCTGCCG 444

Qy       230 CAGAAA------------------GGGAA-------GAGAAGCG-
AGTCCTC-------- 255
             ||| |                    || |     ||| || | |||| |
Db       445
CAGTCACTTCCAGTATTGTGTGGTGGTCACAACCGTGAGCCACGCTGTCCACCTCACAGC 504

Qy       256 -GGTCTGGT----------GCTGCTGC-------GAGGGG-
AGAATCTGGT--------- 287
              || ||          || || ||     |||||| || | |||
Db       505
TAATCATGTCCCAGCGGCGGCAGCGGCCGAGATGGAGGGGCAGCAGCCGGTGTTCGAGCA 564
```

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Qy        288 -CT---------CAATGACAGTAGAGGGAC--------CTCCTC--
CCAAAG------- 319
                 ||          |  ||  |  | || ||  |      || | |  || |
Db        565
GCTGGAGGAGAAGCTGTGTGAATGGATGGGCAACATGAACTACACGGCCGAGGTGTTCCA 624

Qy        320 -ATACTGGTATTGCT----CGAGTT-----CCACTT-------------
GCTGGAGCTGC 356
                 | | |||||||    | |||     ||||||            ||| ||
|
Db        625
TGTCCCGTTATTGCTTGCCCCTGTTGCTCCCCACTTTGCCTTGACTCCAGCTTTTGCATC 684

Qy        357 ----------CGGGGGCCCAGGGAT--------------------
CGGCAGGGCTGCTG 385
                 | |   ||| ||||                  || | || |
|
Db        685
CCTTTTCCCACTGCTACCCCAGGATGTGCACCTCCTTAATAGCGCCCGACCGGACAAGAG 744

Qy        386 GCAG--AGGAATCCCAGCTG----GGGTTCC------CATGCCCCAG----
GCTCCTGCA 429
                 | ||   |||| ||  ||    || |||      |  |||||||    |||
|||||
Db        745
GAAGCTGGGAAGCCTGGGTGATGTGGACTCCACTACGCTAACCCCAGAGCTGCTGCTGCA 804

Qy        430 GGAC--TTGC----TG---GGCC------------------------
AGTCCGTGGG-- 453
                 | |   |||    ||   ||||                    ||| || | |
Db        805
GATCAGATGCCTAGTGTCAGGCCTCAGTTCTCTGTGTGAACATTTAGGAGTACGGGAGGA 864

Qy        454 ----------GTTGG----------CGGGCCATCCCAACAG---------
GTGATGACCC 484
                 || ||         | || |||| | | |            | |||
|||
Db        865
GTGTTTTGCTGTAGGTTCCTTAAGTCAGGTCATCGCTGCGGATCTGGCCAATTATGCCCC 924

Qy        485 CACAAGGAAGAGGT-----ACTGTTGCAGCC---GCTGCAG------
CTGCTGCCACAGC 530
                 ||| ||| |||     |||| ||||| | ||  || |||       || | ||| |
|
Db        925
TGCAAAGAACAGGAAGAAGACTGCTGCAGGCAGGGCATCAGTGGTTTTTGTGGACAGAAC 984

Qy        531 C---AGTATTGCCGGGGC---------TC-------
CAACCCAGTA-------------- 557
                 |   | | | ||| || ||         ||       |||| ||||
Db        985
CCTGGATCTCACAGGAGCAGTTGGACATCATGGAGACAACTTAGTAGAGAAGATCATTTC 1044

Qy        558 --------CCCA----CCTGGCC-----------GTGGGGGT---CCT-----
CCCCCAC 586
                 ||||    || ||||         ||| ||| | |      | |
|||
Db        1045
AGCACTTCCCCAGCTCCCCAGGCCACACAAATGATGTGATGGTTAACATGATAGCGCTCAC 1104
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Qy        587 ----
CTATGGGCCGAGGAG------------------------------------------ 601
                   ||    |  ||||||
Db       1105
TGCACTCCATACTGAGGAGGAAAATTATAATGTGGTTGCACCAGGCTGTCTTTCACAATT 1164


Qy        602 ------CACCCCTCC-AGGCATGATGG-----------GCCCAC----
CTC-------- 631
                    |||| |  || | ||    ||||         |  |||   | |
Db       1165
CAGTGACACCACAGCCAAAGCCCTATGGGAAGCTTTACTGAACACTAAGCACAAAGAGGC 1224


Qy        632 ----CTGG----TATGAGACCTCCTATGG----GTC------------CC--
CCA----- 660
                   |||    |  ||||| ||   |||    | |          || |||
Db       1225
AGTGATGGAAGTTCGGAGACATCTAGTGGAAGCGGCAAGCAGAGAAAACCTGCCAATCAA 1284


Qy        661 -------ATGGGGA---TCCCCCCTGG----------------------------
AAGAG 682
                   ||||||||   || | |||  ||
||||
Db       1285
GATGAGTATGGGGAGAGTCACACCGGGACAGCTCATGTCCTATATTCAGCTCTTCAAGAA 1344


Qy        683 GGA--------CTCCAATGGG-CAT----GCCCCCTCCG----
GGAATGCGGCCTC---- 721
                   |    ||| |||| |||   ||| ||||   ||| | |||| |
Db       1345 CAACCTCAAAGCTCTAATGAATCATTGTGGCCTCCTCCAGCTTGGACT--
GGCCACAGCT 1402


Qy        722 ------------CTCCCCC-----------TGGGA----------------
TGCGAGG--C 741
                   | |||| |        ||||| |          || |||
|
Db       1403
CAAACGTTGAAACACCCACAGACTGCCAAGTGGGACAACTTTCTGGCTTTTGAAAGGCTC 1462


Qy        742 CTTCTT----------------------TGACCCTTG----------------
GCCACAG 763
                   ||||||                   || || |||           |||
|
Db       1463
CTTCTTCAGAGCATTGGGGAGTCAGCAATGTCCGTTGTGTTAAATCAGCTGCTGCCCATG 1522


Qy        764 AGTATGGAAGTAGC-------TCCGCAGAGG--------
CGTGGG--------------- 793
                   | || | ||| |        || |||| |       | || |
Db       1523
ATTAAGCCTGTAACCCAGAGAACCAACGAGGACTACAGCCCTGAGGAACTGCTGATCCTT 1582


Qy        794 CTCG---------ATTC---CTCAGG---GC-CACGTTA-
CCACAGACCTGTTTGTTTCT 836
                   |||     |||| | | ||   || |||| ||  || ||||||||| ||
|
Db       1583
CTCATATATATTTATTCTGTCACTGGAGAGCTCACGGTAGACAAAGACCTGTGTGAAGCA 1642


Qy        837 TATG------------------------CTGTTGTTC---
GTGGAGTCTCATGGGATTGTC 870
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                 | |                        | |  | |||    |  ||| |||
||||||||
Db      1643 GAAGAAAAAGTCAAGAAAGCATTGGCTCAGGTCTTCTGTGAGGAATCT----
GGATTGTC 1698

Qy       871 TGGTTTCC------------
CTTACAGGGCCCCCTC----------------------C 895
                   ||| |                |  || ||| |  | ||
|
Db      1699
ACCTTTGCTGCAAAAAATTACGGACTGGGACTCTTCAATTAATCTGACATTTCACAAATC 1758

Qy       896 C-------CCGGGAATGCGCCCACCAAGGCCCT---------------------
AGACT 926
                 |        ||| | |||  | |     |   | ||             ||
||
Db      1759
CAAAATTGCCGTGGATGAACTCTTTACTTCACTTCGGGATATTGCTGGAGCTCGGAGTCT 1818

Qy       927 C------------------------ATCTTGG--------CCCTCCT--
CAGCT----- 946
                 |                        || |||      ||| ||   || ||
Db      1819
CCTGAAACAGTTTAAGTCTGTATATGTTCCTGGAAATCATACCCACCAGGCATCTTATAA 1878

Qy       947 -CCCT-------GCCTGTT-----------------
TCCCGTAAGGCTGTACATAGTCCT 981
                   || |        || |||               ||||| ||||    || |
|||
Db      1879 GCCATTGTTGAAGCAAGTTGTGGAGGAAATATTTCATCCCGAGAGGC----
CAGATTCCG 1934

Qy       982 TTTAT------CTC----CTTGTGGCCT-----------ATGAAACTGG-
TTTATAATAA 1019
                   || ||      | |    ||| |||||          | ||||||| ||||  ||
Db      1935
TTGATATTGAACACATGTCTTCAGGCCTCACTGATCTCCTTAAAACTGGATTTAGCATGT 1994

Qy      1020 ACTCTTAAGAGA-------ACATTATAATTGC 1044
                   |   | | ||        ||| || |  |
Db      1995 TCATGAAGGTGAGCCGGCCTCATCCTAGTGAC 2026


RESULT 7
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
```

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  Query Match              41.7%;  Score 2715;  DB 1;  Length 2198;
  Best Local Similarity   36.7%;  Pred. No. 4.8e-170;
  Matches  666;  Conservative   0;  Mismatches  365;  Indels  786;
Gaps   96;

Qy        1 GAATTCCCTGAGGAGGCGAATCCGGCGGGT--
ATCAGAGCCATCAGAACCGCCACCATG- 57
            |    ||||||||| ||    || | |||   | |    ||| ||| |    || |||
|
Db     1885
GTGGGCCCTGAGGAAGCACCACCAGAGGGAGGAGCTCCACCACCAGGAAATCCCCCAGGC 1826

Qy       58 ---ACGGTGGGCAAG--
AGCAGCAAGATGCTGCAGCATATTGAT---------------- 96
            |    |||| |    | |||   || | |||| |   ||||
Db     1825
ATTCCTCCTGGCATGCCTCCTGCACTCTGGTACAGCTTGGTGATGATGGGGTTGCAAACT 1766

Qy       97 ---TACAG--------GATGAGGTGCA------TCCTGCAGGACGGCCGGA-
TCTT---- 134
             | |||        | ||| || ||     |||| |   | | | || ||||
Db     1765
TTCTCCAGCTCTTTCTGTTGATGTTCAAATTCTTCCTTCTCAGCAGTCTGATTCTTATCA 1706

Qy      135 ---CA-
TTGGCACCTTCAAGGCTTTTGACAAGCA-------------------------- 164
             || ||| |  |||| |   | ||| | || |
Db     1705
AGCCAGTTGATAATTTCATTACACTTGTCCAGAATCTTCTGTTTGTCCTCATCGTTAATC 1646

Qy      165 ----
CATGAATTTGATCCTCTGTGACTGTGATGAGTTCAGAAAGATCAAGCCAAAGAACT 220
             | |||| || |  || ||   || || || |||    | | ||| || ||
|||
Db     1645 TTGCCTTGAAGTTTCTCATCTTCAACAGT--TGCTTTC---
ATGTTGAAGGCATAGGACT 1591

Qy      221 CCAAACAAGCAGAAAGGGAAGAGAAGCGAGT-CCTCGG--
TCTGGTGCTGCTGCGAGGGG 277
             |   |   | |      ||| ||  | | | || || |    ||| | || | ||    |
Db     1590 C---AAGTGAATTCTTGGATGA-CACCTTGTCCCTCTGCTTCTCAT-
CTTCAGCTTTGTA 1536

Qy      278 AGAATCTGGTCTCAATGAC----AGTAGAGGGACCTCCT-----------
CCC------- 315
             || | | ||   |||     || | | ||||                 |||
Db     1535 CTTCTCAGCT-
TCCTGGACCATACGTTCAATGTCTTCCTTGCTCAAACGGCCCTTGTCAT 1477

Qy      316 -AAAGATACTGGTATTGCTCGAGTTCCACTTGCTGGAG-CTGC--
CGGGGGC-------- 363
             |  |||| | | ||| ||   || | | || ||   | |  |  | | | |
Db     1476
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TAGTGATAGTAATCTTGTTCTCTTTTCCCGTACTCTTGTCCACAGCAGAGACATTGAGTA 1417

Qy        364 --CCA--GGGATC---GGCAG----GGCTGCTGGCAGAGGAATCCC------
AGCTG--- 403
                  ||| || ||| | ||      | ||| | | |||||| ||        || |
Db       1416
TACCATTGGCATCAATGTCAAAAGTGACTTCAATCTGAGGAACACCTCGGGGTGCAGGAG 1357

Qy        404 ----------GGGTTC-------CCATGC----------CC----------
CAGGCT--- 423
                        | ||||        ||| ||          ||         || |||
Db       1356
GTATGCCTGTGAGTTCAAACTTGCCAAGCAGGTTGTTATCCTTTGTCATGGCACGCTCGC 1297

Qy        424 ---------CCT------GCAGGACTTGCTGG--GCCA---------------
GTCCGTG 451
                      |||      ||| | ||||| | ||             |||
|||
Db       1296
CTTCATAAACCTGAATAAGCACACCAGGCTGGTTGTCAGAATAGGTAGTGAAGGTCTGTG 1237

Qy        452 ----------GGGTTG-------------GCGGGCCATC------
CCAACAG--G 475
                       || ||             | || | ||    ||| |||
Db       1236
TCTGCTTGGTAGGAATGGTGGTATTACGCTTGATGAGGACAGTCATGACTCCACCAGCAG 1177

Qy        476 TGATGACCCCACAAGGAAGAGG-------
TACTGTTGCAGCC------------------ 510
               | | ||| | |||||        | |    |||||
Db       1176
TTTCAATACCAAGGGAAAGAGGAGTGACATCCAAGAGCAGCAAATCTTGAACATTCTCAG 1117

Qy        511 --------------------GCTG------CAGCTGCTGCCACAGC--
CAGTATTGCCGG 542
                                  ||||     |||||| | ||| ||| | |
|
Db       1116
ACTTGTCTCCAGACAAGATGGCTGCCTGGACAGCTGCACCATAAGCAACAGCTTCATCAG 1057

Qy        543 G------GCTCCAACCCAGTAC----CCACCTG-----
GCCGTGGGGGTCCTCCCCCACC 587
                  |    ||||| | |||| |   ||| ||   | |||| |   || |    |
Db       1056 GGTTGATGCTCTTATTCAGTTCTTTTCCA-
TTGAAGAAGTCTTGGAGAAGCTTCTGAATC 998

Qy        588 TATGGG--CCGAGGAGCACC-CCCTCCAGG-------
CATGA------------------ 619
                  | |||  |||| || || || ||||     |||||
Db        997
TTGGGGATACGAGTAGAACCACCAACCAGGACAATATCATGAATCTGTGACTTGTCTAGT 938

Qy        620 -------------------------TGGGCCCA-----CCTC----
CTGGTATG----- 639
                                  |||| ||| || |  | ||| |
Db        937
TTGGCATCTCGAAGGGCTTTCTCTACTGGGTCCAGGGTGCCACGGAACAGGTCAGCATTC 878
```

```
Qy        640 AGACCTCCTAT--------GGG----------------------
TCCCCCAATGGG---- 665
              ||  || |       |||                 |||  || | |
Db        877
AGTTCTTCAAATCGGGCACGGGTAATGGAGGTATAGAAGTCGATTCCTTCATAGAGAGAA 818

Qy        666 --GATCCC--------CC------CTGGAAGAGGGACTCCAATGGGCATGCCCCCTC-
CG 708
                ||||  |        ||    |||||||||| | | | ||| | |
                                                                      |
Db        817
TCGATCTCAATACTGGCCTGGGTGCTGGAAGAGAGGGTACGCTTAGCACGTTCACAAGCA 758

Qy        709 GGAATGCGGCCTCCTCC----CCCTGGGATGC----GAGGCCTTCTT----
TGACCCTTG 756
              | | ||| || |    | || |      | | ||||||  | |
              |||
Db        757
GTACGGAGGCGTCTTACAGCTCTCTTGTTCTCACTGATGTCCTTCTTATGCTTGCGCTTA 698

Qy        757 GCCACAG----AGTATGG-------------------------------
AAGTAG--- 776
              | |||    |  ||||                          |||| |
Db        697
AACTCAGCAATAAAATGGTTGACCATTCGGTTGTCAAAATCTTCTCCACCCAAGTGGGTG 638

Qy        777 -CTCC--GCAG-AGGCGTGGGCTC---
GATTCCT------------------------ 803
               |||| || | || || |   ||||||
Db        637
TCTCCAGCTGTAGACTTGACCTCAAAGATTCCATCCTCAATAGTGAGGATTGACACATCA 578

Qy        804 --------------CAGGGC---------CACGTTAC------
CACAGACCTGTTTGTTT 834
                           |||| |    |||||| |     | |  |||| |||||
                                                                      |
Db        577
AAAGTGCCACCTCCCAGGTCAAAGATGAGCACGTTTCTTTCTGCTCCAACCTTTTTGTCT 518

Qy        835 ----------------CTTATGCTGTT--------------------
GTTCGTGGAGTC-- 857
                             |   || |||              || | | ||| |
Db        517
AAGCCGTAAGCAATAGCAGCAGCAGTTGGCTCATTAATAATTCTAAGTACATTGAGACCA 458

Qy        858 ---------------TCATGGGATTGTCTG--GTTTC----CCTTACAG------
GGCCC 890
                              || || | ||| | |     | ||| ||     |||
                                                                      |
Db        457 GCAATAGTTCCAGCATCTTTGG-
TAGCCTGACGCTGAGAGTCATTAAAGTAAGCTGGCAC 399

Qy        891 -----CCTC------------------CCCCGGGAATGC----
GC--------------- 908
                   || |             ||| || | || ||
Db        398
TGTGACCACAGCATTGGTAACAGTCTTCCCAAGGTAGGCTTCTGCAATTTCCTTCATCTT 339

Qy        909 --------------------CCACCAAGG--------------------CCCTAG-
ACTC 927
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                            ||  ||   |                      ||||  | |
||
Db       338
TGTCAGAACCATAGAAGACACCTCCTCTGGATAGAAGCTTTTGGTCTCTCCCTTGTATTC 279

Qy       928 ATCTTGGCCCT----CCT--CAGC-----TCCCTGCC------------
TGTTTCCCGTA 964
                  ||||| |||    ||| ||||    || |  ||          ||||||
|
Db       278
TACTTGGACCTTGGGCCTGCCAGCATCATTCACCACCATAAAGGGCCAATGTTTCATATC 219

Qy       965 AGGCTG---TACATAGTCCTTTTATC----TCCT--------
TGTGGC------------ 997
                  || |||    |||   || |   |||    |||        | ||||
Db       218
AGACTGGACAACAGCATCATCAAATCTGCGTCCAATCAGACGTTTGGCATCAAAAACTGT 159

Qy       998 ------------CTATGAAACTGGTTTAT-------------
AATAAACTCTTAAGAGAA 1032
                            |  || |||| | || |           || |||  || || |
Db       158
GTTGGTGGGGTTCATTGCAACTTGATTCTTTGCGGCATCACCGATCAACCGTTCAGTGTC 99

Qy       1033 CATTA-----TAATTGC 1044
                  | | |     || ||
Db         98 CGTAAAGGCGACATAGC 82


RESULT 8
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;  LENGTH: 2198
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match           41.4%;  Score 2696;  DB 1;  Length 2198;
  Best Local Similarity   42.8%;  Pred. No. 1.1e-168;
  Matches  643;  Conservative   0;  Mismatches  351;  Indels  510;
Gaps   93;

Qy        1 GAATTCC----CTGAGGAGGCGAAT------CCGG-----CGGGTATCAGAGCCA-
TCAG 44
```
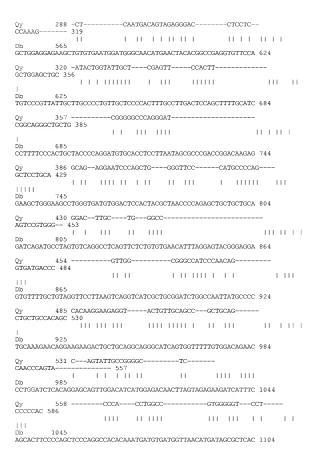
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                     |  ||||    |  ||  ||  |||          ||        |||  |  |  ||  |||  ||
Db          21
GTTTTCCAGCACGGAAAAGTCGAGATAATTGCCAATGATCAGGGAAACCGAACCACTCCA 80

Qy          45 AAC-----CGCC-------ACCATGA---------CGGTGG----
GCAAGAGCAGCAAGA 79
                     |  |     ||||        ||  |||        |||||     ||||  ||  |
||||
Db          81 AGCTATGTCGCCTTTACGGACACTGAACGGTTGATCGGTGATGCCGCAA-
AGAATCAAGT 139

Qy          80 TGC--TG--------CAGCA----TATTGATTACAG------
GATGAGGTGC-------- 111
                     |||  ||       ||  ||    |  |||||  ||       |||   |   ||
Db          140
TGCAATGAACCCCACCAACACAGTTTTTGATGCCAAACGTCTGATTGGACGCAGATTTGA 199

Qy          112 --ATCCTGCAGGACGGCCGGATCT---TCATTGGCCACCTTCAAG---------
GCTTTTG 157
                     ||  |||   |  |  |  |||  |   |||||||  ||||  | |           |  |
Db          200 TGATGCTGTTGTCCAGTCTGATATGAAACATTGGC-
CCTTTATGGTGGTGAATGATGCTG 258

Qy          158 ACAAGCACATGAATTTGATCCTCTGTG---
ACTGTGATGAGTTCAGAAAGATCAAGCCAA 214
                     ||  ||  ||       |  ||     |   |  |||   ||  ||     ||  |
|||
Db          259 GCAGGCCCA------
AGGTCCAAGTAGAATACAAGGGAGAGACCAAAAGCTTCTATCCAG 312

Qy          215 AGAA-----CTCCAA--------ACAAGCAGAAAGGGAAG---
AGAAGCGAGTCCTCG-- 256
                     ||  |       ||  |  |           ||||   |  ||||  ||    ||||||      |||  |
Db          313 AGGAGGTGTCTTCTATGGTTCTGACAAAGATGAAGGAAATTGCAGAAGC-
CTACCTTGGG 371

Qy          257 --GTCTGGTGCTGCTGCGAGGGGAGAATCTGGTCTCAATGACAG-----
TAGAGGGAC-C 308
                     |  |||  |  |   |||          |  |||||  ||  ||  |||       |   |   |||
|
Db          372 AAGACTGTTACCAATGC----------
TGTGGTCACAGTGCCAGCTTACTTTAATGACTC 421

Qy          309 TC---------CTCCCAAAGATACTGG---TATTGC---------------
TCGAGTT-- 339
                     ||          ||  ||||||||  ||||     ||||||               |  ||  ||
Db          422
TCAGCGTCAGGCTACCAAAGATGCTGGAACTATTGCTGGTCTCAATGTACTTAGAATTAT 481

Qy          340 -------CCACTTGCTGGAGC---
TGCCGGGGGCCCAGGGATCGGCAGGGCTGCTGGCAG 389
                     |||  |||||  ||  |||     |||  ||  |  ||  ||
                                                                                     ||||
Db          482 TAATGAGCCAACTGCTGCTGCTATTGCTTACGGCTTAG---ACAAAAAGGTTG-
GAGCAG 537

Qy          390 AGGAATCCCAGCTGGGGTTCCCATGCCCCAGGCTCCTGCAGGAC--
TTGCTGGGCCAGTC 447
                     |  |  |  |||      |  ||  ||  ||      ||   ||  |||  ||  ||  |  ||
```

```
                         | |
Db          538 AAAGAAACGTGCT----CATCTTTGACCTGGGAGGTGGC---
ACTTTTGATGTGTCAATC 590

Qy          448 C------GTGGGGTTGGC-------GGGCCATCCCAACAGGTGATGAC-CCCAC-
AAGGA 492
                          |       || || |||       || ||   | |||| ||  ||| |||||
                         | |
Db          591 CTCACTATTGAGGATGGAATCTTTGAGGTCAAGTCTACAGCTGGAGACACCCACTTGGGT 650

Qy          493 AGAGGTACTGTTG-CAGCCGCTGCAGCTGCTGCCACAGCCA--
GTATTGCCGGG-----G 544
                            |||    | ||| || |||      || |    || |||   |||||| |
                         |
Db          651 GGAGAAGATTTTGACAACCG-----AATGGT----
CAACCATTTTATTGCTGAGTTTAAG 701

Qy          545 CTCCAACC------------CAGTACCCACCTG---GCCGTGGGGGTCCTCC--
CCCACC 587
                            | | |            ||||     ||  |  |||| |    |  ||||| |
                         |
Db          702 CGCAAGCATAAGAAGGACATCAGTGAGAACAAGAGAGCTGTAAGACGCCTCCGTACTGCT 761

Qy          588 TATGGGC---CGAGGAGCACCCCCT----------
CCAGGC------------------- 615
                            | || |   | | | |||| ||            ||||||
Db          762 TGTGAACGTGCTAAGCGTACCCTCTCTTCCAGCACCCAGGCCAGTATTGAGATCGATTCT 821

Qy          616 ----ATGATGGG------------CCCACCT---------
CCTGGTATGA---------- 640
                              |||| ||              || ||            || | |  |||
Db          822 CTCTATGAAGGAATCGACTTCTATACCTCCATTACCCGTGCCCGATTTGAAGAACTGAAT 881

Qy          641 ---GACC--TCCTATGGGTCC-----
CCCAATGGGGATCCCCCCTGGAAGAGGGACTCCA 690
                              |||| |  ||| ||     |||| | | ||   ||| | ||       ||
                         |||
Db          882 GCTGACCTGTTCCGTGGCACCCTGGACCCAGTAGAGAAAGCCCTTCGA-----
GATGCCA 936

Qy          691 A--TGGGCATGCCCCC--------------TCCGGGAATGCGG-CCTCCTC----
CCCCT 729
                            |   | | || | |              ||| ||   | ||   || |||
                         ||||
Db          937 AACTAGACAAGTCACAGATTCATGATATTGTCCTGGTTGGTGGTTCTACTCGTATCCCCA 996

Qy          730 GGGATGCGAGGCCT-TCTTTGAC-----CCTTGGC----CACAGAGTATG-
GAAGTAGCT 778
                            |  | ||  || || |  |||      |  |||       || || || | |  |
                         |
Db          997 AGATTCAGAAGCTTCTCCAAGACTTCTTCAATGGAAAAGAACTGAATAAGAGCATCAACC 1056

Qy          779 CCGCAGAGGCGTGGGCT--CGATTC--CT---CAGG--GCCA-
CGTTACCACAGACCTGT 828
```

```
                  | |  || ||    |||   | | |  ||   ||||  |||| | |  |   ||||
||
Db      1057
CTGATGAAGCTGTTGCTTATGGTGCAGCTGTCCAGGCAGCCATCTTGTCTGGAGACAAGT 1116

Qy       829 TTGT-----TTCTTATGCTGTTGTTCGTGGA------------
GTCTCATGGGATTGT-- 869
                ||      |||     || || || ||||         || | |||| ||||
Db      1117
CTGAGAATGTTCAAGATTTGCTGCTCTTGGATGTCACTCCTCTTTCCCTTGGTATTGAAA 1176

Qy       870 ---CTGGT----------------------------------TTC---
CCTTACAG- 885
               |||||                                 |||    ||
|||
Db      1177
CTGCTGGTGGAGTCATGACTGTCCTCATCAAGCGTAATACCACCATTCCTACCAAGCAGA 1236

Qy       886 ----GGCC--CCCTCCC---------------CCGGGAATGCGCCCACC--------
AAG 916
               | ||  | || ||              || ||   |||     |
|||
Db      1237
CACAGACCTTCACTACCTATTCTGACAACCAGCCTGGTGTGCTTATTCAGGTTTATGAAG 1296

Qy       917 GC-------CCTAGACT------------CATCTTGGC--------CCTCCTCAGC-
TCC 948
               ||       ||  |||            |  ||||||      |||    || |
|
Db      1297
GCGAGCGTGCCATGACAAAGGATAACAACCTGCTTGGCAAGTTTGAACTCACAGGCATAC 1356

Qy       949 CTGCCTGTTTCCCGTAAGGCTGTACAT--------AGTC-
CTTTTATCTCCTTGTGGCCT 999
               || ||||  |||| ||| ||| |     ||||  |||||    | |||
|||
Db      1357 CT-CCTGCACCCCG--AGG-TGTTCCTCAGATTGAAGTCACTTTTG--
ACATTGATGCCA 1410

Qy      1000 ATGAAA------------CTGGTTTATAATAAACTC----TTAAGAGAAC---
ATTATAA 1040
               ||| |               ||| |  |  | | |      ||||||||   ||||
|
Db      1411
ATGGTATACTCAATGTCTCTGCTGTGGACAAGAGTACGGGAAAAGAGAACAAGATTACTA 1470

Qy      1041 TTGC 1044
               | |
Db      1471 TCAC 1474


RESULT 9
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
```

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;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match            40.4%;  Score 2635;  DB 1;  Length 2495;
  Best Local Similarity  36.6%;  Pred. No. 5.5e-164;
  Matches  683;  Conservative   0;  Mismatches  322;  Indels  862;
Gaps  103;

Qy         2 AATTCCCTGAGGAGGCGAATCCGGC----------------GGGTA--
TCAGAGCCATCA 43
             | | || ||| || |  | |||| |              ||| |  ||| ||
||||
Db       280 ATTACCATGATGAATC--
ATCCAACTGATGCCTGGAAAGAAGGGCAATTCAAAGATATCA 337

Qy        44 GAACC------GCCACCATG--
ACGGTGGGCAAGAGCAGCAAGATGCTGC---------- 85
               |||     |||| ||  || || |   |||||| |  |  || |
Db       338
TTACCAAGGTTGCCAATGTGGAACTATACTACAGAGCAATACAGTTCTACTTAGAATTCA 397

Qy        86 AGC--ATATTGATTACAG----GATGA-
GGTGCATCCTGCAGGACGGCCGGATCTTCATT 138
               |||   | ||| | |  |     | ||| |||||   || |   |||| ||||| ||
|
Db       398 AGCCTCTGTTGTTAAATGATTTGCTGATGGTGCTGTCTCC---ACGGTTGGATC-
ACACT 453

Qy       139 GGCACCTTCAAGGCTTTTGACAAG-------------CAC--------
ATGAATTT---- 173
             |  |  |||| |||   ||| |||              |||        |  | ||||
Db       454
CGTGCAGTCAATTATTTCAGCAAGGTTAAACAGCTACCACTGGTGAAACCGTATTTGCGT 513

Qy       174 --------GATCC-----------TCTGTGACTG------TGA---------
TGAGTTCA 199
                     || ||            ||||||| ||       |||          | | |
||
Db       514
TCAGTTCAGAACCATAACAACAAATCTGTGAATGAATCATTGAACAATCTTTTTATTACA 573

Qy       200 GA--AAG---ATCAAGC-CAAAGAACTCCAA----------------------
ACAA---- 228
             || |||  |||| || |   |||| |||                        ||||
Db       574
GAAGAAGATTATCAGGCTCTGCGAACATCAATAGATGCTTATGACAACTTTGACAATATC 633

Qy       229 ------GCAGAAAGGGAAGAGAAGCGAGTCCTC-----GGTCTGGTGC--
```

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TGCTGC---- 271
                        ||  |  |    || || |  |  |||    |  || ||  |  ||||||
Db        634
TCGCTTGCTCAGCGTTTGGAAAAACATGAACTCATTGAGTTCAGGAGAATTGCTGCTTAT 693

Qy      272 -------GAGGGGAGAAT--CTGGTCTCAATG------ACAGT---
AGAGGGACCTCCT- 312
                         |||  | |||  ||||  ||  |     | ||   |||  |||
||||
Db        694
CTCTTCAAAGGCAACAATCGCTGGAAACAGAGTGTAGAGCTGTGCAAGAAAGACAGCCTT 753

Qy        313 ------------------------------
CCCAAAGATACTGGTATTGCTCGAGTTCCA 342
                                          |  ||||||||||   |  |||  ||  |
Db        754
TACAAGGATGCAATGCAGTATGCTTCTGAATCTAAAGATACTGAATTGGCTGAAGAACTC 813

Qy        343 CT------------------------------TGC--TGGAGC---------
TGCCGGG 360
                         ||                    |||  |||||       |  | ||
|
Db        814
CTGCAGTGGTTTTTGCAGGAAGAAAAAAGAGAGTGCTTTGGAGCTTGTCTGTTTACCTGT 873

Qy        361 GGC------------CCAGGGATCGGCAGGG---CTGC-
TGGCAGAGGAATCCCAGCTGG 404
                           |         ||||   ||| |   |    |||| ||| |   ||| ||
|||
Db        874 TACGATCTTTTAAGGCCAGATGTCGTCCTAGAAACTGCATGGAGGCACAATATCA--
TGG 931

Qy        405 GGTTC-
CCATGCCCCAGGCTCCTGCAGGACTTGCTGGGCCAGTCCGTGGGGTTGGCGG-- 461
                        ||  |||||||| |  || ||||||| |  ||| || |  ||| | ||    || ||
Db        932 ATTTTGCCATGCCCCTA-TTTCATCCAGGTCATGAAGG---
AGTACTTGACAAAGGTGGAT 987

Qy        462 ---------GC-----CATCCC----AACAGGTGATGACC---
CCACAAGGAAGAGGTAC 500
                          ||     ||| |    || || || || |   | ||| ||
|
Db        988
AAATTAGATGCTTCAGAATCACTGAGAAAAGAAGAAGAACAAGCTACAGAGACACAACCC 1047

Qy        501 --TGTT-----GCAGCCGCTGCAGCTGCTGCCA-CAG---
CCAGTATTGCCGGGGCTCCA 549
                          ||||      |||||| | |  | ||||| || |||   ||||| ||||| |
Db        1048 ATTGTTTATGGTCAGCCCCAGTTGATGCTGACAGCAGGACCCAGTGTTGCC---
GTCCCT 1104

Qy        550 ACCCAGTACCCACCTGGCCGTGGGGGTCCTCCCCCACC-
TATGGGCCGAGGAGCACCCCC 608
                          |||||  ||  |||  ||| |  | | |  |||| |||||| |       ||
|
Db        1105 CCCCAGGCACCTTTTGGTTATGGTTATACCGCACCACCGTATGGACAG-------
CCACA 1157

Qy        609 TCCAGGCAT----------------GATG-GGCCCACCTCCTG---------------
```

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          GT 636
                    || ||| |                |||| || |    |||||
          ||
Db     1158
GCCTGGCTTTGGGTACAGCATGTGAGATGAAGCGCTGATCCTGTAGTCACCTATTTTCGT 1217

Qy       637 A-TGAGACCTC--CTATGGGTCCCCC------------
AATGGGG--------------- 666
                        | ||| ||| || || |   ||| |         |||||||
Db     1218 ACTGAAACATCGTCTTT---
ACCCACTTCTCAGTTTATAATGGGGGAAAACAGGCAACGT 1274

Qy       667 ------ATCCCC-------CCTGGAAGA-------------------------
GGGAC 686
                          |  ||      | | | ||                       ||
          |
Db     1275
GTTCTTGTAACCTTTATTTCATGAAGGACTTCTTTTTGTTTCTAACTATAAACTTGGATC 1334

Qy       687 TCCAATGG--------------GCATGCCCCCTCC----------------------
GGGA 711
                        || |||        ||| || | ||
          ||||
Db     1335
ACCTATGTTAAAACCTTATTTCACATTCCACATCATTTTAGAATTTATTTTCGAAGGGGA 1394

Qy       712 AT------------------GC---GGC-----CTCCTCCCCCT-----------
GGGAT 734
                        ||               |  |||    || |||||          |
          |
Db     1395
ATAGTTTCAATGTTTTATTCACTTGGGCTTTTTTCTTCCCCCTCTTTCTTTAAAGAACT 1454

Qy       735 GC-------------------GAGG---CCTTCTTTGACC--------------------
CT 754
                        ||                   || | ||| |||| |
          |
Db     1455
GCTCAATATTCAATCTGTTGTGAAGAACCTGATTTGCACTCTGTAGTGTTTAAAGAAACA 1514

Qy       755 TGGCCAC-----------------------
AGAGTATGGAAGTAGCTCCGCAGAGGCGT 790
                          |  ||              || ||||| ||  |||| ||  || |
          |||
Db     1515 AAGAAACTCTAATATTGAATCTCTTAAATTTAGTGTATGTAAACAGCT-
TACAAATACGT 1573

Qy       791 G--GGCTCGATTC----------------------------------------
CTCAGGG 808
                        | ||  || |                                 | |
          ||
Db     1574
ATTGTCTAAATGCATTTAAATCTGTTTTATTCAAAGAAAAGCTAAAGCAAAAACACTGG- 1632

Qy       809 CCACGTTACCA--CAGACCTGTTTGTTTCT--------------
TATGCTGTTGTTCGTGG 853
                        || | |||| || |||| ||  |         || | |   ||||
Db     1633 -
CATATGACCATGCAAGACTGTCAGTGCCAACAAAGACAACACTAATCAGCACATCGT-- 1689
```

```
Qy        854 AGTCTCATGGGATTGTCTGGTTTCCC----------------TTACAGG------
GCC-- 889
                  ||  ||||||    |  |||||                 ||||||      |||
Db       1690 ----
ACACTGGATTGCAGTGCTTCCCAGATTATTGAAAAATGTTACAGACAACTTGCCTG 1745


Qy        890 ----------------------CCCTC----------------
CCCC------------G 899
                                   |||||                |||||
|
Db       1746
ATTTTTAAATGAGCGTAAAAGGCCCTCTAACCTATGCAGGTTTCCCCATTATGCATATAG 1805


Qy        900 GGAATGC-----------GCCCAC-----------CAAG-GCCCT----------
AGACT 926
                     |||||           ||  |||         ||  |  |||||            |
Db       1806
AAAATGCTAGTATGTTTTGCTCACTTCATATGTAACAGGTGCCCTTATGTTGTGCTGTAT 1865


Qy        927 CAT---CTT--------GGCCC--TCC--TC----------AGCTCCCTG---
CC----- 953
                     |  |   |||        ||  ||  |||  ||          ||| ||  ||    ||
Db       1866
CCTGTGCTTTTTCTGTGGGACCATTCCATTCAGGAGCAAAGAGCACCATGATTCCAATCT 1925


Qy        954 ------TGT----------TTCCC----------
GTAAG-------------------- 966
                       |||          |||||           |||  |
Db       1926
TGTGTGTGTTTACTAACCCTTCCCTGAGGTTTGTGTATGTTGGATATTGTGGTGTTTTAG 1985


Qy        967 ---GC----TGTAC----------------------
ATAGTCCTTTTATCTCC------- 990
                        |    |||||                   ||| | ||  |   ||| |
Db       1986 ATCACTGAGTGTACAGAAGAGAGAAATTCAAACAAAATATTGCTGT--
TCTTCAGTTTTG 2043


Qy        991 -TTGTGGCCTATGAAA-----CTGGTTTATAATAA--------
ACTCTTAAGAGAACATT 1036
                     ||||||  |  |||||      |    ||||  |||||        |||  |   |  |  ||||
Db       2044
TTTGTGGAATTTGAAATTACTCAAATTTAAAATAAATTACTGGACTGTGGAAATAACA-T 2102


Qy       1037 ATAATTG 1043
                    |  ||||||
Db       2103 AGAATTG 2109


RESULT 10
US-10-478-914-62
; Sequence 62, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE: 2003-11-26
```

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  Query Match            40.3%;  Score 2623.5;  DB 1;  Length 1946;
  Best Local Similarity  41.8%;  Pred. No. 5.9e-164;
  Matches  629;  Conservative    0;  Mismatches  362;  Indels  515;
Gaps   92;

Qy         1 GAATTCCCTGAGGA-----GGCGAATCCGGCGGG----
TATCAGAGCCATCAGAACCGCC 51
             ||||||| ||| |     ||| | | ||| |    |||| || |||| | | |
|
Db        39 GAATTCCTCGAGCACTGTTGGCCTA-CTGGCTGAGGCTTATCTGA--CATCT-
CATTGTC 94

Qy        52 ACC----------------------------------------------
ATGACGGTG 63
               ||                                         || | |
|
Db        95 CCCTGGTGTGTGTGTGTGTGTGGTGTTTTTGTGTGTGTGGGGTGTGAGTGTGGCAGAG 154

Qy        64 GGCAA----GAGCAGCAAGATGCTGCAG------------CATATTGATTAC------
AG 101
             | ||    |||| |   ||| ||| ||            | | || || |
|
Db       155 AGGAAAGGGGAGCTGTTTGATTCTGTAGTTCCTTTTCTGCCTTCTTCCTTTCTCTGTAAA 214

Qy       102 GATGAGGTGC--ATCC----TGCAGGACGGCCG-----
GATCT---------------T 134
             | | | | ||||   | | ||||| |    |  ||
|
Db       215 CTTTGGATACTTATCCAAATTACT-
AACGGCAGATTGAGCCCTATGCAGATGGCATGTGT 273

Qy       135 CATTGGCACCTTCAAGGCTTTTGACAAGCACATGAATTTGAT--CCT-------
CTGTGA 185
             | ||  || | ||  ||| |  ||| | | ||    || |  |||      | |
|
Db       274 CTGTGACAACCTCT--GCTCTCCACAT-
CTCTTGGGCCTGTTTACCTGCGCTCCCAGAGC 330

Qy       186 CTGTG-ATGAGTTCAGAAAGATCAAGCCAAAGAACTC-------CAAACAAGCAG--
AAA 235
             || |  | | | |  || || || | ||    ||  | || ||| ||| |
Db       331 CTCCGCCAGCATCCCAGAATCTCCATCCCCATCTCTCACTTATACACACAT-
CAGTCATC 389
```

```
Qy          236 GGGAAG--AGAAGCGAGTCCTCGGTC-----
TGGTGCTGCTGCGAGGGGAGAATCTGG-- 286
                || |   |  | ||| | || | ||      | |  | |  |  |    |||||
Db          390
GGTTATCCATTAGCTAAACCGCCTTCCTTAATAGCTTTACACTGTTTGCTTTCTCTGGAA 449


Qy          287 -----------------TCTCAATGACAGTAGAGGGACCTCCTCCCA----
AAGATACTG 325
                               || |||| |||| |        | | ||   |||| ||
|
Db          450 CATTTTTAGTTAAAATTTCATAATG-CAGTTG---------
CACACAAATGAAGACACAG 499


Qy          326 GTATTGCT--------CG--AGTTCCAC----TTGCTGG-
AGCTGCCGGGGGCCCAGGGA 370
                  || |||       ||   |||| |  | | || |||||    ||
||||||
Db          500 --ATGGCTGCATCCTCCGTCTCTTCCCCTCGTTTACAGGAAGCTGC----
GGATCAGGGA 553


Qy          371 TCGG---CAGGGCTGCT-----------GGCAGAGGAATCCCAGCTGGGGTTCCCA-
TGC 415
                  ||     |||| | |           ||||||||     ||   |||| |||| |
Db          554 GGGGTGTTAGGGTTACCCACATGGTAAGGGCAGAG-----
ACAAGAGGGGACCCCAGTTT 608


Qy          416 CCCAGGCTCCTGCAGGAC-
TTGCTGGGCCAGTCCGTGGGGTTGGCGGGCCATCCCAACAG 474
                  ||| ||| |    || ||||||||   | |  || |||| ||    || ||   |
Db          609 TCCATGCTGCACATGGTCATTGCTGGG---GAC--
TGAGGTTTGCACATCACCCTGCCCT 663


Qy          475 GTGATGACCCCACAAGGAAGAGGTAC-----TGTTGC-
AGCCGCTGCAGCTGCTGCCACA 528
                || | | | || | ||| || |||      || || ||| || || ||| |
|
Db          664
GTTCTCCCTCCGCTGGGGAGAAAGTCAGGGATGGGAGCAAGCTGCAGCATCTTCTGAAAAA 723


Qy          529 GCCA-----GTATTG---
CCGGGGCTCCAACCCAGTACCCACCTGGCCGTGGGGGTCCTC 580
                  | |    |  ||| ||| | |||| | |||  ||| |||||| || |  |  |
||
Db          724 GAAAAGGTGGCCTTGTCTCCAGGTCTCCCCTCAAGT-CCCACCTTCCCAT-
AGTTTCTG 781


Qy          581 CCCCACCTATGGG----CCGAGGAGCAC--CCCCTCCAGGCATGATGGGC-------
CCA 627
                  || | ||| | | ||     | ||  |   | |   | ||   | |||| |
|||
Db          782 CCACTTCTCTTGATTTTCC-----TCTCTGCCACTTCT--
CTTGATTTTCCTCTCTGCCA 834


Qy          628 C--CTCCTGGTATGAGACCTC----------CTATGGG--------
TCCCCCAATGGGGA 667
                  |  ||| ||| |   ||||        || || |      || ||  |||
|
Db          835 CTTCTCTTGATTT---
TCCTCTCTGCAGCTGCTTTGAGGTGGGTTTTCTCCAGATGCACA 891
```

```
Qy        668 ---TCCCC---------------CCTGGAAGAGGGAC--
TCCAATGGGCAT-------- 698
                 |||||              |||| ||| | ||  || || |  |||
Db        892
CTTTCCCCTGCTTTGCGTCCTTATTCTGGTAGAAGCACAATCTAAAGCTCATTAAGGGAA 951


Qy        699 ---GCCCCCTCCGGGAATGCGGC---CTC-------CTCC-CCCTGGGA--------
TGC 736
                 |    || |  | |||  ||   |||        | || | ||| |
| |
Db        952
CTAATCAATTCTGTGCATGGCGCTAGCTCAGCAGATCACCACACAGGCAGCACTATTAGC 1011


Qy        737 GAGGCCTTCTTTGACCCTTGGCC--ACAGAGTATGGAAGTAGCTCC---GCAG----
AGG 787
                   || |   | || || | |||   |   | || || | ||  | ||
|||
Db       1012
AAGTCGGTGCTTAACACATGGCACTTCCATGAATCGATATGGAGCCCGTGTAGAACAAGG 1071


Qy        788 CGTGGG-----CTCGATTCC---TCAGGGCCAC-GTTACCA------------
CAGA--- 823
                 | ||||      || ||||  | ||  || | |||            ||||
Db       1072
CATGGGTTTTTTTCTCTTCCCATTAAGAAAAACTGATGCCAAAAATAACTTCTCAGATAT 1131


Qy        824 --------------------------------CCTGTTTGTTT-----------
CTTATG- 840
                                              | | |||||||          |||
Db       1132
TTTCAAGTATGACTTTTATGAAGGGAAAAAGCATTTTTGTTTGCAAAATCATGCTTCAGT 1191


Qy        841 ------CTGTTGT---TCGTGGAG---------TCTCATGGGATTGT--CT-----
GGTT 875
                   | |||||   | ||| |         |||| |||| ||| ||
||||
Db       1192
GCAGGCCAGTTGTGAATTGTGATGGCTTTTATTTCTCCTGGGGCTGTAACTTTAAGGGTT 1251


Qy        876 T----------------CC---CTTA-
CAGGGCCCCCTCCCCCGGGAATGCGCCCACCA 914
                 |             ||  || || | | | | | | | |      | | |||
Db       1252 TAGAATTTGGAACCACAGCCTAGCTAATCATGACACACACACAC------
ACACACACAC 1305


Qy        915 AGGGCCCT---AGACTCAT---CTTGGCCCTCCTCAGCTCCCTGC------------
CTGT 956
                 | ||  | |   | || |||   |  ||    |  || || | |             |
Db       1306
ATGCACACACATACACATACACAAAGCATCACGAAGAACCATACAAATTGTACATTATTT 1365


Qy        957 TTCCCGT-AAGGCT-----GTACATAG--TCC--------TTTTATCT---
CCTTGTGGC 997
                 | | | |  |||||      | |||| ||       | ||| || ||||||
Db       1366
TACACATGGAGGCTCACTCTAAAATAGATACCATTTTAAATATTAACTAAAACTTGTGCT 1425


Qy        998 CTATGAA----------------ACTGGTTTATAATAAAC---
```

```
TCTTAAGAGAACATTAT 1038
              |  || |                      |||| ||| | || ||   ||||  | | | ||
Db      1426
CATTGTATGTTCATTCTATATGTACTGATTTGTTATTCACATTTCTTTCAAAATCGTTCA 1485

Qy      1039 AATTGC 1044
             |||| |
Db      1486 AATTTC 1491


RESULT 11
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match             39.2%;  Score 2555.5;  DB 1;  Length 2495;
  Best Local Similarity   37.3%;  Pred. No. 2.3e-158;
  Matches  665;  Conservative   0;  Mismatches  370;  Indels  749;
Gaps  102;

Qy        1 GAATTCCCTG--------AGGAGGC-----------------GAATCCGGCGGG-
TATCA 34
              |     ||||        || |||                 |||| ||| | |
||
Db      1791
GGGAAACCTGCATAGGTTAGAGGGCCTTTTACGCTCATTTAAAAATCAGGCAAGTTGTCT 1732

Qy       35 GAGCCAT---------------CAGAACCGCCACCATG---
ACGGTG------------ 63
              |   |||              || || || | |  ||| ||
Db      1731
GTAACATTTTCAATAATCTGGGAAGCACTGCAATCCAGTGTACGATGTGCTGATTAGTG 1672

Qy       64 -----------GGCAAGAGCA-----GCAAG-----ATGC---------TGC---
AGCAT 90
                       ||||    ||    ||| |    ||||        |||   |||
|
Db      1671
TTGTCTTTGTTGGCACTGACAGTCTTGCATGGTCATATGCCAGTGTTTTGCTTTAGCTT 1612

Qy       91 ---ATTGATT---ACAGGATGAGGTGCATCCTG-CAGGACG---------
```

```
GCCG------ 128
                |||| |   |||| | |  ||||| | | |  |||       || |
Db      1611
TTCTTTGAATAAAACAGATTTAAATGCATTTAGACAATACGTATTTGTAAGCTGTTTACA 1552

Qy       129 --------------------------GATCTTCATTG---------
GCAC-------- 143
                                            || |||  |||         |||
Db      1551
TACACTAAATTTAAGAGATTCAATATTAGAGTTTCTTTGTTTCTTTAAACACTACAGAGT 1492

Qy       144 ------------CTTCAAGGC--------
TTTTG------------------------ 157
                |||||   |      | |||
Db      1491
GCAAATCAGGTTCTTCACAACAGATTGAATATTGAGCAGTTCTTTAAAGAAAGAGGGGGA 1432

Qy       158 -----ACAAGCACA--TGAAT------TTGA------TCCTCTGTGA---------
CT-- 187
                | |||| ||  |||||     ||||      ||| ||  ||         ||
Db      1431
AGAAAAAAAGCCCAAGTGAATAAAACATTGAAACTATTCCCCTTCGAAAATAAATTCTAA 1372

Qy       188 -GTGATGAGTTCAGAAAGATCAAG------CCAAAGAACTCCAA----------
ACAAGC 230
                |||||| |    | | ||| |      | | |  |||||       | ||
                                                                      |
Db      1371
AATGATGTGGAATGTGAAATAAGGTTTTAACATAGGTGATCCAAGTTTATAGTTAGAAAC 1312

Qy       231 AGAAAGG----------GAAGAGAAG----CGAGTCCTCG--
GTCTGGT----------- 263
                | ||||           |||  |||         | |  | ||| |
Db      1311
AAAAAGAAGTCCTTCATGAAATAAAGGTTACAAGAACACGTTGCCTGTTTTCCCCCATTA 1252

Qy       264 ---GCTGCTGCGAGGGGGAGAATC-TGGTCTCAAT--GACAGTAG--------
AGGGAC-- 307
                |||    | ||| |   | | ||   | | |  |||||          ||| |
Db      1251
TAAACTGAGAAGTGGGTAAAGACGATGTTTCAGTACGAAAATAGGTGACTACAGGATCAG 1192

Qy       308 --------CTC-----CT---CCCAAAGATACTGG-
TATTGCTCGAGTTCCACTTGCTGG 350
                |||      ||   ||||||   | | | |||    |||| |
                                                                     |||
Db      1191 CGCTTCATCTCACATGCTGTACCCAAAG--CCAGGCTGTGGCT----
GTCCATACGGTGG 1138

Qy       351 AGCTG-----------CC---GGGGGCCCAGGGA---TCGGCA-----GGG--
CTGCTGG 386
                || |            ||    || || ||| ||||     ||||||      |||
                |||||||
Db      1137
TGCGGTATAACCATAACCAAAAGGTGCCTGGGGAGGGACGGCAACACTGGGTCCTGCTGT 1078

Qy       387 CAGAG-------------------------------
GAATCCCAG---------------- 400
                |||                                  |  || | |
Db      1077
```

```
CAGCATCAACTGGGGCTGACCATAAACAATGGGTTGTGTCTCTGTAGCTTGTTCTTCTTC 1018

Qy        401 ------CTGGGGTTCCCATGC--------------CC-----CAGG--
CTCCTGCAGGAC 433
                  |  |  |||  |  ||                  ||      ||  |  ||||| ||
|||
Db      1017
TTTTCTCAGTGATTCTGAAGCATCTAATTTATCCACCTTTGTCAAGTACTCCTTCATGAC 958

Qy        434 TT------------GCTGGGCCAG------------------TCCGTGGGGTT-----
GGC 459
                  |           ||  |||  |              |||  ||  |||       |
Db       957
CTGGATGAAATAGGGCATGGCAAAATCCATGATATTGTGCCTCCATGCAGTTTCTAGGAC 898

Qy        460 G------GGCC-------ATCCCAACAGGTGA--TGACC--
CCACAAGGAA--------- 493
                  |     ||||      |||  ||||||| |   |||    |  ||| | |
Db       897
GACATCTGGCCTTAAAAGATCGTAACAGGTAAACAGACAAGCTCCAAAGCACTCTCTTTT 838

Qy        494 GAGGTACTGTTGCAGCCGCTGCAG-----
CTGCTGCCA--------------------- 526
                   |  |||   | ||  ||||||      ||  |  ||||
Db       837
TTCTTCCTGCAAAAACCACTGCAGGAGTTCTTCAGCCAATTCAGTATCTTTAGATTCAGA 778

Qy        527 --CAGCCAGTATTGC------------------------CGGGGCTCCA-
ACCCAGTAC 558
                   ||  |  | |||||                      |    ||||  |  ||  |  ||
Db       777
AGCATACTGCATTGCATCCTTGTAAAGGCTGTCTTTCTTGCACAGCTCTACACTCTGTTT 718

Qy        559 CCACC-----TGGCCGTGGGGG-------------TCCTCCCCCAC-
CTATGGG------ 593
                   ||| |     |  ||| | |             |  |||  ||  | ||| |
Db       717
CCAGCGATTGTTGCCTTTGAAGAGATAAGCAGCAATTCTCCTGAACTCAATGAGTTCATG 658

Qy        594 ---------CCGAGGAGCACCC----------CC------TCC-AGGCA-----
TGATGG 622
                   ||  |||||  |           |       ||  |  |||
|||||
Db       657
TTTTTCCAAACGCTGAGCAAGCGAGATATTGTCAAAGTTGTCATAAGCATCTATTGATGT 598

Qy        623 GCCCACCTCCTGGTATGAGACCTC-------------------
CTATGGGTCCCCCAATGG 664
                   |  || ||||  ||       |  ||                |  |||   ||    ||
|
Db       597
TCGCAGAGCCTGATAATCTTCTTCTGTAATAAAAAGATTGTTCAATGATTCATTCACAGA 538

Qy        665 -----------GGATCCCCCCTGGAAG-----AGGG--ACTCCAATGG--GC--
ATGCCC 702
                   ||  ||   |||  |   |   |  ||   |  ||| |||   ||     |
|
Db       537
TTTGTTGTTATGGTTCTGAACTGAACGCAAATACGGTTTCACCAGTGGTAGCTGTTTAAC 478
```

```
Qy        703 CCTCCGGGAATGC-GGCCTCCTC---------CC--
CCTGGGATGCGAGGCCTTCTTTGA 750
               |  |  |  | |||    |  || |  |         || || ||| |    || ||
 |
Db        477
CTTGCTGAAATAATTGACTGCACGAGTGTGATCCAACCGTGGAGACAGCACCATCAGCAA 418


Qy        751 --CCCTTGGCCACAGAGTATGGAAGTAGCTCCGCAGAGGCGTG-GGCTC--------
GAT 799
                 |  || | ||||| | |||| | || | ||| || | |||
 |
Db        417 ATCATTTAACAACAGAGGCTTGAATT--
CTAAGTAGAACTGTATTGCTCTGTAGTATAGT 360


Qy        800 TCCTCA-GGGCCACGTTACCACAGACCTGTTTGT-------TTCTT---
ATGCTGTTGTT 848
                ||| ||  ||| || ||   |  || | ||||       ||||| | ||
 |||
Db        359
TCCACATTGGCAACCTTGGTAATGATATCTTTGAATTGCCCTTCTTTCCAGGCATCAGTT 300


Qy        849 CGTGGAGTC-TCATGGG---------ATTGTCTGGTT-----TCC----
CTTACAGGGCC 889
                |  || || ||||||         ||| || || |    | |   || ||||
 |
Db        299
GGATGATTCATCATGGTAATTATGGCATTATCATATTCTTCATACTTGTCATACAAAAAC 240


Qy        890 CCC---TCC-CCCGGGAATGCGC--------C--CACCAAGGCCCTAG-----
ACTCATC 930
               ||   || ||| |||   ||        | | || ||| |    | |||
Db        239
ACCAGTTCTGCCCAAAGATGAGCTTGTTCTGCAGCTCTTAGCACCTTGGGAATATTCACT 180


Qy        931 TTGGCCCTCCTCAGCTCC-----CTGCCTGTTTCCCGTAAGGCT----------
GTACA- 974
               | | ||   ||||||||     || ||| || | | |||||           |||
 |
Db        179 CTAGACCAGAACAGCTCCAGGTGCTCCCTCATTTTC-
TGAGGCTTAAATTTAGAGTATAG 121


Qy        975 ------TAGTCCTTTTATCT---CCTTGTGG-------------
CCTATGAAACT----G 1008
               || |  | |   ||  || ||||            || ||   ||
Db        120
AATAGCTAATTCAGTAAACATTCCCATGTGAGCTCGCTCAAGTCCCAGTGCTGCTTCCAA 61


Qy       1009 GTTTATAATAAACTCTTAAGA--------GAACATTATAATTGC 1044
               |  | ||| | ||||| | |        || | ||| | ||
Db         60 CATGGTGATCAGCTCTTCAAAATAGCCACGATCCTGATAGTAGC 17
```

RESULT 12
US-10-478-914-57/c
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA

```
  Query Match           38.4%;  Score 2502;  DB 1;  Length 2336;
  Best Local Similarity   36.2%;  Pred. No. 8.7e-155;
  Matches   626;  Conservative   0;  Mismatches  366;  Indels  736;
Gaps   95;

Qy        3 ATTCCCTGAGGAGGCGAATCCGGCGGGTATC-----AGAGCCATC-----
AGAAC----- 47
            |  || ||| | |  |||| |  | || || || ||    | | ||
Db     1689
AACCCATGAAGGGAAAAATCCTCCTTTTTTCCCCCAAGTGCATTCTACTTATTACTTTGC 1630


Qy       48 ------CGCC-----ACCATGACGGTG----GGCAAGAGCAGCAAG-----ATGC--
TGC 85
                | ||      |||      ||    |  | || || | ||||    ||||
|||
Db     1629
ATTTTTCTCCCAAAGTCCAAATTTATGCAAAGAAAATAGAAACAAGTTCAAATGCAATGC 1570


Qy       86 -------------AGCATATTGATTACAGGATGAGGTGCATCCT--GC--------
AGGA 122
                       | || |   | ||   | |  || ||| ||        ||
Db     1569
ATTAACCAAATAAAACAAGTCTCCTTCAAATTAGGAACCAACCTAAGCATTTGTAAAGTG 1510


Qy      123 CGGCCGGATC----TTC--------------ATTGGCACC------------
TTCAAGG- 151
               || | |||    |||          |||| |||         ||||
Db     1509
TAGCAGAATCAGAATTCTTTTAAAAATTAGATTTGGAACCTGAACTATATAATTCATAAT 1450


Qy      152 ----------CTTTTGACAAGCACATGAATTTGATCCTCTGTGACTGTGATGA-
GTTCA- 199
                        || | || ||  | |  | ||  |||| | |  ||| |  | ||
||
Db     1449
TCTCATTTTTCTGTGGAAAATTATTTTATCTTTCTCCTGTATACCTGAAAAAATGTCCAT 1390


Qy      200 ------GAAAGATCAAGCCAAAGAACTCCAAACA---AGCAG--
AAAGGGAAGAGAAGCG 248
                        || | ||| ||        | ||| ||    ||| |  |||| | |
|
Db     1389
AGGCTTAAAGGGTCATGCTTTTACATTCCTTCCATATCACAGGTACTATGAAGTAAGGAG 1330
```

```
Qy        249 A----------------GTC-----
CTCGGT--------------------------- 258
              |              |||   ||| |
Db       1329
ACTTTTAGGTTTCTTTTTGTCTTAAACTCAGACAGCTTTGTAAGCAGTAGTGTGTAGATT 1270

Qy        259 ------------------CTGGTGCTGCTGCGA----------
GGGGAGAATCTGG---- 286
                           | || ||   ||| ||      |||||||| || |
Db       1269
ACAAGAGTTAGACAAAAGCAGGCGCGACTGAGAAGAGTTGGTGGGGGGAGAAGCTTGGGGC 1210

Qy        287 ----------TCTCA----ATGACAG-----TAGAGGG------------------
ACCT 309
                        ||||    || |||     || |
||
Db       1209
ACTTCCTGTCACTCAACACATTCCAGATCACTAAAAAATTTCCACACCCTCTGCATTCCC 1150

Qy        310 CCT--CCCA---
AAGATACTGGTATTGCTCGAGTTCCA--------------------- 342
              ||| |||| || | |||||||  ||  |||||
Db       1149 CCTTGCCCACTCCAGTTCCCGGTATT-
TTCTGATTCCATATGTTGTGGTATTTACCATAC 1091

Qy        343 -------------------CTTGCTGGA--GCTGCCGGGGG--------
CCCAGGGATCG 373
                              || || || ||| | |||        ||    |||
|
Db       1090
TTCTCTCCCTCACTAGGCTCTGGCAAGACTGCTTCAGAGGGGATGCATTCCTTTAGATTG 1031

Qy        374 ------GCAGGGCT---------GCTGGCAG---AGGAATC------------
CCAGCTG 403
                     || | |||       |||||||||   |||||          | ||
Db       1030
CACAAAGCGGAGCTGGGAAAATGGCTGGCAGTTTCAGAATCTAGTCACGATCGCACGCAT 971

Qy        404 GGGTTCC-CATGCC-
CCAGGCTCCTGCAGGACTTGCTGGGCCAGTCCGTGGGGTTGGCGG 461
                     | | || ||  ||| |  ||| || |||    | | || || || | ||||
|
Db        970
GAGCACCTCACACATCCATGTCCCTACCCGCCCCCCCGCTCCCGCCCCTGCAGCTGGCTG 911

Qy        462 GCC--ATCCCAACAGGTGATGACC-------CCACAAGGAAG---
AGGT------------ 498
                    || || || |  || || ||       |  | |||| |||
Db        910
ACCTGTCTCACCCACTGCTGGCCTATCGAACGGCCAGGACTGTCTGGTTTTGGCTCGTGC 851

Qy        499 ---------------------------ACTGT---TGC-
AGCCGCTGCAGCTGCTGCCAC 527
                                     ||||   |||  ||| || | |  | | |||
|
Db        850
CTTTGTCCATGTCTGGCTTAGTTCCTCTCTGTCTATGCTTGCCTCTACCCCCACCGCCCC 791

Qy        528 AG------CCAGTATT--GCC----------------------GGGG------
```

```
CTCCAA 550
            ||      | ||| || |||                         | ||        ||
|||
Db       790
AGGCGGCACAAGTGTTTGGCCACACAAAACTAGAGATAGAAAAGGTGGTAAAAAACTTCAA 731

Qy       551 CC------CAGTAC-CCACCTG-----GCCGTGGGGG-----TCCT----------
CCCC 583
             |        | | ||| | |       | ||| |      ||||          |
||
Db       730
ACTTTTCTAAATTCTCCAACAGTTTATTTCTTGTGAATTTCTTCCTTCTTTAAATACTCC 671

Qy       584 C------------------------ACCTATGGGCCGAG------
GAGCACC------- 605
                                  | |||| ||| ||     |||| |
Db       670
ATTTTAAGAAAACAAAAAAATTAATTATCTAAAGGCAAAGAATGGAAAGCAACCTTTGTG 611

Qy       606 ---------------------------CCCTCCAG--GCATGATGGG---------
CCCA 627
                                  | |||||| || | |||||
|
Db       610
TTCCTTATAATAACTGACTTCATAACTCTCTCCAGCTGCGTTATGGGATGTGTATAAAAA 551

Qy       628 CCTCCTGGTATGAGACCTCCTATGGGTCCC---C--CAATGGG-----
GATCCCCCCTGG 677
             || ||| | |||||   ||| | |  | |    |||| |      |    ||
|||
Db       550 GCTTCTGTTCTGAGA---
ACAAAGGAGCACGTGCAGAAATGAGACGAAAAAATCCACTGA 494

Qy       678 AAGAGGGACTCCA-----------------------ATGGGCATGCCCC-
CTCCGGG--- 710
             ||  | ||||                          | | || ||||| |  | |
Db       493 CAGT---
ATTCCATTACACAAATTACTTAAAAGATTTTAGTCAAGCCCCTCAACAGATTC 437

Qy       711 ------AATGCGGCCT---------------------------
CCTCCC----------- 726
             ||    ||| |                               | | ||
|
Db       436
AATTTTAAAATGGCTTTTAGTTAAAAAAAAAAAATTGAAAGTGCTTACCCAGTAAAAGAA 377

Qy       727 ----------CCTGG---GATGCG-AGGCCTTCTTT------
GACCCTTGGCCACAGAGT 766
                           ||||    | | || | ||| ||        || | ||| | ||
|
Db       376
CCGAAGTAGTCCTGAACTGTTACGTAAGACTTTTTACAGTTGGATCTTTGTCAAAAGGGG 317

Qy       767 ATGG-------------AAGTAGCTCCG-----CAGAGGCGT--GGGCT-
CGATTCCTCA 805
             ||||              ||| |||| ||    || |  || ||||| |  | ||
|
Db       316
ATGGGGGTGATGGGGAGAAAGCAGCAACGACAATCAAAAAAGTTCGAGCTGCTGTGGCTAG 257

Qy       806 GGGCCACGTTACCACAG----ACCTGTTT-
GTTTCTTATGCTGTTGTTCGTGGA------ 854
```

```
                   || ||     || | |     || |  | | |||| ||||||| |    ||||
Db      256 AGGACA----ACTTCTGTGTTTCCAGATAGGATTCT--TGCTGTAG-
AAATGGAACTTCC 204

Qy      855 -----------------GTCTC---------
ATGGGATTGTCTGGTTTCCC--------- 879
                             ||| |        ||| | ||||| | |    |
Db      203
AGCCAGCACAGCATCCTGTCCCAGTAGAGAAATGAGTTTGTCAGTTAAAACAAAAAAAAA 144

Qy      880 -----TTACAGGGCCCC---
CTCCCCCGGGAATGCGCCCACCAAGGCCCTAGACTCATCT 931
                       ||| || ||| || | || ||   || |   ||| ||| |
||
Db      143 ATTAGATACTGGAACCCAGGCTAGACGAGGTATTGAACCGC----GCC--AGA-
TTTCCT 91

Qy      932 TG--GCCC--TC--
CTCAGCTCCCTGCCTGTTTCCCGTAAGGCTGTACATAGTCCTTTTA 985
                || |||| || |||||||| |       |||| ||| | |   ||| | |
|
Db       90 TGCAGCCCTGTCTGCTCAGCTCGC------ATTCCAGTAGGCC--
AACAGTGCTCGAGGA 39

Qy      986 TCTCCTTGTGGCCTATGAAACTGGTTTATAATAAACTCTTAAGAGAAC 1033
                ||| | || | | | | |    || ||| |||    | ||
Db       38 ATTCC--GCAGCTTTTAGAGCAG------AAGTAACACTTC--CGTAC 1


RESULT 13
US-10-478-914-57
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;  LENGTH: 2336
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match          38.3%;  Score 2498;  DB 1;  Length 2336;
  Best Local Similarity  33.1%;  Pred. No. 1.7e-154;
  Matches  681;  Conservative   0;  Mismatches  309;  Indels 1070;
Gaps  112;

Qy       2 AATTCCCTG-------AGGAGGCGAATCCGGCGGGTA--TCAGAGCCATCAG-----
AAC 47
```

```
                    | ||| ||        |||| ||    | ||| || |  ||      |  |||        |
                                                                                 |
Db       171
ATTTCTCTACTGGGACAGGATGCTGTGCTGGCTGGAAGTTCCATTTCTACAGCAAGAATC 230

Qy        48 C------GCCACCATGACGGTG------
GGCAAGAGCAGCAAGA---------------- 79
                  |     |  ||   || |  ||         || | |||||| | ||
Db       231
CTATCTGGAAACACAGAAGTTGTCCTCTAGCCACAGCAGCTCGAACTTTTTTGATTGTCG 290

Qy        80 -TGCTGCAG-------------------CATATTGA--------
TTACAGGATGAGGTGC 111
                |||||||                     |  | ||||      || |  | | ||
                                                                              |
Db       291
TTGCTGCTTTCTCCCATCACCCCCATCCCCTTTTGACAAAGATCCAACTGTAAAAAGT-C 349

Qy       112 ATCC-------TGCAGGACGGC--CGGATCTT---C---ATTGGCACCTTCAA-----
GG 151
                  | |      | ||||||  | |||  |||| |  |  |  |||| |||||
Db       350
TTACGTAACAGTTCAGGACTACTTCGGTTCTTTTACTGGGTAAGCACTTTCAATTTTTTT 409

Qy       152 CTTTTGAC---AAGCACA---TGAATTTGATCCT---------
CTGTGAC---------- 186
                 |||| ||   |||| ||   | || |||| ||         || ||||
Db       410 TTTTTAACTAAAAGC-CATTTTAAAATTGAATCTGTTGAGGGGCT-
TGACTAAAATCTTT 467

Qy       187 -----------TGTGAT-GAGTTCAGAAA----------------------
GATCAAGC 211
                         ||| || || || |   |                         |  |
                                                                                ||
Db       468
TAAGTAATTTGTGTAATGGAATACTGTCAGTGGATTTTTTCGTCTCATTTCTGCACGTGC 527

Qy       212 ---------CAAAGAAC------------------TCCAAACAAGCA----
GAAAGGGAA 240
                  |  |||||                     ||| |  | ||| |  || | |
Db       528
TCCTTTGTTCTCAGAACAGAAGCTTTTTATACACATCCCATAACGCAGCTGGAGAGAGTT 587

Qy       241 GAGAAGCGAGTCCT----CGG---TCTGGTGCTGC-----------
TGCGAGGGGAGAA- 281
                 |||| ||| |      ||    |  | |||           |||      ||
                                                                                ||
Db       588
ATGAAGTCAGTTATTATAAGGAACACAAAGGTTGCTTTCCATTCTTTGCCTTTAGATAAT 647

Qy       282 -------TCTGGTCTC----AATG--------ACAGTAGAGGGACCTCCTCCC-
AAAGAT 321
                  | || ||     ||||        | | ||  || | | |   |||
Db       648
TAATTTTTTGTTTCTTAAAATGGAGTATTTAAAGAAGGAAGAAATTCACAAGAAATAA 707

Qy       322 ACTG-----------------------GTATT--------------
GCTCGAGTT---- 339
                  ||||                     || ||                  ||| ||||
```

```
Db        708
ACTGTTGGAGAATTTAGAAAAGTTTGAAGTTTTTACCACCTTTTCTATCTCTAGTTTTGT 767

Qy        340 ----CCACTTGCTGGAGCTGCCGGGGGCCCAGGGATCGGCAG--GGC-TGC--
TGGCAGAG 391
                    |||    || | || ||| ||||   |||   || || ||| |||   |
|||||
Db        768 GTGGCCAAACACTTGTGCCGCCTGGGGCGGTGGG---
GGTAGAGGCAAGCATAGACAGAG 824

Qy        392 -GAATC----CCAG-------CTGGGGTTCCCATGCC----CCAGGC--TCCT-
GCAGGA 432
                   | | |    ||||      |   || |  |||    |||| |  |||| || |
Db        825 AGGAACTAAGCCAGACATGGACAAAGG--
CACGAGCCAAAACCAGACAGTCCTGGCCGTT 882

Qy        433 CTTGCTGGGCCAGTCCGTGGGGTTGGCGGGCCATCC--
CAACAGGTGATGACCC------ 484
                   | | | ||||||| | ||||   | | || ||| |  |||| | |   |
Db        883 C--GATAGGCCAG-
CAGTGGGTGAGACAGGTCAGCCAGCTGCAGGGCGGGAGCGGGGGG 939

Qy        485 -C--------ACAAGGA----AGAGGTACTGTTGC-AGC---CGCTGC-
AGCTGCTGCCA 526
                   |      ||| |||     ||||| || ||| || |  | | ||| |||
|
Db        940
GCGGGTAGGGACATGGATGTGTGAGGTGCTCATGCGTGCGATCGTGACTAGATTCTGAAA 999

Qy        527 CAGCCAG---TATTGCCGGGGCTC--------CAACCCA---------
GTACCCAC--- 562
                   | ||||| | || |  ||||       ||| | |        | ||| |
Db        1000 CTGCCAGCCATTTTCCC--
AGCTCCGCTTTGTGCAATCTAAAGGAATGCATCCCCTCTGA 1057

Qy        563 ------CTGGCC--------GTGGGGG--------------
TCCTCCCCCACCTATGG-- 592
                   || |||        ||| |||                 || | || |||||
Db        1058
AGCAGTCTTGCCAGAGCCTAGTGAGGGAGAGAAGTATGGTAAATACCACAACATATGGAA 1117

Qy        593 ---------------------------------------
GCCGAGG--------------- 599
                                                        || ||||
Db        1118
TCAGAAAATACCGGGAACTGGAGTGGGCAAGGGGGAATGCAGAGGGTGTGGAAATTTTTT 1177

Qy        600 ----------------------------AGCACCCC------
CTCCAGGCATGATGGGC 624
                                               || ||||     ||||
|
Db        1178
AGTGATCTGGAATGTGTTGAGTGACAGGAAGTGCCCCAAGCTTCTCC------------C 1225

Qy        625 CCACCTCCTGGTATGAGAC-CTCCT--
ATGGGTCCCCCAATGGGGATCCCCCCTGGAAGA 681
                   |||||  ||  | | || | |||   |  |||   | | |  ||| | |
Db        1226
CCACCAACTCTTCTCAGTCGCGCCTGCTTTTGTCTAACTCTTGTAATCTACAC------- 1278
```

```
Qy          682 GGGACTCCAATGGGCATGCC---CCCTCCGGGAATGCGGC------------------
CT 720
||
Db         1279 ---ACTACT----
GCTTACAAAGCTGTCTGAGTTTAAGACAAAAAGAAACCTAAAAGTCT 1331


Qy          721 CCTCCC---------CCTGGGAT-----------------
GCGAGGCCTTCTTTGACCCT 754
                ||| |     |||| ||                 ||  |  ||  |||| |
|||
Db         1332 CCTTACTTCATAGTACCTGTGATATGGAAGGAATGTAAAAGCATGACC--
CTTTAAGCCT 1389


Qy          755 -TGGCCA------CAGAGTAT---GGAAGTAGC-----------
TCCGCAGAGGCGTGGG 793
                ||| ||      ||| ||||   |||   ||          ||| ||||    ||
|
Db         1390 ATGGACATTTTTCAG-
GTATACAGGAGAAAGATAAAATAATTTCCACAGAAAAATGAG 1448


Qy          794 C-----------------TC-GATTCC---------------------------
TCAGGG 808
                                  || | ||||                           || |
Db         1449
AATTATGAATTATATAGTTCAGGTTCCAAATCTAATTTTTAAAAGAATTCTGATTCTGCT 1508


Qy          809 CCACGTTACCAC--------------------------
AGACCTGT------------- 828
                |||| |||| |                              |||| |||
Db         1509
ACACTTTACAAATGCTTAGGTTGGTTCCTAATTTGAAGGAGACTTGTTTTATTTGGTTAA 1568


Qy          829 ----------------TTGTTTCT------
TATGC------------------------- 841
                                |||||||||     | |||
Db         1569
TGCATTGCATTTGAACTTGTTTCTATTTTCTTTGCATAAATTTGGACTTTGGGAGAAAAA 1628


Qy          842 TG----------------TTGTTCGTGGAG-----------------TC---
TCATGGGA 865
                ||                    || | |||| |                    ||
|||||||
Db         1629
TGCAAAGTAATAAGTAGAATGCACTTGGGGGAAAAAAGGAGGATTTTTCCCTTCATGGGT 1688


Qy          866 TTG----------------------TCTGG-----------
TTTCCCTTAC--------- 883
                | |                      ||| |       | || |||||
Db         1689
TGGAAAGTATTTTAAAGGGTTGTTTTCTTGAAAAAACAAGCTCTCTCTTACTTTCTGCAT 1748


Qy          884 ------------------------------------
AGG---------------------- 886
                                                |||
Db         1749
CTATGCTATAAAGATAACTATGCTATAATAAATGTAAGGTAGAAAACTTTAAAGAGAAAA 1808


Qy          887 -----------------------------GC-----CCC---
CTCCCCC---------- 898
```

```
                                    ||      |||    ||| |  |
Db      1809
TAACAGTGTTCTAAGTGAAAAGCTACTTAGCATTTTCCCAAACTCACACATTATCAACAG 1868

Qy       899 ----------------GGGAATGCGCCCACC-----
AAGGCCCTAGACTCAT------- 929
                             | ||  |||  ||| |     ||    |||| || ||
Db      1869
AAACACTAAAAATTAAGAGAAAAGCGGCCAACTAATTAAATAGCTAGCCTTATTTTGGGG 1928

Qy       930 --------------------------------------CTTGG----------
CCCTC---- 939
                                    |||||        |||||
Db      1929
GTATGGGATAGAAAATTAAGTGTGAATAAAATGATACTTGGGAATGTTTCTCCCTCGTAC 1988

Qy       940 --C---------------TCAGC---------------TCCCTGCCTGTTTC----
CCGT 963
                 |           |||||            |||  || || ||    ||
|
Db      1989
CACAAAGGATGTTAGTGGTCAGCCTACGAGTTAATCCTTCCTAGCATGGCTCTGAGCCTT 2048

Qy       964 AAGGCTGTAC------------------------ATAGTCCTTT----
TATCTCCTTGT 994
                 | || |   |                       |  ||||| ||   ||||||
Db      2049
CATGCCGAGCAGACGTTATTCACATGACGATTCGAAAAGTCCATTCATATATCTC----- 2103

Qy       995 GGCCTATGAAACTGGTTTATAATA-------------AACTCTTAAG----AG--
AACAT 1035
                 ||     | | |||| ||  ||||          || |||| ||    || |
Db      2104 -GC-----
TACCTGGATTTGAATAGAAACCAGACAGCAATTCTTTAGTTCCAGCCACCAT 2157

Qy      1036 T-----------ATAATTGC 1044
                 |           | |||| ||
Db      2158 TCGCCCCACTGGACAATAGC 2177


RESULT 14
US-10-478-914-62/c
; Sequence 62, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
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;    LENGTH: 1946
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-62

  Query Match            38.2%;  Score 2489.5;  DB 1;  Length 1946;
  Best Local Similarity   34.9%;  Pred. No. 1.8e-154;
  Matches  643;  Conservative   0;  Mismatches  377;  Indels  823;
Gaps   99;

Qy         1 GAATTC--CCTGAGGAGGCGAATCCGGCGGGTATCAGAGCCA----
TCAGAACCGCCAC- 53
             ||| ||  || |  |  |  |  | |||  ||| |  |  ||||     | | |||||
||
Db      1827 GAAATCCACCCGTCGCTG-
GGATCCACAGGGGAGTAACGCCAAAACACGGCACCGCTACT 1769

Qy        54 --CATGACGG---TGGGCAAGAGCAGCAAGATGCT--------
GCAGCATATTGATTACA 100
               | | | |   |  | | ||| |||    | ||        | | | | |||
|
Db      1768
GTCTTCGCAGCTTTTAGGATGAGGAGCCTATTTCTCTCCCATCACTGTAAAATAATTTTA 1709

Qy       101 GGATGAGGTGCATCCTGCAGGACG--------GCCGGATCTT-----
CATTGGCACCTTC 147
               | | | || ||| | || | ||          |   | ||||     ||| |  |||
Db      1708 TG-TATGTTG--TCCAGTAGAACAATGATGTTGAGAGTTCTTTCTACAATTTG--
CCTCA 1654

Qy       148 AAGGCTTT--------TGAC---------
AAGCACATGAATTTGATCCTCTGTGACTG-- 188
               | |||||         |||        ||| ||||  |||| ||  || ||||
Db      1653 GAAGCTTTTTAGTATGTGACATTAGTTTTAAGATCATG----
TGATACTTAGTTACTGAC 1598

Qy       189 ----------------
TGATGAGTTCAGAAAGA-------------------------- 205
                ||||| |  ||| ||
Db      1597
AAAGTATGAGCAGTATTGATAACACCAGTGGGAAAAATAGATTTGAATTTATTTTGTGCG 1538

Qy       206 -TCAAGCC-----AAAGAACTCCAAA-----------------CAAGCA----
GAAAG-- 236
              ||| |   |||| |||  ||                 | || |    ||| |
Db      1537
CTCATGTTTGTAGAAAGTACTATTAATATTTAATTGATGTGGGCTAGAAATTGAACGAT 1478

Qy       237 ---GGAAGAGAAGCGAGTCCTCGGTCTG----------
GTGCTGCTGCGAGGGG------ 277
                | |||| | | | |  |||        || | | | | | |
Db      1477
TTTGAAAGAAATGTGAATAACAAATCAGTACATATAGAATGAACATACAATGAGCACAAG 1418

Qy       278 ----AG---------AATCTGGTCTCAATGACAGTAGAGGGA-
CCTCC------------ 311
                 ||       || |||| || ||  ||||| || |||||
Db      1417 TTTTAGTTAATATTTAAAATGGTATCTAT---
TTTAGAGTGAGCCTCCATGTGTAAAATA 1361
```

```
Qy         312 ------------------
TCCCAAAGATACTG--------------------------- 325
                              ||    ||| ||

Db        1360
ATGTACAATTTGTATGGTTCTTCGTGATGCTTTGTGTATGTGTATGTGTGTGCATGTGTG 1301


Qy         326 --------------------GTATTGCTCG-----AGTTCCA-----------
CTTGCTG 349
                                   |  |  | ||  |     ||||||         |||
|
Db        1300
TGTGTGTGTGTGTGTCATGATTAGCTAGGCTGTGGTTCCAAATTCTAAACCCTTAAAG 1241


Qy         350 GAGCTGCC---GGGG--------GCC----
CAGGGATCGGCAGGGCTGC----------- 383
                |  ||||   || |        |||   ||    |  | || |||  |||
Db        1240
TTACAGCCCCAGGAGAAATAAAAGCCATCACAATTCACAACTGGCCTGCACTGAAGCATG 1181


Qy         384 ---TGGCAGAGGAA---------TCCC-----------------------
AGCTGGG-- 405
                  | ||| |  ||        ||||                   | ||| |
Db        1180
ATTTTGCAAACAAAAATGCTTTTTCCCTTCATAAAAGTCATACTTGAAAATATCTGAGAA 1121


Qy         406 ----------------GTT-----------------------
CCCATGC---------C 416
                                |||                    |||||||
|
Db        1120
GTTATTTTTGGCATCAGTTTTTCTTAATGGGAAGAGAAAAAAACCCATGCCTTGTTCTAC 1061


Qy         417 CCAGGCTCC-----------------TGC---------AG----GACTTGC---
TGGGCC 443
                | ||||||                 |||        ||  ||||||||  | |
|
Db        1060
ACGGGCTCCATATCGATTCATGGAAGTGCCATGTGTTAAGCACCGACTTGCTAATAGTGC 1001


Qy         444 AGTCCGTGGGGT----TGGCGGGCCATC-CCA---ACAGG--TGATGA---
CCC------ 484
                | | ||| |||    || | || ||  ||||  |||| |  | |||
Db        1000
TGCCTGTGTGGTGATCTGCTGAGCTAGCGCCATGCACAGAATTGATTAGTTCCCTTAATG 941


Qy         485 --------------------------------CACAAGGAAGAGGTA---------
CTGT 503
                                               | ||| | || || |
|||
Db         940
AGCTTTAGATTGTGCTTCTACCAGAATAAGGACGCAAAGCAGGGGAAAGTGTGCATCTGG 881


Qy         504 TG-----CAGCCGC--TGCAGCTGCTG----------CCA---------
CAGCCAGTATT 537
                |    |  | || | |||||||||         |       |||  || |
Db         880
AGAAAACCCACCTCAAAGCAGCTGCAGAGAGGAAAATCAAGAGAAGTGGCAGAGAGGAAA 821


Qy         538 GCC-------GGGGC-----------TCCAACCCAGTACC---
CACCT----------G 565
```

```
                   |         |  | | |           | |    | | |    |     | | |
                                                                              |
Db        820
ATCAAGAGAAGTGGCAGAGAGGAAAATCAAGAGAAGTGGCAGAAAACTATGGGAAGGTGG 761

Qy        566 GCCGT---GGGGGTCCT-----CCC--CCACCTAT-------------
GGGCCGAGG--A 600
              | | |   || |  || | ||       |   | |||||| |          || | |
Db        760
GACTTGAGGGGAGACCTGGAGACAAGGCCACCTTTTCTTTTTCAGAAGATGCTGCAGCTT 701

Qy        601 GCACC--CCCT---------CCAGGCATGATGGGCCCACCTCCTGGT-
ATGAGACCTCCT 648
              || ||  ||||          ||  ||     | |  | ||    |  ||| ||| |
                                                                          |||
Db        700
GCTCCATCCCTGACTTTCTCCCCAGCGGAGGGAGAACAGGGCAGGGTGATGTGCAAACCT 641

Qy        649 ATGGGTCCCC--CAATG--------------------
GGGATCCCCCCTGGAAGAGGG 684
                   ||||||  |||||                    ||| ||||| || |
                                                                              |
Db        640 C--
AGTCCCCAGCAATGACCATGTGCAGCATGGAAAACTGGGGTCCCCTCTTGTCTCTGC 583

Qy        685 ACT--CCA-ATGGGCATGC------CCCCTCCGGGA-ATGCGGCCTCCT---
CCCCCTGG 731
                   ||  ||| |||| |  |  |       ||||||| ||   || ||  ||||      |
              ||
Db        582
CCTTACCATGTGGGTAACCCTAACACCCCTCCCTGATCCGCAGCTTCCTGTAAACGAGGG 523

Qy        732 GATGCGA----------GGCCTTCTTTGAC--
CCTTGG--------------------- 757
                   ||  | ||        ||| ||||  | |  | |  |
Db        522
GAAGAGACGGAGGATGCAGCCATCTGTGTCTTCATTTGTGTGCAACTGCATTATGAAATT 463

Qy        758 ---------------CC----------ACAGAG---------TATGGAAG------
TAG 776
                             ||         |||| |        || |||||
                                                                              |||
Db        462
TTAACTAAAAATGTTCCAGAGAAAGCAAACAGTGTAAAGCTATTAAGGAAGGCGGTTTAG 403

Qy        777 CT---------
CC------------------------------------------------ 780
                   ||           ||
Db        402
CTAATGGATAACCGATGACTGATGTGTGTATAAGTGAGAGATGGGGATGGAGATTCTGGG 343

Qy        781 ------GCAGAGGC---
GTGGGCTCGATTCCTCAGGGCCAC------------------G 813
                   || |||||  | | || |  |  |||| |||
                                                                              |
Db        342
ATGCTGGCGGAGGCTCTGGGAGCGCAGGTAAACAGGCCCAAGAGATGTGGAGAGCAGAGG 283

Qy        814 TTACCACAGAC---------CTGTTTGTTTCTTATGCTGTTGTTCG-----TGG---
AGT 856
```

```
              ||  |||||||          |||  |    ||  |  |||  ||| |      |||
|||
Db      282
TTGTCACAGACACATGCCATCTGCATAGGGCTCAATCTGCCGTTAGTAATTTGGATAAGT 223

Qy      857 CTCATGGGATT----------------GTCTGGT-------TTCC----
CTTACAGGGCC 889
              ||    | ||             | | |          | |     |  ||||
||
Db      222
ATCCAAAGTTTACAGAGAAAGGAAGAAGGCAGAAAAGGAACTACAGAATCAAACAGCTCC 163

Qy      890
CCCTCCCCCGGGAATGCGCCCACCAAGGCCCTAGACTCATCTTGGCCCTCCTCAGCTCCC 949
              || | || |    ||| | ||| |  ||| ||| ||       | | | || | |
|
Db      162 CCTTTCCTC---TCTGC-CACACTCACACCCCACACACACAAAAACACCACACA-
CACAC 108

Qy      950 TGCCTGTTTCCCGTAAGGCTGTACATAGTCCTTTTA-TCTC--CTTGT-
GGCCTATGAAA 1005
              |       ||    | | |     ||| | | ||| |  || |||| |
Db      107 ACAC---
ACACCAGGGGACAATGAGATGTCAGATAAGCCTCAGCCAGTAGGCCAACAGTG 51

Qy      1006 CT---GGTTTATAATAAACTCTTA-AGAGAACATTATAATTGC 1044
              ||   ||  | | |   || ||| ||   |  |  | || |
Db        50 CTCGAGGAAT-TCCGCAGCTTTTAGAGCAGAAGTAACACTTCC 9


RESULT 15
US-10-478-914-3/c
; Sequence 3, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;    LENGTH: 2083
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-3

  Query Match           38.1%;  Score 2483.5;  DB 1;  Length 2083;
  Best Local Similarity   35.6%;  Pred. No. 7.7e-154;
  Matches  654;  Conservative    0;  Mismatches  365;  Indels  817;
Gaps  103;

Qy        7 CCTGAGGAGGCGAATCCGGCGGGTATCAGAGC-
```

```
CATCAGAAC----------------- 47
        |  | ||  |||| ||| || |   || |||| ||| |  |
Db     2083 CTAGCGGCCGCGA--CCTGCAG--CTC-
GAGCACATGTGGCCTTTTTTTTTTTTTTTTTA 2029


Qy       48 ---CGCCACCATG--ACGGTGGGCAAGAGC--------AGCAAGATG-----------
CT 83
                    ||| | ||  ||||| |   |        | || ||| |
||
Db     2028
TTTTGCCTTCTTGCTCTGGTGGTTAGTCTCCTACTATAAACATGATTTTCCTTCTTCCCT 1969


Qy       84 GCAG-----------------------CATATTGAT-TACAGGA--------
TGAGGT 109
                |||                      |  ||| || ||||| |          ||
|
Db     1968
TCAGAGTCCTGTCAATCTTTACTTTTTTTCTCATTAATATACAGAAGTTATACTACAGAT 1909


Qy      110 GCATCCTG---CAGGACGGC-CGGATCTTCAT---TGGCACCTTCAAGGCTTTTGAC-
AA 161
                |||| |     || ||| ||    | |||| |   |  ||||| |    ||    ||
||
Db     1908 ACATTCAAGCTCATGACTGCTAAAAACTTCCTGAAATGAGCCTTAA----
TTCATACGAA 1853


Qy      162 GCACATGAATTTGATC------------------------CTCTGT-GACTGTGAT-
GAG 195
                || | |||||  ||                          ||||||  | |  | |
|||
Db     1852
TCATTTCTATTTGTTCTTTTTTTTTTGAGACAGACTCTTACTCTGTCGCCCAGGCTGGAG 1793


Qy      196 TTCA---GAAAGATCAAGCCAAAGAACTCCAAAC-AAGCAGAAAGGG--
AAGAGAAGCGA 249
                | ||   | | |||| | |   ||| ||| |  ||  | | | | |  ||||
|
Db     1792 TGCACTGGCATGATCTCGGCT---
CACTGCAACCTCTGCCTCACGAGTTAGGTCAAGCAA 1736


Qy      250 GT------CCTCGGTCT-----GGTGCTG-------------
CTGC-------------- 271
                |     |||| | ||   || |||             ||||
Db     1735
TTCTTCTGCCTCAGCCTCCCGAGGAGCTAGGATTACAGGTCCCTGCCACCATGCCTGAGT 1676


Qy      272 --------------------GAGGGG-------------AG--
AATCTGGTCTCAA--- 292
                            || |||     || ||  || |||||||| |
Db     1675
AATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTAGCCAAGCTGGTCTCGAATT 1616


Qy      293 --TGACAGTAGAGGG-------ACCT---CCTCCCAAAGATACTGGTATTGC--
TCGAGT 338
                |||| || |     ||||  ||||||||| | |||| ||| |   ||
Db     1615 CCTGACCTCAGGTGATCCGCCCACCTCAGCCTCCCAAAG-
TGCTGGGATTACGGGCGTGA 1557


Qy      339 TCCAC--TTGCTGG-----------------
```

```
AGCTGCCGGGGGCCCAGGGATC------- 372
                 |||| | ||||            | | || |||| | |||
Db      1556
GCCACGGTGCCTGGCCTCTATTTTTTATTTTAAATACCTTTTGCCCTGAAATCTATGTCC 1497

Qy      373 -------GGCAGGGCTGCTGG-CAG-----------AGG-------------
AATCCC 398
                 ||  ||||| |||              ||
Db      1496
TCTGATTATCAACACTGCTTACCAGTTTTATTTTTGTTGGTATTTATTTCATTCAATCCC 1437

Qy      399 AGC-----------------------TGG--------------------GGTTC--
CC 411
             |||                     |||                | |||
||
Db      1436
AGCTCTACAACTTACCAGTATAAAAATTTGGATCAGTTACTTAATCTTGCAGTTTCTTCC 1377

Qy      412 -------------------------------------ATGCCC----------------
CAG 420
                                          ||||||                  |
Db      1376
TTTTAAAAATGGAATAATATTATCTATCATATAAAATGCCCAGTTAACAAATATGAACTA 1317

Qy      421 GCTCCTG--------CAGG--ACTTGCTGGG--------------------
CCAGTCCGT 450
             | |||       |||| | | || ||              | ||| |
Db      1316
ACACCTACAATGTGCCAGGCACCATTCTAGGGAATAGAATGTAAATAAGTTCAAGTTCTT 1257

Qy      451 G------------------------
GGGTTGGCGG------------------------ 461
             |                             | | | | |
Db      1256
GACCTGAATAAGTTTACATTTTAGTGAGAAGACAGACAATAAATCAATAACATGTCCATT 1197

Qy      462 --GCCA--------------TCCCAA------------------CAG---
GTGATG---- 480
                 ||||              || |||              ||| | |||||
Db      1196
ATGCCAGATAGTTTTAAATGTCACAAAGAAAAAGGGGGAGCAATCAGATAGTGATGGAAG 1137

Qy      481 -ACCCCACAAGGAAGAG-GTACTGTTGCAG-----------------CCGCTG--
CAG-- 517
                 | | | || ||| || || || ||               | ||| |||
Db      1136
TTACACTCTAGAGAGGGTGGACAGAAAAAGTTTCTCTTAGGAGATGACATCTGAACAGAG 1077

Qy      518 ----------CTG----------------------------------------
CTGC-- 524
                       |||                                    | ||
Db      1076
ATCTAAATGACTGAGTACAAACCCCAATGGAAAAGTGATTGGTGTGTTGTGAAACAGCAA 1017

Qy      525 CACAGCCAGTAT--------------------TGCC------GGGGCT----
CCAACCC 553
             |||||||||| |                  || |   ||| ||    || |
Db      1016
```

```
CACAGCCAGTTTGACTAGATGAGTAGATCAGAATGACTGAGGTGGGACTGTGGTCATCAA 957

Qy        554 AGTACCCACC----TGGCCGTGGGGGTCCTCC-CCCA------CCTATGGGCC----
GAG 598
                  ||    ||     | |||  ||  | || |  | ||       ||| ||||||
|
Db        956
AGAGATCAGAGAGGTAGCCTGGGAAGGCCACATCACAGAATGTCCTTTGGGCCTCTGTAA 897

Qy        599 GAGC---------ACCCCCTCCAGGC-
ATGATGGGCCCACCTCCTGGTATGAGACCTCC 647
                  ||||         | |  ||  || | | | |    || | | | | |
Db        896
GAGCGTTTTGAAAAAACAGTTCTGAGCAAAGGTTAGTCATTTAACTTGACTTACTCTTTA 837

Qy        648 TATGGGTCCC-----CCAATGG--GGATCCCCCCTGGAAGA--------
GGGACTCCAAT 692
                   | || || |     | | ||  ||   |  ||||| |        |||| |
|
Db        836
GAAGGATCACTTTGGCTATTGAGTGGCAAACAACTGGAGAAGTGGTTAGGGGAGCACTGT 777

Qy        693 GGGCATGCCCCCTC--CGGGAATGCGGCCT----CCTCCCCCTG------
GGATGCGAG- 739
                  ||||| |        || || || || |   ||| || |     |||| ||
Db        776
GGGCAGGAATAGAAGGAGGAAAAGCAGACTGGAGCCTAATCCAGTACTTCAGATGAGAAA 717

Qy        740 ----------GCCT------TCTT----TGACCCTTGGC----
CAC-------------- 761
                  ||||        || |  | ||||| |     ||
Db        716
TGACAGATTTGCCTGGTACATCATTTCCTATCCCTTTACTTATAACTTATTGGTGTATTT 657

Qy        762 --------AGAG--------TATGGAAGTAGC----TCCGCAGA------------
GGC- 788
                  || |        ||| | ||| |    | | | |||             |
Db        656
TTATTTTAAGTGTAAATTTTTATAAATGAAGCATAATTTGAAGATTGATATGTTCGGACT 597

Qy        789 -GTGGGCTCGATTCCTCAGGGCCACGTTACCACAGACCTGTT-----------
TGTTTCT 836
                  |||  || ||| ||| ||  | | ||||| |||| ||          ||
||||
Db        596 TGTGTTTTCTATT-ATCATGGTGTC-
TCTCCACATACCTTTTCCCTTTAGTTCTGCTTCT 539

Qy        837 TA---TGC-------------TGTTGTTCGT-------GGAGTCTCATG----
GGATTGT 869
                  ||    |||              | ||||||| |         ||| ||   | |
|||
Db        538
TATTGTGCTCCTCAAGTCTATTTTTGTTCTTTTCCCTCTACTTCTACTGTTTTGAACTGT 479

Qy        870 CTG----GTTTCCCTT---ACAGG----GCCCCCTCC-------------
CCCGGGAATG 905
                  |    |||| ||    ||||    ||||||  | |    |
Db        478
ATATGCTATTTCTATTTTGCCAGGAGTTACCCCCTTCAATTTTCGTTGTACTCTCTCAGT 419
```

```
Qy       906 CGCCCACCAAGGCCCTAG-ACTCATCTTGGCC--CTCCTCAGCTCC-
CTGCCTGTTT--- 958
              |  |   ||  |  |||  |  ||| ||  || ||   |||  |||  ||  || |  |  |
Db       418 CTCAAACACATACCCATGCTCTCTTC-
TGTCCTTCTCTTCATATCATCTTCTAGAATTAG 360

Qy       959 ------CCCGTAAGGCTGTACATAGTCCTTTTATCTCC-
TTGTGGCCTATGAAACTGGTT 1011
                    ||||    |   |||  | |  ||||||| |||  |  |  |  |||  | |
||
Db       359 TTCTACCCCGATTTTC--
TACCAATTTATTTTATTTCCAATCAGTACATTGATTCAGATT 302

Qy      1012 TATAATAAACTCTTAAGAG----AACATTATAATTG 1043
              ||| |  |  |  ||| |  |   | |||| |  |||
Db       301 TATCAATATGTTTTACCAATTTTATCATTTTTTTTG 266


Search completed: March  9, 2010, 15:52:13
Job time : 7.14664 secs


                       GenCore version 6.3
              Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:        March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                         (without alignments)
                                         1134.946 Million cell
updates/sec

Title:         US-10-572-905-25
Perfect score: 10862
Sequence:      1 cagttacagggagcaccacc..........aataaacatcagagtaactc
1828

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:     834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     7335755.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
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                  %
Result         Query
   No.   Score Match Length DB  ID                          Description

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     1   4608  42.4   3210  1  US-10-478-914-4            Sequence 4,
Appl
     2   4473  41.2   2437  1  US-10-478-914-61           Sequence 61,
Appl
  c  3   4350  40.0   3210  1  US-10-478-914-4            Sequence 4,
Appli
  c  4  4300.5 39.6   2437  1  US-10-478-914-61           Sequence 61,
Appl
     5  4272.5 39.3   3589  1  US-10-478-914-21           Sequence 21,
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  c  6  4224.5 38.9   3589  1  US-10-478-914-21           Sequence 21,
Appl
     7  4221.5 38.9   2120  1  US-10-478-914-64           Sequence 64,
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     8   4214  38.8   2495  1  US-10-478-914-20           Sequence 20,
Appl
  c  9   4211  38.8   2120  1  US-10-478-914-64           Sequence 64,
Appl
  c 10   4192  38.6   2198  1  US-10-478-914-17           Sequence 17,
Appl
  c 11   4134  38.1   2495  1  US-10-478-914-20           Sequence 20,
Appl
    12   4097  37.7   2198  1  US-10-478-914-17           Sequence 17,
Appl
    13   4092  37.7   2336  1  US-10-478-914-57           Sequence 57,
Appl
  c 14  4064.5 37.4   2336  1  US-10-478-914-57           Sequence 57,
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    15   3982  36.7   1946  1  US-10-478-914-62           Sequence 62,
Appl
  c 16  3955.5 36.4   2022  1  US-10-478-914-60           Sequence 60,
Appl
  c 17  3950.5 36.4   2083  1  US-10-478-914-3            Sequence 3,
Appli
    18   3807  35.0   2083  1  US-10-478-914-3            Sequence 3,
Appli
  c 19   3742  34.5   1813  1  US-10-478-914-63           Sequence 63,
Appl
  c 20   3670  33.8   1946  1  US-10-478-914-62           Sequence 62,
Appl
    21   3666  33.8   1813  1  US-10-478-914-63           Sequence 63,
Appl
    22   3649  33.6   2022  1  US-10-478-914-60           Sequence 60,
Appl
    23  2217.5 20.4    938  1  US-10-478-914-69           Sequence 69,
Appl
    24  2206.5 20.3    889  1  US-10-478-914-5            Sequence 5,
Appli
    25   2193  20.2   1020  1  US-10-478-914-68           Sequence 68,
Appl
    26  2187.5 20.1    867  1  US-10-478-914-6            Sequence 6,
Appli
  c 27   2178  20.1   1020  1  US-10-478-914-68           Sequence 68,
Appl
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  c  28  2120.5   19.5    889  1  US-10-478-914-5          Sequence 5,
Appli
  c  29    2099   19.3    938  1  US-10-478-914-69         Sequence 69,
Appl
  c  30  2095.5   19.3    867  1  US-10-478-914-6          Sequence 6,
Appli
  c  31    2089   19.2    889  1  US-10-478-914-9          Sequence 9,
Appli
  c  32  2084.5   19.2    909  1  US-10-478-914-67         Sequence 67,
Appl
     33    2078   19.1    909  1  US-10-478-914-66         Sequence 66,
Appl
     34  2063.5   19.0    889  1  US-10-478-914-9          Sequence 9,
Appli
     35    2053   18.9    816  1  US-10-478-914-15         Sequence 15,
Appl
  c  36    2051   18.9    811  1  US-10-478-914-37         Sequence 37,
Appl
     37    2047   18.8    839  1  US-10-478-914-16         Sequence 16,
Appl
     38  2045.5   18.8    717  1  US-10-478-914-42         Sequence 42,
Appl
  c  39  2045.5   18.8    816  1  US-10-478-914-15         Sequence 15,
Appl
  c  40    2031   18.7    816  1  US-10-478-914-38         Sequence 38,
Appl
     41  2020.5   18.6    794  1  US-10-478-914-13         Sequence 13,
Appl
     42  2019.5   18.6    845  1  US-10-478-914-18         Sequence 18,
Appl
     43    2015   18.6    816  1  US-10-478-914-38         Sequence 38,
Appl
  c  44    2012   18.5    891  1  US-10-478-914-10         Sequence 10,
Appl
  c  45  2001.5   18.4    839  1  US-10-478-914-16         Sequence 16,
Appl
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ALIGNMENTS

RESULT 1
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4

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;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match             42.4%;  Score 4608;  DB 1;  Length 3210;
  Best Local Similarity   38.0%;  Pred. No. 8.5e-303;
  Matches 1164;  Conservative   0;  Mismatches  623;  Indels 1280;
Gaps  163;

Qy         1 CAGTTACAGGGAGC-----------
ACCACCAGGGAACATCTCGGGGAGCCT-------- 41
             ||   ||| |||||         || ||      | | |     ||||
Db       133
CAAGGACAAGGAGCTGCTGTTCGAAACAGCCTTCCTGCTCCCCAACCTGCCTCCCACCCA 192

Qy        42 ---GGTT-----------------------GGAAGCTGCAGGCTTAGT--
CTGTCGGCT 72
                |||                      ||| | | || |  | ||| |
||
Db       193 ACAGGTTTTGCATATACTCTACTGGGAAGAGGGACACACCCGACTGCATCACTGCC--
CT 250

Qy        73 GCGGGTCTCTGACTGCCCTG------------------------
TGGGGAGGGTCTTGC 107
              | | |||||| ||||||||                      |||||| |  |||
|
Db       251 CCAAGTCTCTCCCTGCCCTGTCCAGCATCCAGGAGCACCCCTAGTTGGGGAAG--
CTT-C 307

Qy       108 CTTAACATCCCTTGCAT-----TTGGCTGCAAAG----------AAATCTGC--
TTGGAA 150
                | || ||| | ||     | || || |  | |  ||   | | |||   ||
|
Db       308
TGTGACTCCCCCTACAACAGCCTAGGATGGAGTGGGGTTTGTGAACAAATGCAGAAGGCA 367

Qy       151 G----AAGGGGTTACGCTG--------------TTTGGCCGG------
GCAGAAACT--- 183
              |    | ||| |  ||||              | |||| ||      ||||| ||
Db       368
GTCTTAGGGAGGTCAGCTGACATGCCCCTGGCCTGTGGCTGGGAAGTAGCAGAGGCTAAG 427

Qy       184 --------CCGCT-------------GAGCAGAACTTG--CCGCCAG-----
AATGCTCC 215
                     |||||            ||| || ||| |  | ||| 
|  |||
Db       428
GTTCTTCCCCGCTCTGGGGTTGCCAGGAGTAGCACTGGATCAGTCAGGTGACAGGGCT-C 486

Qy       216 TCCTGTTGCTGAGTA-------------TCATC--GTCCTCCACGTCG------
CGGTG- 253
              |||| |  ||||| |             | || | |||||| |        |
||
Db       487
TCCTCTCTCTGAGCAGGTCCGGTGGCAGCCTTCAAGGTCGCCACGCCGTATTCCCTGTAT 546

Qy       254 --CTG----GTGCTGCTGTTCGTCTCCACGATCGTCA-GCCAATGGATC--
GTGGGCAAT 304
              |||      | | || |  |||| ||   | | || || |   ||| | ||||
||| |
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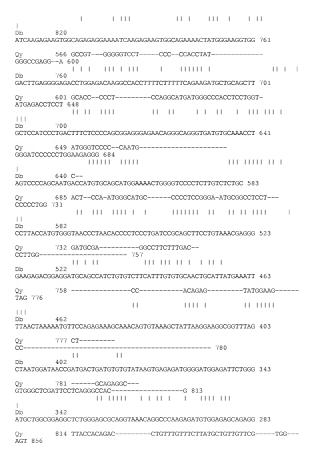
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Db      547
GTCTGTCCCGAGGGGCAGAACGTCACCCTCACCTGCAGGCTCTTGGGCCCTGTGGACAAA 606

Qy      305 GGACACG------------------------CAACTGATCTCTG--------
GCAGAAC 331
           || ||||                     |  | ||  |     |||||
|
Db      607
GGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGGGGCGAGGTGCAGACC 666

Qy      332 TGT----AGCAC---CTCTTCC-------------
TCAGGAAAT--------------- 355
           ||   ||| |   | ||        ||||| |
Db      667
TGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCACCTGCACCATGGA 726

Qy      356 GTCCACCA--CTGTTT--------CTCATCAT--
CACCCAAACGAATGGCTGCAGTCTGTC 403
           | |||||| |||        | |  | | | |    | | ||||| |||| |
|
Db      727
GGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGCTGGAGTCGGCC 786

Qy      404 -CAGGCCACCATG--
ATCCTGTCGATCATCTTCAGCATTCTGTCTCTGTT---------C 451
            | | |||||||| | | | || |||| |  ||| ||| | ||| |
|
Db      787
TCCGACCACCATGGCCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGC 846

Qy      452 CTGTTCTTCTGCC-----------AACT--CTTCACC-
CTC------------------- 478
           || | || |||||          | |   | |||| |||
Db      847
CTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGTCCATGGT 906

Qy      479 ACCAAGGGG-
GGCAGGT------------------------------------------- 494
           ||| || |  ||||||
Db      907
GCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACTGTGTGGTGTACCCA 966

Qy      495 TTTACATCACTGGAATCT-----------TCCAAATTCTTGC------TGG--
TCTGTGC 535
           |   | || ||| |      |||| |||||||      ||| |||
||
Db      967
TCCTCCTCCCAGGAGAGTGAAAGTAAGGGACCAACCTCTTGCCCCTTTTGGGTTCTCTGT 1026

Qy      536 GTGAT-------GAGTGCTGCGGCCATCTACACGGTGAGGCACCCGGAGTGGCATC-
TCA 587
           | |        | |||| |||  || | || || || |     |||| ||
|||
Db      1027 TTTCTTCTGTCCTCATCCTGCACCCA--GACCCTGTTTGGAACTC----
TGGCCTCATCA 1080

Qy      588 ---------ACTCGGAT--------TACTCCTACGGTTTCGC----------------
CTAC 616
           ||| ||        | |||||| | || ||                  ||
|
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```
Db        1081
CCCCAAGCCCTCAGAACCCCCCGGTCCTCCTCCTTTTCTGCTGCTGCACATCCCTTCTGC 1140

Qy        617 ATCCTGGCCTGGGTG-------------------GCCTTCC-----CCCTGG---
CCCT 648
              ||||  ||| ||||             ||||||   | ||||    |
                                                              ||
Db        1141 TTCCT--
CCTTGGTGCAATCCCCAGAAGCCCACTCTCCTTCCATCTGCTCTGGAGTCTCT 1198

Qy        649 TCTC------------------AGCGGTGTCATCTATGTGATCTT--GC--
GGAAACG-- 684
              |||             || ||| |  |||| ||| || || | |
Db        1199
GCTCCTCTTGACTCTCTGGAGTGGCTGTGCCTTGGCAGTGACCTTTGGCCAGGGCAAGTG 1258

Qy        685 -CGAATGA---------GGCG-CCCAGACGGTCTGTCTGAGGCTCTG------
AGCGTAC 727
              |  ||||       || | |||||| |  || || || ||     |||
                                                               |
Db        1259 CCTCATGACAGGTACTGGGTGCCCCAGGCAG-
CTAAGTGCCGCCCTGCCCACCAGCCCCC 1317

Qy        728 -----ATAGGGAAGGGAGGAAG-------GGAAAACA----
GAAAGC------------- 758
              | ||||||||  ||  |       || ||||   |||| |
Db        1318
TATGGCTTGGGAAGGCTGGGGGTCCTCTTGGCCAACAGGGTGAAACCCCATCTCTACTAA 1377

Qy        759 AGACAAAGAAAAAA-------------GAGCTAGCCCAAAATCCCA--AACTCAA---
AC 800
              | ||| | ||| |            | || |||   | ||||| |||||||
                                                               |
Db        1378
AAACACAAAAATTAGCCAGGCATGGTGGTGCGCGCCTGTAGTCCCAGCTACTCAAGAGGC 1437

Qy        801 CAAACCAA-------
ACAGAAAGCAGTGGAGGTGGGGGTTGCTGTTGATTGAAGAT---G 850
              |  |||     |  | |||| |  | |||||| | |||    ||||
                                                               |
Db        1438 TGAGGCAAGAGAATCGCTTGAACCCG-GGAGTCAGAGGTTGCAG-
TGAGCCGAGATCGCG 1495

Qy        851 TATATAATATCT--CCGGTTTATAAAAC------
CTATTTATAACACTTTTTACATATAT 902
              |  ||  || | ||| |        | ||| || |         |  |
                                                               ||
Db        1496
CCACTGCACTCCAGCCTGCTGATAGAGCAAGACTCCATCTCAAAAAAAACAACCCAAAAT 1555

Qy        903 GTACATAGTATTGT---TTGCTTTTTATGTTGACCATCAGC--
CTCGTG----------- 946
              | | | || ||       || | ||| ||  |||| |||| |
Db        1556 TTGCCTGGCATGGTGGCAGGC---ATCTGTAATCC--
CAGCTACTCGGGAGGCTGAGACA 1610

Qy        947 ----------TTGAGCCT----
TAAAGAAGTAGCTAAGGAACTTTACATCCTAACAGTAT 992
                        |||| |||     |||||| ||   |  |  | ||| | || |
Db        1611 TGAGAGCTGCTTGAACCTGGGAGGCAGAAGTTGCAGTGAGCC--
```

```
GAGATCACACCACTGC 1668

Qy        993 AATCCAG------------------CTCAGT--------
ATTTTTGTTTTGTTTTTGT 1025
                  |  |||||                  ||| ||        ||          |
|||||
Db       1669
ACTCCAGCCTGGGTGACAGAGCGAGACTCTGTCCCAAAAAATCAAAAAAATCACTTTTGG 1728

Qy       1026 TTGT---------TTGTTTTGTTTTACCCAGAAATAAGAT-
AACTCC------------A 1063
                  | |          | | | || || ||||||        | ||||||
|
Db       1729 TAGAGATGCACTCTCGCTATG--
TTGCCCAGGCTGGTCTTGAACTCCTGGGCTCAATTGA 1786

Qy       1064 TC-TCGCCCCTTCCCTTTCAT----CTG-----AAAGAAGATA-CCTCCCT-
CCCAGTC- 1110
                  || || | |||| | || | ||       |||      | || | || | || | || ||
|
Db       1787 TCTTCCCACCTTGACCTCCAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCTAGCCT 1846

Qy       1111 ------------------------------------CACC-
TCATTTAGAAAACC----A 1129
                                                       |||| || | |    | ||
|
Db       1847 CAGGGAATTCTTATAAGAACTCTATGAAGTAGGCATCACCATCTTCTCTGTATCCATGGA 1906

Qy       1130 AAGTGTGG-GTAGAAA--------------CCC-----
CAAATGTCCAA----------- 1158
                  ||| | || |||| |              |||      || || || |
Db       1907 AAGAGAGGCCTAGAGATGTATGCTAACTTGCCCAAGCTCACATAGCCCAGGGTAGCATAG 1966

Qy       1159 -----------------AAGCC------------------------------------
CTT 1166
                                    | |||
||
Db       1967 CTGGGATGTTGAGCTGAGGCCGGAGGAGAAGTAGCAGTCGCTGGCAGAGCACACAGGCTG 2026

Qy       1167 TTCTGGTGGGTGACCCAGTGCAT------------CCAACAGAAACAGCCGC-
TGC---- 1209
                  ||||| || ||| |  |||| |          ||| ||    || ||| ||
Db       2027 CTCTGGGGGATGAGCTGGTGCGTTTAAGGAACAGGCCAGCACTGGCATTCGCAAGCAGTG 2086

Qy       1210 ----------------CCG-----------AACCT--
CTGTGTGAAGC------------ 1228
                                   |||          | |||| || | || ||
Db       2087 GGGAAGGGGAGAGATGCCGAGGTGGTCAGTATCCTGACTTTCAGAGGCCTTTTTTTGTTT 2146

Qy       1229 ---------TTTAC----------------------------
GCGCACACGGA------- 1244
                           ||| |                             | | || |||
Db       2147 GTTTTAATTTTTGCTAGATTGATATTAAAAACTCATGTGGAGGAACTCAAGGAATGTTTA 2206
```

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Qy       1245 ------CAAAA-TGCCCAA--ACTGGAGCCCTTGCAAAAA------------
CACGGCT- 1282
                   ||||| | ||||| || ||| |    |||| |             | |
                                                                  | |
Db       2207
GAAGACCAAAAGTCCCCAATGACAGGAACAAAAGCAACCAATTTTAACTTTCTCTTCTC 2266

Qy       1283 -----TG-TGGCATTGGCATAC------TTGCCCTT----ACAGG-------
TGG----- 1314
                   || | ||||| || |     | ||||    ||||      |||
Db       2267
ATTCCTGTTTTCATTGATTTCCCACATGTAGTCCTTTGCTCAGGAAGTCTTTGGGGAAA 2326

Qy       1315 ---AGTATCTTCGTCACACATCT-AAATGAGAAATCAG------------
TGACAACAAG 1358
                   || ||||| |    | ||| |||| | |||||          || ||| |
                                                                       |
Db       2327 TTAAGGATCTTTGAAGC---TCTGAAATAGGTGATCAGGTTAGTGGTGTCTGTCAGC-
TG 2382

Qy       1359 TC-------TTTGAAATGGTGCTA----------------------------
TGGATTT 1382
                   ||       || |||| | |||                             |
             |||||
Db       2383
TCTAAGAGGTTGGAAAATGAACTACTCAAGATAGTCACGAAAATACTGAAAGTTTGATTT 2442

Qy       1383 ACCATTCCTTATTATCACTAA--TCATCTAAACAACTCACTGG---------------
AA 1425
                    | |||| |||| |    ||| | | |||    ||| |   ||
             ||
Db       2443
TTCTTTCCATATTTGAATTAATTTTTTCTGTTTGACTGGAAGGGGTTTTTGTATAACTAA 2502

Qy       1426 ATCCAATTAACA--------ATTTTACA-----
ACATAAGATAGAATGGAGACCTGAATA 1472
                    | || || |||  |||| | ||||| ||| | | ||
             ||
Db       2503 AACCTCAGCGCATAAAGGAGATTTAAAAGGAGCACATGATTTAGTGGGTGGGCC---
ATG 2559

Qy       1473 ATTCT-----------------GTGTAAT-----
ATAAATGGTTTATAA----------- 1499
                    |  ||            ||| ||   ||| ||| |||
Db       2560
AAACTAGAGATGGGATTTGGGGGTGAATTTGTCAATATCTGGATTTTAATCCAGACATCT 2619

Qy       1500 CTGCTTTTGTACC--TAGCTAGGC--------TGCTATTATTACTAT----
AATGAG--- 1542
                    |||||   | | ||| | ||| |    ||||| | ||| || || |
Db       2620
CTGCTAACGAGCCTTTGGTAAGTCACTTCAGATACTTTTCCTCCTTTTTACAAAGAGAGG 2679

Qy       1543 ------TAAATCAT-----AAAG--CCTT-----
CATCACTCCCACA------------- 1571
                    | | || ||    |||| ||||    | | | ||||
Db       2680
GCTGGCTTAGTTATTTGCCAAAGCCCCTTCCAGGCCTGAATTCCACAAGTACGATTTACT 2739
```

```
Qy      1572 --------TTTT---TCTTACG-GTC----------GGAGCATCAGA-
ACAAGCGTCTAG 1608
                  || |   |||| |  |||        ||||||| ||| | ||||
||||
Db      2740 GTAGTGTCTTATCACTCTTTCATGTCACAATAGCGTGGAGCATTAGAGAAAAGC--
CTAG 2797

Qy      1609 ACT------------CC-----------------------------
TTGGGACCG---- 1622
                 |||             ||                            || |||
Db      2798
ACTTTTAGTTGATAGCCAGTTGAAATATCATTGATAGAATTTTAGTTTTAGGAAAAATTG 2857

Qy      1623 ---TGAGTTC-----------CTA----------GAGCTTGG---------------
CT 1642
                |||  |||            |||         |||||||||
                                                                   |
Db      2858
GTTTGATTTCTAGCTTTATTACTATTAGGTATGTGAGCTTGGGCAAATCGCTTAATCTTT 2917

Qy      1643 GGGTC------------------------TAGGCTG------
TTCTGTGCCTCCA---- 1667
                | |||                        ||||||     ||| | |  ||||
Db      2918
GAGTCTAGTTTTCTCTCAAAATGAGAACATTAGGCTAAATGATTTCCGAGTTTCCAGCTA 2977

Qy      1668 -------AGGACTGTCTGGCAA------
TGACTTGTATTGGCCACCAACTGTAGATGTAT 1714
                  ||  || | |  | |    ||| || | ||  |   |   || | |
||
Db      2978
GTCCTAGAGTTCTATATTTCTACATAGTTGAATTATTTTATCATGCTGTTGCTGGGGAAT 3037

Qy      1715 ATATGGTGCCCTTCTGATGC---------TAAGAC------
TCCAGACCTTTTGTTTTTG 1759
                 ||    ||||| ||| ||         || | |     |  || || |   | ||
Db      3038
ATGACTAACCCTTTTGAAGCTACTAATTTTATGTCGAGCTTTAAAGTCCATAATTGTTAT 3097

Qy      1760
CTTTGCATTTTCTGATTTTATACCAACTGTGTGGACTAAGATGCATTAAAATAAACATCA 1819
                 |||  ||     |  | | |||  || || || ||   | | ||| ||  |||
|
Db      3098 CTT--CAGAAAATATTATTTGACCTACAGTATGTCC--
AAATCAATTTAATAAAATCGCT 3153

Qy      1820 GAGTAAC 1826
                  ||||
Db      3154 TTATAAC 3160


RESULT 2
US-10-478-914-61
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
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  Query Match          41.2%;  Score 4473;  DB 1;  Length 2437;
  Best Local Similarity   44.1%;  Pred. No. 4.9e-294;
  Matches 1100;  Conservative    0;  Mismatches  659;  Indels  736;
Gaps  157;


Qy        3 GTTACAGGGAGCACCACCAG----
GGAACATCTCGGGGAGCCTGGTTGGAAGCTGCAGG- 57
            |||||    || | |  ||  ||||   |||   ||||   |||||   || |
||
Db        1 GTTACT-TCTGCTCTAAAAGCTGCGGAATTCCTC---GAGCACTGTTGGC--
CTACTGGG 54


Qy       58 ----CT---TAGTCTGTC---GGCTGCGGGTCTCTGACTGCC-----
CTGTGGG------ 96
               ||   || ||||| | || | ||  | | | ||    | ||| |
Db       55
TGTACTGTGGAGACTGTCAAAGTCTCCCGGAGCCCAATTTCCGGAAGCGGTGAGTTCTGA 114


Qy       97 --GAGGGTCTTG--CCTTAACATCCCTTGCATTTGGCTGCAAAGAAAT---
CTGCTTGGA 149
              || | || ||  || ||   ||||  |  | |  | | |    ||   | ||
||
Db      115 AAGAAGTTCCTGCACCGTAGTTTCCCAAGTCTGCGAATCCCCAACCATGAGCGCCTCGGG 174


Qy      150 AGAAGGG---GTTACGCTGTTTGGCCGG--GCAGAAACT--CC------------
GCTGA 190
              | |   |  |||| | |   || ||  |||| |  ||  ||
||||
Db      175
CGTACTGTCCTTTACCCAGCAAGGATGGGAGCAGGTGCTGGCCAAAGTGAAACGGGCTGT 234


Qy      191 G------CAGAACTTGCCGCCAG---AATGCTCCT--CCTGTTGCTGAGTATCAT--
CGT 237
              |       | | || |||||| |     |  ||||   ||| |  |||| | |||
|||
Db      235 GGTTTACCTGGAC--
GCCGCCTGCGCCGAGAGCCTGCACTGGGGCTGCGGATCCACCCGT 292


Qy      238 CCTCCACGTCGCGGTGCTGGTGCTGCTGTTCGTCTCC-ACGA----TCGT---CAGC-
CA 288
              ||||  |  ||||||  || || |||   ||| ||  |||     |||    | |
||
Db      293 -CTCCTGGAGGCGGTG-GGGGGCC-
CTGACTGTCACCTGCGAGAGTTCGAGCCCGACGCA 349
```

```
Qy        289 ATGGATCGTGG-GCAATGGA-CAC---GCA--------ACTGATCT-----CT----
GGC 326
                 || |  |||| || | | | |   |||         |||| ||     ||
|||
Db        350
ATTGGTGGTGGAGCCAAGCAGCCCAAGGCAGTGTTTGTGCTGAGCTGCCTGCTGAAAGGC 409

Qy        327 AGAACTGTAG-------------CA-
CCTCTTCCTCAGGAA------------------ 353
                | || || |                 || | ||| || ||| |
Db        410
CGGACCGTGGAGATCCTACGGGACATCATCTGCCGCAGTCACTTCCAGTATTGTGTGGTG 469

Qy        354 -------------------ATGTCCAC--
CACTGTTTCTCATCATCACCAAAC------- 385
                                  |||||||| ||| |  || ||||| || | |
Db        470 GTCACAACCGTGAGCCACGCTGTCCACCTCACAG---
CTAATCATGTCCCAGCGGCGGCA 526

Qy        386 ------------GAATGGCTGCAGTC--
TGTCCAGGC---------------------- 408
                               || ||| |||| | ||| | ||
Db        527
GCGGCCGAGATGGAGGGGCAGCAGCCGGTGTTCGAGCAGCTGGAGGAGAAGCTGTGTGAA 586

Qy        409 --------CACCATGATC----CTGTCGA------TCATCTTCAGCATT---------
CT 441
                      || ||||| |    | | |||       ||| | | | |
||
Db        587
TGGATGGGCAACATGAACTACACGGCCGAGGTGTTCCATGTCCCGTTATTGCTTGCCCCT 646

Qy        442 GT-------CTCTGTTCCTGTTCTTCTGC-----CAACTCTTCACCCTC----
ACCAAGG 485
                ||        | || ||| || | ||     || | ||| ||| |    |||
Db        647
GTTGCTCCCCACTTTGCCTTGACTCCAGCTTTTGCATCCCTTTTCCCACTGCTACCC--- 703

Qy        486 GGGGCAGGTTTTACATCACTGGAAT--CTTCCAAAT--TCTTGCTGGT-
CTGTGCGTGAT 540
                 |||| | || | |||  | ||  | | |        | | | ||| |
|
Db        704 ----
CAGGATGTGCACCTCCTTAATAGCGCCCGACCGGACAAGAGGAAGCTGGGAAGCCT 759

Qy        541 GAGTGCTGCGGCCATCTACACGGTGGAGGCACCCGGAGTGGCATCT-
CAACTCGGATTACT 599
                | ||| ||| | | || | | |||  | || ||| || || || || ||
|| |||
Db        760 GGGTGATGTGGACTCCACTACGCTAA---
CCCCAGAGCTGCTGCTGCAGATCAGATGCCT 816

Qy        600 ---------CCTACGGTTTC---GCCTACATCCTGGCCT--
GGGTGG------------- 632
                          ||| | |||  | |  |||| || | ||| ||
Db        817
AGTGTCAGGCCTCAGTTCTCTGTGTGAACATTTAGGAGTACGGGAGGAGTGTTTTGCTGT 876

Qy        633 -----CCTTCCCCCTGGCCCTTCTCAGCGG---TGTCATCTATGTGATCTTGCGGA-
```

```
                               AAC 683
                               ||||      |  ||   |  | |  |  ||||    || |    |  |  ||   |  |||   |
|||
                               Db       877 AGGTTCCTTAAGTCAGG-TCATCGCTGCGGATCTGGCCAAT-
TATGCCCCTGCAAAGAAC 934


                               Qy        684 GCGAATGAGGC-GCC-CAGACGGTCTGTCTGAGGCTCT----
GAGCGTACATAGGG---- 733
                                 |||   ||  | |  ||   |||  |  |     ||  | ||  |  |      ||   |  ||      ||
                               Db       935
AGGAAGAAGACTGCTGCAGGCAGGGCATCAGTGGTTTTTGTGGACAGAACCCTGGATCTC 994


                               Qy        734 AAGGGAGGA-AGGGAAAACAGAAAGCAGACAAAG-AAAAAAGAGCT----
AGCCCAAAAT 787
                                 |  |||| |   ||| |  ||   ||    ||    | | |||  |        |||  |
|
                               Db       995 ACAGGAGCAGTTGGACATCATGGAGACAACTTAGTAGAGAAGATCATTTCAGCAC---
TT 1051


                               Qy        788 CCCAAACTCAAACCAAACCAAACAGAAAGCAGTGGAGG---------
TGGGGGTTGCTG- 837
                                 ||| | |||    |||  ||| |||  | | |  |||   ||           |  | ||
|||
                               Db      1052 CCCCAGCTC---CCAGGCCACACA-
AATGATGTGATGGTTAACATGATAGCGCTCACTGC 1107


                               Qy        838 ----
TTGATTGAAGATGTATATAATATCTCCGGTTTATAAAACCTATTTATAACACTTT- 892
                                          | |||  ||  | | || |  |  ||||      |  | || | | |||  ||
                               Db      1108 ACTCCATACTGAGGAGGAAAATTATA-
ATGTGGTTGCACCAGGCTGTCTTTCACAATTCA 1166


                               Qy        893 -TTACATATATGTACATAG---
TATTGTTTGCTTTTTATGTTGACCATCAGCCTC----- 943
                                          |  |||    |  | || |   ||| |    ||||    |   | ||| ||   | |  |
                               Db      1167 GTGACACCACAG-CCAAAGCCCTATGGGAAGCTT----
TACTGAACACTAAGCACAAAGA 1221


                               Qy        944 ----GTGTT---------GAGCCTTAAAGAAGTAGC--TAAG--
GAACTTTACATCCTAA 986
                                          ||| |        ||| |  |   || |  ||| | |||  ||     |  ||
|
                               Db      1222
GGCAGTGATGGAAGTTCGGAGACATCTAGTGGAAGCGGCAAGCAGAGAAAACCTGCCAAT 1281


                               Qy        987 C------AGTAT------AATC---------
CAGCTCAGTATTTTTGTTTTGTTTTTTGT 1025
                                          |   |     |||||   |  | ||        |||||||       |||  | | |
|
                               Db      1282 CAAGATGAGTATGGGGAGAGTCACACCGGGACAGCTCA-------
TGTCCTATAT----T 1330


                               Qy       1026 TTGTTTGTTTTGTTTTACC-CAGAAATAAGATAACTCCATCTCGCCCCTTCC--
CTT--- 1079
                                          |  |  |   |    |  ||| | |  |  |  | |  |  | ||| |  ||  |||  |||
                               Db      1331 CAGCTCTTCAAGAACAACCTCAAAGCTCTAATGAATCATTGTGGCCTCCTCCAGCTTGGA 1390


                               Qy       1080 ------TCATCTGAAA-GAAGATACCTCC-----CTCCCA-----GTCCAC---CT--
CA 1117
```

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                          || ||  ||| |  || || ||       || |||      | | ||    ||
                          |
Db      1391
CTGGCCACAGCTCAAACGTTGAAACACCCACAGACTGCCAAGTGGGACAACTTTCTGGCT 1450

Qy      1118 TTTAGAAAAC--------CAAAGTGTGGGTAGAAACCCCAAATGTCC--------
AAA-- 1159
                          |||  || |       || || | ||  | |   |||||||        |||
Db      1451 TTTGAAAGGCTCCTTCTTCAGAGCATTGG--
GGAGTCAGCAATGTCCGTTGTGTTAAATC 1508

Qy      1160 ------AGCCCTT-TTCTGGTGGGTGACCCAGTGCATCCAAC-AGAA--
ACAGCCGCTGC 1209
                          |||| |  |    |    || |||||| | ||||| || |  ||||||
                          |||
Db      1509 AGCTGCTGCCCATGATTAAGCCTGTAACCCAGAG-AACCAACGAGGACTACAGCC-
CTGA 1566

Qy      1210 -------CCGAACC-TCT-GTGTGAAGCTTTAC----------GCGCACACGG-
ACAAAA 1249
                          | || || ||  |             | || ||||| | |
                          ||
Db      1567
GGAACTGCTGATCCTTCTCATATATATTTATTCTGTCACTGGAGAGCTCACGGTAGACAA 1626

Qy      1250 TGCCCAAACTGGAGCCCTTG-------CAAAAACAC---GGCT---------
TGTG---- 1286
                          | ||   || |||   |        ||| || |   ||||         ||||
Db      1627
AGACCTGTGTGAAGCAGAAGAAAAAGTCAAGAAAGCATTGGCTCAGGTCTTCTGTGAGGA 1686

Qy      1287 ----GCATTGGCATACTTGC-------
CCTTACAGGTGGAGTATCTTCG----------- 1324
                          | |||| ||  ||||         |||| |   | |  |||||
Db      1687
ATCTGGATTGTCACCTTTGCTGCAAAAAATTACGGACTGGGACTCTTCAATTAATCTGAC 1746

Qy      1325 ---TCACACATCTAAA-------TG--
AGAAATCAGTGACAACAAGTCTTTGAAATGGTG 1372
                          ||||| ||| |||       ||   ||| || | ||  ||    ||| |  ||
                          ||
Db      1747 ATTTCACAAATCCAAAATTGCCGTGGATGAACTCT-TTACTTCA---
CTTCGGGATATTG 1802

Qy      1373
CTATGGATTTACCATTCCTTATTATCACTAATCATCTAAACAACTCACTGGAAATCCAAT 1432
                          ||   | |     |||| | ||| | || |         ||| | | | |||||||||
                          |
Db      1803 CTGGAGCTCGGAGTCTCCTGA--
AACAGTTTAAGTCTGTATATGTTCCTGGAAATCATAC 1860

Qy      1433 TAACAA------TTTTACAACAT-----AAGATAG-AATGGA-
GACCTGAATAATTCTGT 1479
                          || |        || || |||        ||| ||  |||| ||  |   | || |
                          |
Db      1861
CCACCAGGCATCTTATAAGCCATTGTTGAAGCAAGTTGTGGAGGAAATATTTCATCCCGA 1920

Qy      1480 G-----TAATATAAATGGTTTATAAC---
TGCTTTTGTACCTAGCTAGGCTGCTATTATT 1531
```

```
                 |        ||      || |  |  |||    ||  ||     |||  ||    || |   |||
Db      1921 GAGGCCAGATTCCGTTGATATTGAACACATGTCTTCAGGCCTCACTGATCTCC--
TTAAA 1978

Qy      1532 ACTATAATGAGTA-AATCATAAAG------C--CTTCATC---------
ACTCCCACATT 1573
                 |||   |  || |   |||| |||      |   | |||||      || ||| |
|
Db      1979
ACTGGATTTAGCATGTTCATGAAGGTGAGCCGGCCTCATCCTAGTGACTACCCCCTCCTG 2038

Qy      1574 TTTCT-----------TACGGTCGGAGCATCAGAA-----------
CAA---------- 1600
                 | ||            |  |||| ||  ||  ||           |||
Db      2039
ATCCTCTTTGTGGTAGGTGGGGTCACAGTCTCTGAAGTGAAAATGGTCAAAGATCTTGTG 2098

Qy      1601 GCGTC-TAGACTCCTTGGGAC---------CGTG-AGT---------TCCTAGAG---
CT 1637
                 || || ||| ||  || ||  ||        |||| ||     |||| ||
Db      2099 GCATCGTTGAAGCC-
AGGAACCCAGGTAATCGTGCTGTCCACACGACTCCTGAAGCCACT 2157

Qy      1638 TGGCTGGGTCTAGGCTGTTCTGTGCCTCC-AAGGACTG---
TCTGGCAATGACTT----G 1689
                 | |        || ||||||| ||| ||  |  | |||||     |  | |  || |||
|
Db      2158 TAAC-
ATTCCTGAGCTGTTATTTGCAACTGACCGACTGCATCCAGACCTTGGCTTCTGAG 2216

Qy      1690 TATTGGCC-----------ACCAACTGTAGATGTATAT----ATG-------
GTGCC--- 1724
                 || ||           ||| ||| || || | ||   |||        ||||
Db      2217
CATCCGCTAAGAAGATAAGACCTACTCAAGCTGGAAATGCCGATGCAATTTTCTGCCACC 2276

Qy      1725 -CTTCTGATGCTAAGACTCCA--------GACCTTTT--GTTTTTGC-------
TTTGCA 1766
                  || |   || ||      |||||       | || |  |   ||||        | |
|
Db      2277 ACTCCAAATACT---
CCTCCACAACCAGCGTCCCTGTCACTAATTGCGAGAATGATGGAA 2333

Qy      1767 TTTT--CTGAT-----TTTATACCAACT--GTGTGG---------------
ACTAAGATG 1802
                 || |  ||||      || ||||| |||  ||| ||                  ||
|||
Db      2334
TTCTGCCTGAAGGGTCTTGATACCTACTCAGTGAGGTACTTTGCTTGGATTGCTGTGATT 2393

Qy      1803 CATTAAAATAAACAT---------CAGAGTAACTC 1828
                 | | ||||  ||| |           || |   |||
Db      2394 CTTAAAAAAAAAAAAAAAAAAAGGCCACATGTGCTC 2428


RESULT 3
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
```

```
  Query Match            40.0%;  Score 4350;  DB 1;  Length 3210;
  Best Local Similarity   39.8%;  Pred. No. 1e-284;
  Matches 1083;  Conservative    0;  Mismatches  675;  Indels  966;
Gaps  155;

Qy         2 AGTTACAG-GGAGCACCACCAGGGA----ACATCTCGGGGAGCCT--
GGTTGGAAGCTGC 54
             | || | |  || || | | |||    | | |||| |  | |  || | ||||
|
Db      3108 ATTTTCTGAAGATAACAATTATGGACTTTAAAGCTCG----
ACATAAAATTAGTAGCTTC 3053

Qy        55 ---AGGCTTAGTC-TGT----CGGCTGCGG-------
GTCTCTGACTGCCCTGTGGGGA- 98
               ||| ||||| | |   | || | |      |   |  |  ||| |
|
Db      3052
AAAAGGGTTAGTCATATTCCCCAGCAACAGCATGATAAAATAATTCAACTATGTAGAAAT 2993

Qy        99 ----------GGGTCTTGCCTTAACATC-
CCTTGCATTTGGCTGCAAAGAAATCTGCTTG 147
                || || ||  || ||      ||||| ||  || |   ||
|||
Db      2992 ATAGAACTCTAGGACTAGCTGGAAACTCGGAAATCATTTAGCC-
TAATGTTCTCATTTTG 2934

Qy       148 GAAGA-----------
AGGGGTTACGCTGTTTGGCCGGGCAGAAACTCC-----------185
               |||      |  | ||||  ||||| ||  ||  | | ||
Db      2933
AGAGAAAACTAGACTCAAAGATTAAGCGATTTGCCCAAGCTCACATACCTAATAGTAATA 2874

Qy       186 --GCT---GAGCAGAAC----TTGCC----GCCAGAATGCTCCTCCTGTT------
GCTG 226
               |||    | ||| |    || ||     | | ||| ||    || |
|||
Db      2873
AAGCTAGAAATCAAACCAATTTTTCCTAAAACTAAAATTCTATCAATGATATTTCAACTG 2814

Qy       227 AGTATCATC-----GTC-----------------CTCCACG---
```

```
TCGCG----------G 251
           ||||| |     |||               |||||||   | |
|
Db     2813
GCTATCAACTAAAAGTCTAGGCTTTCTCTAATGCTCCACGCTATTGTGACATGAAAGAG 2754


Qy       252 TGCT--GGTGCTGCTGT---TCGTCTCCACGATCGTCA-GCC--
AATGGATCGTGGGCAA 303
              || | |   || | ||  ||||       |   ||| |||   | ||  | |
|||||
Db     2753
TGATAAGACACTACAGTAAATCGTACTTGTGGAATTCAGGCCTGGAAGGGGCTTTGGCAA 2694


Qy       304 TGGAC-ACGCAACTGATCTCT---------GGCAGAA------
CTGTAGCACCTCTTCCT 347
              || | | |    |||||        ||  |||       ||| ||   || |
||
Db     2693 ATAACTAAGCCAGCCCTCTCTTTGTAAAAAGGAGGAAAAGTATCTGAAGTGACT-
TACCA 2635


Qy       348 CAG-----------GAAATGTC---------------------------
CACCACTGTT 368
              ||           || |||||                           |||| |
Db     2634
AAGGCTCGTTAGCAGAGATGTCTGGATTAAAATCCAGATATTGACAAATTCACCCCCAAA 2575


Qy       369 TCTCATC-------------ATCACC-----
AAACGAATG-------------------- 390
              || ||||             ||||      || |    ||
Db     2574
TCCCATCTCTAGTTTCATGGCCCACCCACTAAATCATGTGCTCCTTTTAAATCTCCTTTA 2515


Qy       391 ---GCTGCAGT-----CTGTCCAGGCCACCATGATCCTGTCGATCA---------
TCTTC 433
              ||||  ||      | ||      || |   || ||| | |
|||
Db     2514 TGCGCTGAGGTTTTAGTTATACAAAAACCCCT--
TCCAGTCAAACAGAAAAAATTAATTC 2457


Qy       434 --------------------AGCATTCTGTCTCT--GTTCCT----------
GTTCTTCT 461
                                 | | ||| || | |  || ||        |||| |
|
Db     2456
AAATATGGAAAGAAAAATCAAACTTTCAGTATTTTCGTGACTATCTTGAGTAGTTCATTT 2397


Qy       462 GCCAA-CTCTT-------------CACC-
CTCACCAAGGGGGGCAGGTTTTACATCACT 505
              |||| |||||             |||| || ||   | || | || ||
||
Db     2396 TCCAACCTCTTAGACAGCTGACAGACACCACTAACCT----
GATCACCTATTTCAGAGCT 2341


Qy       506 ----GGAATCTT-------CCAAATTCTTGCTGGTC------------
TGTG-------- 534
              || |||        |||||  ||| |||  |              ||||
Db     2340
TCAAAGATCCTTAATTTCCCCAAAGACTTCCTGAGCAAAAGGACTACATGTGGGAAATCA 2281


Qy       535 ------------CGTGATGAGT-------------
```

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GCTGC----------------- 549
                  |  || |||                          |  |||
Db      2280
ATGAAAACAGGAATGAGAAGAGAAAGTTAAAAATTGGTTGCTTTTGTTCCTGTCATTGGG 2221

Qy      550  -------GGCCATCTACACG----GTGAG----
GCACCCGGAGT---------------- 578
                  || | |||| ||    ||||    |  |  ||||
Db      2220
GACTTTTGGTCTTCTAAACATTCCTTGAGTTCCTCCACATGAGTTTTTAATATCAATCTA 2161

Qy      579  ------------------------GGCATCT-CAACTCGGATTACT-----
CCTACGG- 606
                                   ||| |||  || || |  ||||     |||
 |||
Db      2160  GCAAAAATTAAAACAAACAAAAAAAGGCCTCTGAAAGTCAGGATACTGACCACCT-
CGGC 2102

Qy      607  ---TTTCGCCTACATC-CTG---------GCCTGGG-TGGCC--TTCC-------
CCCTG 643
                  |  || ||| |   |  ||||         ||| | | |||||  ||||        |  |
Db      2101
ATCTCTCCCCTTCCCCACTGCTTGCGAATGCCAGTGCTGGCCTGTTCCTTAAACGCACCA 2042

Qy      644  GCCCTTCTCAGCGGTGTCATCTATGTGATCTTGCGGAAAC-GCGAATG------
AGGC-- 694
                  || |  || |   |  | |    || |||| |||  | |  || || |          |||
Db      2041  GCTCATCCCC-
CAGAGCAGCCTGTGTGCTCTGCCAGCGACTGCTACTTCTCCTCCGGCCT 1983

Qy      695  ----------
GCCCAGACGGTCTGTCTGAGGCTCTGAGCGTACATAGGGAAGGGAGGAAG 744
                  |||||   || |    | |||| |||  | | ||| |||  || |
Db      1982  CAGCTCAACATCCCAGCTATGCTACCCTGGGCTATGTGAG--
CTTGGGCAAGTTAGCAT- 1926

Qy      745  GGAAAACAGAAAGC--------------AGACAAAGAAAAAAGAGCTAGCC-----
CA-- 783
                  |  |   | ||             |  ||| |||| |  | | |||        ||
Db      1925  --ACATCTCTAGGCCTCTCTTTCCATGGATACAGAGAAGATGGTGAT-
GCCTACTTCATA 1869

Qy      784  -------------AAATCCCAAA---------------CTCAAACC---
AAACCAAACAG 812
                  || |||| |               |||| |||   || || |
 ||
Db      1868
GAGTTCTTATAAGAATTCCCTGAGGCTAGGCATGGTGGCTCACACCTGTAATCCCAGCA- 1810

Qy      813  AAAGCAGTGGAGGT----GGGGGTTG--CTGTTGA---------TTGAAGA------
TG- 850
                  |  ||||||||   | ||| |  | ||||        || ||||
 ||
Db      1809  ----
CTTTGGAGGTCAAGGTGGGAAGATCAATTGAGCCCAGGAGTTCAAGACCAGCCTGG 1754

Qy      851  --TATATA----------ATATCTCC-----------------
GGTTTATAAAACCTATTT 882
                  |  |||          || ||| |                | ||| |      |
 |
```

```
Db      1753
GCAACATAGCGAGAGTGCATCTCTACCAAAAGTGATTTTTTTGATTTTTTGGGACAGAGT 1694

Qy       883 ATAACACTTTTTACATATAT---GTACATAGTATTGTT----------
TGCTTTTTATGT 929
             |  |  | | |    |      |     | | | |    | | |         | | |    | |
||
Db      1693
CTCGCTCTGTCACCCAGGCTGGAGTGCAGTGGTGTGATCTCGGCTCACTGCAACTTCTGC 1634

Qy       930 TGACC-------ATCAGC-CTCGTGT-
TGAGCCTTAAAGAAGTAGCTAAGGAACTTTACA 980
             | |              | | | | |  | | | |  | | | | |      | | | | | | |  |
| | | | |
Db      1633 CTCCCAGGTTCAAGCAGCTCTCATGTCTCAGCCTCCC--GAGTAGCTGGG----
ATTACA 1580

Qy       981 ---TCCTAACAGTATAATCCAGCTCAGTATTTTTGTTTTGTTTTTTGTTTGTT--
TGTTT 1035
                 | | |    | | |    | | |   | | | |   | |    | | | | |  | | | | | | | | | |  |     | |     | |
|
Db      1579 GATGCCTGCCACCATG--CCAG-GCA--
AATTTTGGGTTGTTTTTTTTGAGATGGAGTCT 1525

Qy      1036 TGTTTTACC------
CAGAAATAAGATAACTCCATCTCG--------------------C 1069
             | | | | | |     | | | |    |   | | |
|
Db      1524
TGCTCTATCAGCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCTCTGACTC 1465

Qy      1070 CC-----------CTTCCCTTTCATCTG-----AAAGAAGAT-----------------
AC 1097
                | |            | | | | | |  |  | | |        | |  | |  |
| |
Db      1464
CCGGGTTCAAGCGATTCTCTTGCCTCAGCCTCTTGAGTAGCTGGGACTACAGGCGCGCAC 1405

Qy      1098 CTCCCTCCCAGTCCACCT------CATTTAGAAAA---------
CCAAAGTGTGGGT--- 1139
             | | | | | | | | | |       | | | | | |     | |     | | | |  ||
Db      1404
CACCATGCCTGGCTAATTTTTGTGTTTTTAGTAGAGATGGGGTTTCACCCTGTTGGCCAA 1345

Qy      1140 -AGAAACCCCAAATGTCCAAAAGCCCTT---
TTCTGGTGGGTGACCCAGTGCATCCAACA 1195
             | | | | | | | |    | | |   | | | | | |    | | | | | | | |     | | | | |  |
|
Db      1344 GAGGACCCCCAGCCTTCC-CAAGCCATAGGGGGCTGGTGGG-----
CAGGGCGGCACTTA 1291

Qy      1196 GAAACAGCC----GCTGCCCGAACCTCT-GTGTGAAGCTTTAC---GC----
GCACACGG 1243
             |  |   | | |      | |  | |  | | | |  |  | |  |     | | |   | |     |    | | |
|
Db      1290 G---
CTGCCTGGGGCACCCAGTACCTGTCATGAGGCACTTGCCCTGGCCAAAGGTCACTG 1234

Qy      1244 ACAA---AATGCCCAAACTG-GAGCCCT----
TGCAAAAACAC----------------- 1278
```

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                 |||   |  |||    |  | |||  |      ||| | || |
Db       1233
CCAAGGCACAGCCACTCCAGAGAGTCAAGAGGAGCAGAGACTCCAGAGCAGATGGAAGGA 1174

Qy       1279 -----GGCTTGTGGCATTGGCAT-------------------ACTTGC-----
CCTTACA 1309
                    ||||| |||   | |||                | |||      |   |
|
Db       1173
GAGTGGGCTTCTGGGGATTGCACCAAGGAGGAAGCAGAAGGGATGTGCAGCAGCAGAAAA 1114

Qy       1310 GGTGGGAGTATC------TTC--------------------------GT--
CACACA---T 1332
                  || |||| |  |      |||                        || || |||
|
Db       1113
GGAGGAGGACCGGGGGGTTCTGAGGGCTTGGGGTGATGAGGCCAGAGTTCCAAACAGGGT 1054

Qy       1333 CTAAATG-----AGAAATCAG-
TGACAACAAGTCTTTGAAATGGTGCTATGGATTTACCA 1386
                  ||  ||      ||  |||     |||            ||| || || |  | ||
|
Db       1053
CTGGGTGCAGGATGAGGACGAAGAAAACAGAGAACCCAAAAGGGGCAAGAGGTTGGTC- 995

Qy       1387 TTCCTTATTATCACTAATC----------ATCTAAACAACTCAC---TGGA--
AATCCAA 1431
                  ||||| | ||||| |       ||   ||| | |||   ||||      |
Db       994 --
CCTTACTTTCACTCTCCTGGGAGGAGGATGGGTACACCACACAGTTGGATGGTGCATC 937

Qy       1432
TTAACAATTTTACAACATAAGATAGAATGGAGACCTGAATAATTCTGTGTAATATAAATG 1491
                  || |  | | || |  ||| |  |||| |||| |  || |    | ||| |  |
Db       936 TTTGCCTGTCTGCACCTGCAGCTC-CATGGCACCATGGA-----
CCCTGTGCTCCGAGTG 883

Qy       1492 GTTTATAACTG--CTTTTGTACCTAGCT-------AGGCTGCTATT------------
AT 1530
                  |  |  | ||| ||       ||| ||        |||| |||||
|
Db       882 G-
TGGTGCCTGATCTCCACCACCAGGCAGCAGTAGAGGCCGCTATCCAGCAGGGTCAGGT 824

Qy       1531 TAC----TATAATGAGTAAAT---CAT--------AAAGCCTTCATCACTCCC---
ACAT 1572
                  | |     | ||| || |  |||         | |||  | ||    |||      |
Db       823 TGCGCATGGTGATGGAGAAGTTGCCATGGTGGTCGGAGGCCGAC-
TCCAGCCCGTGGCGC 765

Qy       1573 TTTTCTTACGGTCGGAGCATCAGAACAAGCGTC----TAGACTCCTTGGGACC-GTG-
AG 1626
                  |   |  | ||||| |||  |    ||  |   | | |||| ||| |  | |||
||
Db       764 TGAGC--CAGGTCGTGGCT--
GGTGTTGGCAGCCTGGTGGCCTCCATGGTGCAGGTGAAG 709

Qy       1627 TTCCTAGAGCTT--------GGCTGGG-------TCTAGGCTGTTCTGTGCCT----
CCA 1667
```

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                ||||  || |  |          ||  ||||       |||  || |  ||||   |||
||
Db       708
GTCCTGGAACGTGAGGTTGCGGATGGGCCGGCGCTCTGAGCAGGTCTGCACCTCGCCCCT 649

Qy      1668 AGGACTGTCTGGCAATGACTTGTA-------------------TTGGCCA------
CCAA 1702
                | |||     | | | ||||||                        ||| |||
||||
Db       648
CGAGCTGCGGTACCACGTCTTGTAGAAGGTCACATCGTGCCCTTTGTCCACAGGGCCCAA 589

Qy      1703 ----CTGTAGATGTATATATGGTGCCCTTCTGATGCTAAGACTCCAGACCTTTTG---
TT 1755
                  ||| || ||     | |||| | |||||  || |   ||||| |   |
|
Db       588 GAGCCTGCAGGTG-----AGGGTGACGTTCTGCCCCTCGGG--
ACAGACATACAGGGAAT 536

Qy      1756 TTTGCTTTGCATTTT------CTGATTTTATACCAACT----GTGTGGACTAAGATG-
CA 1804
                || | ||    |       ||| | |||   ||| ||   | | |||      ||
||
Db       535
ACGGCGTGGCGACCTTGAAGGCTGCCACCGGACCTGCTCAGAGAGAGGAGAGCCCTGTCA 476

Qy      1805 TTAAAATAAACATCAGAGTAACTC 1828
                | | | |  ||| |  ||||
Db       475 CCTGACTGATC--CAGTGCTACTC 454


RESULT 4
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

   Query Match           39.6%;  Score 4300.5;  DB 1;  Length 2437;
   Best Local Similarity   42.7%;  Pred. No. 5.9e-282;
   Matches 1033;  Conservative    0;  Mismatches  716;  Indels  669;
Gaps  147;
```

```
Qy          2 AGTTAC---------AGGGAGCA----CCACCAGG--GAA------CA-
TCTCG------ 33
                |||  |        ||| | ||   ||  |||| |||    || |||||
Db       2373
AGTACCTCACTGAGTAGGTATCAAGACCCTTCAGGCAGAATTCCATCATTCTCGCAATTA 2314

Qy         34 ------GGGAGCCTGGTTG----------------GAAGCTGCAG------
GCTTAGTCT 65
                   ||||  |||||||              |  |  ||||    || | |
|
Db       2313
GTGACAGGGACGCTGGTTGTGGAGGAGTATTTGGAGTGGTGGCAGAAAATTGCATCGGCA 2254

Qy         66 GT--CGGCT---GCGGGTC------TCT----GACTGCCCTGTGGGGAGGGTCT---
TGC 107
                |  | |||   |  ||||      |||    | ||| | |  |  |||||
|||
Db       2253
TTTCCAGCTTGAGTAGGTCTTATCTTCTTAGCGGATGCTCAGAAGCCAAGGTCTGGATGC 2194

Qy        108 CTTAACATCCCTTGCATTTGGCTGCAAAGAAATCT------GCTT-GGAAGAAG---
GGG 157
                   |   ||  |||||  |  ||| |         |     |||| | || |
||
Db       2193 AGTCG-
GTCAGTTGCAAATAACAGCTCAGGAATGTTAAGTGGCTTCAGGAGTCGTGTGGA 2135

Qy        158 TTACGCTGTT---TGG---
CCGGGCAGAAACTCCGCTGAGCAGAACTTGCCGCCAGAATG 211
                 | | ||   ||| ||  || |||  ||| || | | ||| ||   | |
|
Db       2134 CAGCACGATTACCTGGGTTCCTGGCTTCAACGATGCC-ACAAGATCTT--
TGACCATTTT 2078

Qy        212 CTCCTCCTGTTGCTGAGTATCATCGTCCTCCACGTCGCGGTGCTGGTG----------
CT 261
                | |||| | | | || ||  ||   || |  || |  | || | |||
||
Db       2077 C-ACTTCAGAGACTGTGACCCCAC--
CTACCACAAAGAGGATCAGGAGGGGGTAGTCACT 2021

Qy        262 G---------CTGTTCGTCTCCACGATCGT----CAGCCAAT-------GGATC---
GTG 298
                 | ||  || || || | |    | ||| |       |||| |
|
Db       2020
AGGATGAGGCCGGCTCACCTTCATGAACATGCTAAATCCAGTTTTAAGGAGATCAGTGAG 1961

Qy        299 GGCAATGGACACGCAACTGATCTCTGGCAGAACTGTAGC--
ACCTCTTCCTCAGG----- 351
                | |  |||| |   || |  | ||| ||| ||| |  ||  |   ||| ||
Db       1960 GCCTGAAGACATG----TGTTCAATATC--AACGGAATCTGGCCT----
CTCGGGATGAA 1911

Qy        352 AAATGTCCACCACTGTTTCTCATCATCA----
CCAAACGAATGGCTG------------- 394
                | || ||| |||   | |||| ||   |  |     ||| |||
Db       1910 ATATTTCCTCCACAACTT-
GCTTCAACAATGGCTTATAAGATGCCTGGTGGGTATGATTT 1852
```

```
Qy        395 ------------CAGTCT------GTCCAG--GCCACCATGATCCTG-----
TC---- 423
                          ||| ||        | ||| | | || | ||| |      ||
Db       1851
CCAGGAACATATACAGACTTAAACTGTTTCAGGAGACTCCGAGCTCCAGCAATATCCCGA 1792


Qy        424 -------------
GATCATCTTCAGCATTCT---------------------------- 441
                          | ||||| | ||| | |
Db       1791
AGTGAAGTAAAGAGTTCATCCACGGCAATTTTGGATTTGTGAAATGTCAGATTAATTGAA 1732


Qy        442 --GTCTCTGTTCCTGTTCTTCTGC--CA------ACTCTTCA---
CCCTCACCAAGG--- 485
                      ||| | ||| | | | || ||| ||      || | ||  |||||| | |
Db       1731
GAGTCCCAGTCCGTAATTTTTTGCAGCAAAGGTGACAATCCAGATTCCTCACAGAAGACC 1672


Qy        486 -GGGGCAGGTTTTACATCACTGGAATCTTCCAAATTCTTGCTGGTCTGTG-----
CGTG- 538
                        | | ||    || | ||   |||| |   ||| | ||||| |
||||
Db       1671 TGAGCCAATGCTTTCTTGACT-TTTTCTT-
CTGCTTCACACAGGTCTTTGTCTACCGTGA 1614


Qy        539 -------------------------ATGAGTG----CTGCGG-
CCATC----------T 557
                              |||||      | || | | ||
|
Db       1613
GCTCTCCAGTGACAGAATAAATATATATGAGAAGGATCAGCAGTTCCTCAGGGCTGTAGT 1554


Qy        558 ACACGGTGAGGCACCCGGAGT----GGC---ATCT----CAACT-CGGATTACTC-
CTAC 604
                        | | || | || | | ||   |||  |||    || | ||||| | |
||
Db       1553 CCTCGTT--
GGTTCTCTGGGTTACAGGCTTAATCATGGGCAGCAGCTGATTTAACACAAC 1496


Qy        605 GGT--TTCGCCTACATCC---TGGCCTG----GGTGGCCTTCCC----CCTG------
GCC 646
                          || | || || || || |   || ||| |     | ||||| |    || |
|
Db       1495
GGACATTGCTGACTCCCCAATGCTCTGAAGAAGGAGCCTTTCAAAAGCCAGAAAGTTGTC 1436


Qy        647 CTTCTCAGCGGTGTCATCTATGTGATCTTGCGGAAACGCGAATGAGGCGCCCAG-
ACGGT 705
                          | || || | | ||| ||||| | |||     |||| | | | ||||| |
Db       1435 CCACTTGGCAG-----TCTGTG-GGTGTTTC---
AACGTTTGAGCTGTGGCCAGTCCAAG 1385


Qy        706 CTGTCTGAGG-
CTCTGAGCGTACATAGGGAAGGGAGGAAGGGAAAACAGAAAGCAGACAA 764
                          ||| ||||| | | ||| | | | ||| | |||| |     || ||| |||
|
Db       1384 CTGGAGGAGGCCACAATGATTCATTAGAGCTTTGAGGTTGTTCTTGAAG--
AGCTGAATA 1327


Qy        765 AGAAAAAAGAGCTAGCCCAAAAT-------
```

```
CCCAAACTCA------------------- 797
          | | ||||| ||| |    |||| |||||
Db       1326
TAGGACATGAGCTGTCCCGGTGTGACTCTCCCCATACTCATCTTGATTGGCAGGTTTTCT 1267


Qy       798 -----------AACCA--------AACCAAACAGAAAGCAGTG-------
GAGGTGGGGG 831
                      |||        || |||    | || ||       | | |
|
Db       1266
CTGCTTGCCGCTTCCACTAGATGTCTCCGAACTTCCATCACTGCCTCTTTGTGCTTAGTG 1207


Qy        832 TTGCTGT--TGATT-------GAAGATGTATATAATATCTCCGGTTTATAAAA-----
CC 877
                 || | ||   | ||          |   || | |||| |||| | | || ||||
||
Db       1206 TT-
CAGTAAAGCTTCCCATAGGGCTTTGGCTGTGGTGTCACTGAATTGTGAAAGACAGCC 1148


Qy        878 TATTTATAACACTTTTTACATATATGTACATAGTATTGTTTGCT--------
TTTTATGT 929
                | |   | ||| || || || |   | | ||||| | |||            | |
|||||
Db       1147 TGGTGCAACCACATTATA-
ATTTTCCTCCTCAGTATGGAGTGCAGTGAGCGCTATCATGT 1089


Qy        930 TGACCATCAGCCTCG--TGTTGAGCCT------TAAAGAAGTAGCT--
AAGGAACTTTAC 979
               | |||||||| | ||   ||| ||||        |  ||||| ||| || || |||
|
Db       1088 TAACCATCA-CATCATTTGTGTGGCCTGGGAGCTGGGGAAGT-
GCTGAAATGATCTTCTC 1031


Qy        980 ATCCTAA-------CAGTATAATCCAGCTCAGTATTTTTGTT-
TTGTTTTTTGTTTGTTT 1031
               | ||||         |  |     |||| ||      | | | |   |  || |||
|
Db       1030 -
TACTAAGTTGTCTCCATGATGTCCAACTGCTCCTGTGAGATCCAGGGTTCTGTCCACAA 972


Qy       1032 GTTTTGTT-TTACCCAGAAATAAGATAACTCCATC----
TC------------------G 1068
                  | | |||||     |       ||   || | ||      ||
|
Db        971
AAACCACTGATGCCCTGCCTGCAGCAGTCTTCTTCCTGTTCTTTGCAGGGGCATAATTGG 912


Qy       1069 CCCCTTCC----CTTTCATCTGAAAGAAGATACCT---------CCCTC--
CCAGTCCAC 1113
                || ||||     | | | ||||  ||| ||||          | ||| || || |
|
Db        911
CCAGATCCGCAGCGATGACCTGACTTAAGGAACCTACAGCAAAACACTCCTCCCGTACTC 852


Qy       1114 CTCATTTAGAAAAC-CAAAG---TGTGGGTAGAAACCC--CAAATGTCCAAAAGCC-
CTT 1166
                || | | |   || |||| ||  || | ||   ||    | ||  || | |||  |
Db        851 CTAAAT--
GTTCACACAGAGAACTGAGGCCTGACACTAGGCATCTGATCTGCAGCAGCAG 794


Qy       1167 TTCTGGTGGGTGACCCAGTGCATCCAACAGAAACAGCC--GCTGCCCG--
```

```
AACCTCTGTG 1222
             |||||  ||  |   |   ||||  |   |  ||     |  || ||   ||| |||     |||||
||
Db      793 CTCTGG-GGTTAGCGTAGTGGAGTCCAC---ATCACCCAGGCTTCCCAGCTTCCTCT-
TG 739


Qy      1223 TGAAGCTTTACGCGCACACGGACAAAATGCCCAAACTGG---
AGCCCTTGCAAAA----- 1274
             |   |     |||     | ||    |  ||| ||  ||||    ||| | | ||||
Db      738 TCCGGTCGGGCGCTATTAAGG---
AGGTGCACATCCTGGGGTAGCAGTGGGAAAAGGGAT 682


Qy      1275 -
ACACGGCTTGTGGCATTGGCATACTTGCCCTTACAGGTGGAGTATCTTCGTCACACATC 1333
               |  ||| | | || ||||  |               |  ||||  |   |  ||  ||
Db      681 GCAAAAGCTGGAGTCA-AGGCAAAGT-----------
GGGGAGCAACAGGGGCAAGCA-- 636


Qy      1334
TAAATGAGAAATCAGTGACAACAAGTCTTTGAAATGGTGCTATGGATTTACCATTCCTTA 1393
              ||  |  ||  || |  ||| | |  || ||          |   |    |  ||  |||
|
Db      635 ATAACGGGACAT--GGAACACCTCGGCCGTG---TAGTTC-ATG---
TTGCCCATCCATT 585


Qy      1394 TTATCA-CTAATCATCTAAACAACTC-----------
ACTGGAAATCCAATT-------- 1433
              ||  || || ||  |  |   |||              |||     ||||  |
Db      584 CACACAGCTTCTCCTC-
CAGCTGCTCGAACACCGGCTGCTGCCCCTCCATCTCGGCCGCT 526


Qy      1434 ---AACAATTTTACAACATAAGATAGAATGGAGACCTGAATAATTC-----
TGTG----- 1480
              |   |   ||| ||| ||  |   || | | |    | |       ||||
Db      525 GCCGCCGCTGGGACATGATTAGCT-
GTGAGGTGGACAGCGTGGCTCACGGTTGTGACCAC 467


Qy      1481 -TAATATAAATGGTTTATAACTGC------TTTTGTACC-TAG---CTAGGCTG-
CTATT 1528
              |  |  |  |||   |  | |||||    |  ||| ||  ||    ||    |  | |
Db      466 CACACAATACTGG-
AAGTGACTGCGGCAGATGATGTCCCGTAGGATCTCCACGGTCCGGC 408


Qy      1529 ATTACTATAATGAGTAAATCATAAA----GCCTT------CATCACTC--
CCACATTTTT 1576
              ||  |   |   ||   | ||  |||     |||||       |  |   |||  ||||
||
Db      407 CTTTCAGCAGGCAGCTCAGCACAAACACTGCCTTGGGCTGCTTGGCTCCACCACCAATTG 348


Qy      1577 CTTACGG--TCGGA-----GCA--------
TCAGAACAAGCGTCTAGACTCCTTGGGACC 1621
              |  | ||| |||  |         |||       ||||   |   |  | ||||   |
|||
Db      347 CGT-CGGGCTCGAACTCTCGCAGGTGACAGTCAGGGCCCCCCAC-
CGCCTCCAGGAGACG 290


Qy      1622 GTGAGTTCC-TAGAGCTTG-GCTGGGTCTAGGC--------
TGTTCTGTGCCTCCAAGGA 1671
              |    |  ||||  ||  |   |  |  || || ||| |||          ||  |  |     |||
```

```
|
Db        289
GGTGGATCCGCAGCCCCAGTGCAGGCTCTCGGCGCAGGCGGCGTCCAGGTAAACCACAGC 230

Qy       1672 CTGTCTGGCAATGACTTGTATTGGCCACCAACTGTAGATGTATATATG---GT--
GCCCT 1726
             |  || |   || |   || |  | |    ||  ||| |  | | ||   || | |    ||
||||
Db        229 CCGTTTCACTTTGGCCAGCACCTGCTCCCATCC-
TTGCTGGGTAAAGGACAGTACGCCCG 171

Qy       1727 T----CTGATGCT--AAGACTC-CAGACCTTTTGTTTTTGCTTTGCA-------
TTTTCT 1772
             || ||| |   || || |||| ||| |    | |  ||||
||||
Db        170 AGGCGCTCATGGTTGGGGATTCGCAGA-
CTTGGGAAACTACGGTGCAGGAACTTCTTTCA 112

Qy       1773 GATTTTATACCAACTG-----
TGTGGACTAAGATGCATTAAAATAAACATCAG------- 1820
             ||  ||  |   | | |     || |  |   ||  | || |    |  |||
Db        111
GAACTCACCGCTTCCGGAAATTGGGCTCCGGGAGACTTTGACAGTCTCCACAGTACACCC 52

Qy       1821 AGTA----------ACTC 1828
             ||||          |||
Db         51 AGTAGGCCAACAGTGCTC 34


RESULT 5
US-10-478-914-21
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match           39.3%;  Score 4272.5;  DB 1;  Length 3589;
  Best Local Similarity   36.6%;  Pred. No. 5.2e-279;
  Matches 1177;  Conservative    0;  Mismatches  628;  Indels 1409;
Gaps  171;

Qy        1 CAGTTACAGG----------------GAGCACCACCAGGGAACATCTC---
GGGGAG-- 38
```

```
              ||   ||| ||                        |  |  ||  |  | ||    || |   ||||||
Db       390
CAAATACTGGCATGAAGACTGCCTGAAGTGTGCCTGCTGTGACTGTCGCTTGGGGGAGGT 449

Qy        39 -----CCTGGTTGGAAGCTGCAG------------------GCTTAGTCTGTC---
GGCT 72
                    ||    || |  ||  ||                 ||  || || ||
||||
Db       450
GGGCTCCACCCTGTACACTAAAGCTAATCTTATCCTTTGTCGCAGAGACTATCTGAGGCT 509

Qy        73 ----------GCGGGT-----CTCTGACTG------------CCCTG---
TGGGGAGGGT 102
                      ||||    | ||| |||             |||||   | | ||
|||
Db       510
CTTTGGTGTAACGGGAAACTGCGCTGCCTGTAGTAAGCTCATCCCTGCCTTTGAGATGGT 569

Qy       103 ----CTTGCC----------TTAACATCC---CTTGCATT---
TGGCTGCAAAGAAATCT 142
                    | ||||          || ||  ||   ||| ||  || | |    |
||||
Db       570
GATGCGTGCCAAGGACAATGTTTACCACCTGGACTGCTTTGCATGTCAGCTTTGTAATCA 629

Qy       143 GC---------TTGGAAG------------AAGGGGTTAC--
GCTGTTTGGCCGGGCAGA 179
                       |           |||||          || |  ||  | |  || ||| | |
                |
Db       630
GAGATTTTGTGTTGGAGACAAATTTTTCCTAAAGAATAACATGATCCTTTGCCAGACGG- 688

Qy       180 AACTCCGCTGAGCAGAACTTGCCGCCAGA-----ATGCTCCTCCTGTT-GCTGAG-
TATC 232
                     ||| |  ||| |   || |   | |||      |||| ||  |   ||| |||||
||||
Db       689 -ACTAC---
GAGGAAGGTTTAATGAAAGAAGGTTATGCACCCCAGGTTCGCTGATCTATC 744

Qy       233 ATCGTCCTCCACGTCGCGGTGCTG-GTGCTGCTGTTCGT------------
CTCCAC--G 277
                     | | || ||   |      |  | | ||  || | ||| |          ||||||
                |
Db       745 AACATCACCCCATTAAGAATACAGAGCACTAC-
ATTCTTTTATCTTTTTTGCTCCACATG 803

Qy       278 ATCGTCA-----GCCAATGGATC----------------------
GTGGGCA-------- 302
                     | | |    | || ||| |                        |  ||||
Db       804
TACATAAGAATTGACACAGGAACCTACTGAATAGCGTAGATATAGGAAGGCAGGATGGTT 863

Qy       303 --ATGG----ACACGC-AACTG-ATCTCTG-
GCAGAACTGTAGCACCTCTTC-------- 345
                     ||||   | | ||  |||| | | ||    | | || |||
Db       864
ATATGGAATAAAAGGCGGACTGCATCTGTATGTAGTGAAATTGCCCCAGTTCAGAGTTGA 923

Qy       346 ------------------CTCAGGAAATGTCCACC--ACTG-----------
TTTCTCATC 375
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                              | |  ||||| ||      |||            || ||
Db        924
ATGTTTATTATTAAAGAAAAAAGTAATGTACATATGGCTGGATTTTTTTGCTTGCTATTC 983

Qy        376 --------ATCAC----CAAACGA--------ATGG-
CTGCAGTCT-------------- 400
                              ||||   ||   ||      ||| ||    || |
Db        984
GTTTTTGTGTCACTTGGCATGAGATGTTTATTTTGGACTATTGTATATAATGTATTGTAA 1043

Qy        401 -------------------GTCCAG---------GCCACCA----
TGATCCTGTCGATCA 428
                               | |||       |  ||||   || ||| | |
Db      1044 TATTTGAAGCACAAATGTAATACAGTTTTATTGTGTTACCATTTGTGTTCCATTTG--
CT 1101

Qy        429 TCTT-------CAGCATT-----CTGTCTCTG-------TTCCTGTT---------
CTTC 460
                    ||||        |||||     |  ||  ||       || |||
|||
Db      1102
TCTTTGTATTGTTGCATTTAGTACAATCAGTGTTTAAACTTACTGTATATTTATGCTTTC 1161

Qy        461 TG------
CCAACTCT----------------------------------------T 471
                    ||    ||| || |
Db      1162
TGTATTTACCAGCTATTTTAAATGAGCTGTAACTTTCTAGTAAAGAATTGAAAAGCAAAT 1221

Qy        472 CACCCT-------CACCAAGGG---GGGCAGGTTTTACATC---------
ACTGGAA--- 509
                    | | ||       ||| |     ||| |||| || ||          ||| ||
Db      1222
CTCACTAATGATACACAGATAGATAAAGCAAGTCTATCAACATTAAAAATACTAAAAAAT 1281

Qy        510 --------------------------TCTTCCA--
AATTCTTGCTGGTCTGTCGTGATG 541
                              | ||||  | || |||| |  || || || |
Db      1282 AAAGACACACACAGAGCATTTTAGTGACATCCACTACTTATTGCCG--
CTATGAGTTA-G 1338

Qy        542 AGTGCTGCGGCCATCTACACGGTGAGGCACCC---------GGAGT--------
GGC--- 581
                    ||| ||  |  | | | | |    | |||        || ||           ||
Db      1339 AGT-CTAT--
CAGTGTTCTTGTTATAACCCCCTATTTTCAGGGGGTTAAAAATCAGCTTT 1395

Qy        582 ----------------ATCTCAAC-----------TCGGATTACTCCTACG------
GTT 608
                              || ||| |           || |||| || | ||| |
Db      1396
AAAAAAATACATAAAAATTTCATCTTAAAGCACTTTCATTTTATACCAACGTGAAAAGTG 1455

Qy        609 TC--------------------GCCT-ACA----TCC------TGGCC------
TGGGTG 631
```

```
                    |                      | |  | | |      | | |        |   | | |            | |
        |||
        Db      1456
        CCATTTTTAGAATAACTTTAAAGCTTAACAGGTTTCCTTTTAATATCCTTTTTTTGTGTG 1515

Qy       632 GCCTT------CCCCCTGGC---------
        CCTTCTCAGCGGTGTCATCTATGTGATCT-- 674
                      |||      | |  | | | |      | | |  | | | | | |     |    | |  | | | | | | |  | |
        Db      1516
        CTCTTTACTTACACAATGGCTTTGTTTTGCTTTTTCAGCCACACCCCTTATGTGAACTAG 1575

Qy       675 TGC-----GGAAACGCG-------------
        AATGAGGCGCCCAGACGGTCTG-------- 708
                      |||      | |  | | | |             | |  | |  |    |    | | | |
        Db      1576
        TGCCTTTGGGTATCACGTAAAATTTTTTCCAAAGGGTTACTTTAAAAATCTGTTACCACA 1635

Qy       709 --TCTGAG-------------------------------------------
        GCTCTGAG 722
                      |  | | | |                                                    | |  |
        ||
        Db      1636
        ATTATGAGATGATTTTTAAGTGATAAATTAAACTTCTTCTTGTATAAATTCTGCCCAGAT 1695

Qy       723 CGTACATAGGGAAGGGAGG-------------
        AAGGGAAAACAGAAAGCAGACAAAGAAA 769
                      |    |    | |    | | | |         | | |    | | |  |       | | | |
        | | | |
        Db      1696
        CTCTCCACAAGAGCTGAGGGTTTCATAACTTTATGGCTTAATAAATGTATGACACTGAAA 1755

Qy       770 AAA---
        GAGCTAGCCCAAAATCCCAAACTCAAACCAAACCAAACAGAAAGCAGTGGAGGT 826
                      | |   | | |     |   | |  |  | | | |     | |  |  |  | | | |  | |
        |||
        Db      1756 AGATTTGAGTGTG---AATCTACTGAAATCACTATAATGCACATTG-
        AAGCTATGATGGT 1811

Qy       827 G----------GGGGTTGCTGTTGATTGAAG-------
        ATGTATATAATATCTCC----- 864
                      |  | | | |  | |  | | | | | |  |         | | |    | | |   | | | |  |
        Db      1812
        ATTTGAGTAGTGAGGTTACTTTTGATCGGAGCAACATAATGCTCATAGAATCTTCTAGAA 1871

Qy       865 --------------
        GGTTTATAAA---------------------------------- 874
                      |  | |  | | | | |
        Db      1872
        GAAGAGAAACAAAGGGATTGATAAAATGCTGAGAACTAGTGATTATATATTTTTCTGTAT 1931

Qy       875 --ACCT---ATTTAT------------------AACACTTT---
        TTACATATATGT---- 904
                      | | | |    | | | | | |            | | | | | | | |   | |  | | | | |
        Db      1932
        TTACCTGACATTTATTTTAATGTTCAAAAAGTAAACACTTTAAGTTTGATGTGTTTTACT 1991

Qy       905 ---ACATAGTATT--GT--TTGC------------------
        TTTTTATGTTGA-------- 932
                      | | |  | | | |  | |   | | |  | | | |              | | |  | | |  | | | |
        Db      1992
```

```
CTCTCATTGTTTTAAGTAATTGCCAACTCAGAATACATCATTCTTAGGCTGAAATTTGTC 2051


Qy       933 ---CCAT-------------------CAGCCT--CGTGTTGAGCCTT-AAAGAAG-
TAGC 966
                ||||                    |  |||  |||| | ||| |  ||||||||
|||
Db      2052 TTTCCATTTTTTAAGGTGAAATAGTACTACCTTACGTGAT-
AGCATACAAAGAAGAAAGC 2110


Qy       967 ---------------------------------------------
TAAGGAACT-------- 975
                                                             ||||||| |
Db      2111
TCTAGAAAGAGAAATTATGGAGAATGATTATTTAAATTACAATTAAGGAAATGAGAATAT 2170


Qy       976 ---------------------------TTACATC----------
CTAACAGTA------ 991
                                            || | ||         || | |||
Db      2171
GATCCCCTCTTCCGAGTTGCCCACAAACTTGCTTCTTTGCTTTTGCTCCCTGTAATAGAA 2230


Qy       992 ------------TAATC----------CAGCTCAG-------
TATTTT------------ 1010
                            ||||          | || |     ||||||
Db      2231
CTACTTTTCAACAAATCTAATTTTGCACGGCACCGTTAACCATATTTTCACTACAGCAAA 2290


Qy      1011 -----TGTTTT--GTTTTTTGTTTGTTTGTTTTGTTTT---
ACCCAGAAATAAGATAACT 1060
                  || | | ||||| | ||| |||||||| || |    | |    ||| || |
Db      2291
CTTAGTGCTATGGGTTTTCTTTTTCTTTGTTTTTTTCTTGATCACTTGTATAGGAAACAA 2350


Qy      1061 CCATCTC-----------GCC------------CCTTC---------
CCTTTCATCTGAA 1088
                | | ||              ||           |||||        | || ||
||||
Db      2351
CATTTTCCAGTGTTATTTGCATATATATTTTGTCCTTCCAATATATGCATTACAGATGAA 2410


Qy      1089 ----AGAAG--ATACCTCCCTCCC-------
AGTCCACCTCATTTAGAAAACCAAA---- 1131
                | | | |||||| | |         | ||| ||| || | | |
Db      2411
AATTAAATGTTATACCTGAATTCTTGGGTTGGGGCCAAAATATTAAGCTGAAAATAATGC 2470


Qy      1132 --GTGTGG----GTAGAAACCCCAA--------ATGTCCA----------------
AAA 1160
                ||||||    ||  ||  ||      ||| ||                      |
Db      2471
TGGTGTGGATTTGTTTTAAAACAAAGCTTTATTATGAACATGCATGTGAATCTGGATATT 2530


Qy      1161 GCC-CTT-----------------TTCTG------GTGGGTGA-----------
CCCAGTG 1186
                ||| |||                 |||||      ||| |||            || |
||
Db      2531
GCCTCTTATTTTTAAGAAAATGGTTCTGTGAAAAGTGAATGATATGTATTTTTCCAAATG 2590


Qy      1187 CATCC---AACAGAAACAGCCGCTGCCC-
```

```
GAACCTCTGTGTGAAGCTTTACGCGCACACG 1242
          | ||        || |  |   | ||  |  | | |  |  | || | |||          |
                                                                        |
Db     2591
CTTCATGGTTAGGAGTCTTCAAGTTCCATGTTCCCCAGATTTGAGATATACTAAAGAAAG 2650

Qy     1243 GA---CAAAATGCCCAAACTGGAGCCCTTGCAAA-
AACACGGCTTGTGGCATTGGCATAC 1298
             |  | |||||  | |  ||| ||||   ||| |||    || | || || | |
                                                                 |
Db     2651 AAATTCAAAAGTAGCTATTTGGGGCCCACAAAAATAACTATTATTTTAGCCTTAG-
AGCC 2709

Qy     1299 TTGCCC---TTACAGGTGGAGTA---TCTT-CGTCAC------------------
ACATC 1333
             || | |  || || |  || |   ||| | | ||                     |||
Db     2710
TTACACTTGTTTCATGAAGAGAAAGGACTTGCATAACCAAAATAAACAAAGCAAGACAAA 2769

Qy     1334 TAAAT-----------
GAGAAATCAGTGACAACAAGTCTTTGAAATGGTGCTATG----- 1377
             | ||          |||| ||||||||| ||   || ||   |||| ||   ||
Db     2770
TTAAAAATATGTGGGGGAGAGATCAGTGAAAAGTGGTTTTCTTAATGCAGCCCTGCTGGT 2829

Qy     1378 ---GATTTACCATTCCTT-------------------------
ATTATCA--------- 1399
                |||  || ||| |||                       ||| |||
Db     2830
CCCCATTAACAATTGCTTGAAATTCACATGGATGTAAAATTATAATTGTCAGGATCTTAT 2889

Qy     1400 -CTAATCATC--TAAACAACTCACTGGAAATCC----
AATTAACAATTTTACAACATAAG 1452
             |  | ||  | | ||      | ||||| | |     ||| | || |  ||| |||
Db     2890
TCAGATGATCTTTTAAGGTTTAACTGGTTTTGCTTTTGTTTATCTATATGTCAAAATACT 2949

Qy     1453 ATAGAATGGAGACCTGAATAAT-TCTG-----------TGT---
AATATAAATG------ 1491
             ||| | || |  | | ||| |  | | |         |||   | ||| |  ||
Db     2950
TGTAAATTGGGAACAAACTTCTCTCAGCTTCTTGAAGTTGTTCAACTATCCTTGCCACTG 3009

Qy     1492 -------------GTTTATAACTGCTT----TTGTACCTA----
GCTAGG---------- 1520
                          | || | |||||||    || ||| ||     ||| |
Db     3010
GAAGACCAAACAAGGTTTTCACTGCTTTTTCTTTTACATAATATGCTGAGAATTATTTCT 3069

Qy     1521 -CTGCTATT-------------ATTACTATAAT-
GAGTAAATCATAAAGCCTTCATC--- 1562
              |||| ||            ||||||  | || ||||   ||| ||||| |||
Db     3070
TATGCTTTTTACTACAAACAAAATTACTCACCTGGATTAAAGATTAAGGCCTTAATCTGT 3129

Qy     1563 --------------ACTCC--------------------------------
CA----- 1569
                            ||||                                ||
Db     3130
TTAGATTATCTTTAATCTCCATGAAATCGTGAAATAAGACAAGAATAGTGTTTCAGCTGT 3189
```

```
Qy       1570 ----CATTTTTC------TTAC-----GGTCGGAGCAT-----------CAGAAC-
AAGC 1602
                   |||||| |       || |       | | |||||          || ||
||||
Db       3190
AGGCCATTTTACAGCTAATTGCCCATAAATTGTAGCATTTATTGACCTGAAGTACTAAGC 3249

Qy       1603 -----GTCTAGACTCCT-TGGGACCGTGAGTT--------------
CCTAGAGCTTGGCT 1642
                   |||| |||| ||   | || ||| ||             |||     |||
|
Db       3250
TAATTGTCTTGACTACTCAAAGCCCCTGAATTGTTGTCAACTTTCCCCTTTGTGTTGTGT 3309

Qy       1643 GG-------GTC---TAGGCTGT--TCTG-TGCCTCCA--AGGACT-GTCTG-----
GCA 1681
                  |        |||    ||| |||  |||| |||||||| |||||   || |
Db       3310
AGCCCTAACGTCATTTAGCTTGTTGTCTGATGCCTCCAGTAGGACACCTCCGATGGAGCT 3369

Qy       1682 ATGACTT-------GTATTGGCCACCAACTGTAGATGTAT-----
ATATGGTGCCCTTCT 1729
                  ||| ||         |       || || |  ||||| ||     ||| | |||| |
Db       3370 TTGATTTCTGAGCAGCGAAAGCTCCCTTCCTAAGATGCATCTCGCATAGGCTGCC--
TAT 3427

Qy       1730 GATG------------CTAAGACTCCA-----------------------GACCT---
TT 1751
                  ||||              |   ||||||                       |||||
||
Db       3428
GATGAAGGACCGTGCACCTCCACTCCAACAGAGTGCTGAGTTTAAAAGTTGACCTGTGTT 3487

Qy       1752 TGT--TTTTGCTTTGCATTTT-CTGATTTTATACCAACTGTGT--
GGACTAAGATGCATT 1806
                  ||| |||  |||| ||| ||| || || ||  ||| | |||  |     | || |    |
Db       3488 TGTAATTTCACTTT-
CATCTTGCTTAATAAATATCTGCTGGATTCTTTCAAAAAAAAAAA 3546

Qy       1807 AAAATAAACATCAGAGTAA-----------CTC 1828
                  |||| ||| |  | |  ||             |||
Db       3547 AAAAAAAAAAAAAAAAAAAAGGCCACATGTGCTC 3580


RESULT 6
US-10-478-914-21/c
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
```

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  Query Match            38.9%;  Score 4224.5;  DB 1;  Length 3589;
  Best Local Similarity  35.1%;  Pred. No. 1.2e-275;
  Matches 1149;  Conservative    0;  Mismatches  649;  Indels 1477;
Gaps  162;

Qy        1 CAGTTACAG----GGAGCAC-------CACC--AGGGAACATCT-
CGGGGAGCCT----G 42
            | ||| ||   || |||||      || | ||| | | | || |  || |
|
Db     3458
CTGTTGGAGTGGAGGTGCACGGTCCTTCATCATAGGCAGCCTATGCGAGATGCATCTTAG 3399

Qy       43 GTTGGAAGCT---GCAGGCTTAG----------TCTGTCGG----------
CTGCGGGTC 79
            |  || |||| || | ||| ||       || ||||        ||| ||
Db     3398 GAAGGGAGCTTTCGCT-
GCTCAGAAATCAAAGCTCCATCGGAGGTGTCCTACTGGAGGCA 3340

Qy       80 TCTGACTGCC--CTGTGGGGAG---GGTCTTGCC----------------
TTAACATCCC 118
            || ||| |  ||    | |  || ||   |              || ||| |
Db     3339
TCAGACAACAAGCTAAATGACGTTAGGGCTACACAACACAAAGGGGAAAGTTGACAACAA 3280

Qy      119 TT-----GCATTTGGCTG-CAAAGAAATCTGCTTGGAAGAAGGGGT----------
TAC- 161
            ||    || || | | ||| ||| |||| | |      |||
|||
Db     3279
TTCAGGGGCTTTGAGTAGTCAAGACAATTAGCTTAGTACTTCAGGTCAATAAATGCTACA 3220

Qy      162 ---------------GCTGT---TTGGCCG--
GGCAGAAACTC----------------- 184
                          ||||| ||||| || ||||| |
Db     3219
ATTTATGGGCAATTAGCTGTAAAATGGCCTACAGCTGAAACACTATTCTTGTCTTATTTC 3160

Qy      185 -CG----------------------CTGAGCAG------------
AACTTGCCGCCAG- 207
             ||                       || | |||         | |||
|||||
Db     3159
ACGATTTCATGGAGATTAAAGATAATCTAAACAGATTAAGGCCTTAATCTTTAATCCAGG 3100

Qy      208 -------------------------------------
AATGCTCCTCCTGTT--------- 222
                                        ||| |||  | | ||
Db     3099
TGAGTAATTTTGTTTGTAGTAAAAAGCATAAGAAATAATTCTCAGCATATTATGTAAAAG 3040
```

```
Qy        223 -----GCTG---------AGTATCATCGTCC------------------
TCCACGTCGCG 250
                    || |         || | || |||                | || ||
|
Db      3039
AAAAAGCAGTGAAAACCTTGTTTGGTCTTCCAGTGGCAAGGATAGTTGAACAACTTCAAG 2980


Qy        251 GTGCTG-GTGCTG-CTGTTC-----------
GTCT------------------------- 272
                    |||| | |  |  |||||          || |
Db      2979
AAGCTGAGAGAAGTTTGTTCCCAATTTACAAGTATTTTGACATATAGATAAACAAAAGCA 2920


Qy        273 ------------CC----ACGATCGTCAGCCAATGGATCGTG----------------
GG 300
                          ||    | |||| || |  |    |||| ||
Db      2919 AAACCAGTTAAACCTTAAAAGATCATCTG-
AATAAGATCCTGACAATTATAATTTTACAT 2861


Qy        301 CAATG-GA----CACGCAACTGATC------TCTGGCAGAACTGT------
AGCACCTC- 342
                    | ||| ||    || |||| || |      |  |||| |||     | |||
|
Db      2860
CCATGTGAATTTCAAGCAATTGTTAATGGGGACCAGCAGGGCTGCATTAAGAAAACCACT 2801


Qy        343 TTCCTCAGGAAATGTCCACCAC------------------------------------T 365
                    || | | || | ||| ||||
|
Db      2800 TTTCACT-
GATCTCTCCCCCACATATTTTTAATTTGTCTTGCTTTGTTTATTTTGGTTAT 2742


Qy        366 G-------TTTCTCATCAT-CACCAAACGAATGGCT------------------
GCAGTCT 400
                    |     ||||||| |||| | ||| | |||             | |
|
Db      2741
GCAAGTCCTTTCTCTTCATGAAACAAGTGTAAGGCTCTAAGGCTAAAATAATAGTTATTT 2682


Qy        401 GTCCAGGCCACCA--TGATCCTGTCGATCATC-
TTCAGCATTCTGTCTCTGTTC------ 451
                    |  |||| |  | | || | ||   || ||| | | | ||||  ||
Db      2681
TTGTGGGCCCCAAATAGCTACTTTTGAATTTCTTTCTTTAGTATATCTCAAATCTGGGGA 2622


Qy        452 -CT--GTTCTTCTGCCAACTCTTCACCCT-CACCAAGGGGG-----
GCAGGTTTTACA-- 500
                    |  | | || || |||| | ||| | ||  ||    || | | | ||
Db      2621 ACATGGAACT--
TGAAGACTCCTAACCATGAAGCATTTGGAAAAATACATATCATTCACT 2564


Qy        501 --TCACTGGA-----ATCT------------------
TCCAAATTCTTGCTGGTCTGTGC 535
                    |||| | |       |||              |||| |||| |  |  |||
|
Db      2563 TTTCACAGAACCCATTTTCTTAAAAATAAGAGGCAATATCCAGATTC--
ACATGCATGTTC 2506
```

```
Qy        536 GTGATGA------GT-------------GCTGCGGC--------
CATCTACACGGTGAG 567
                | | | |        | |              |  | | |        | | | |  |    |
 |
Db       2505
ATAATAAAGCTTTGTTTTAAAACAAATCCACACCAGCATTATTTTCAGCTTAATATTTTG 2446

Qy        568 GC----ACCC---------GGAGTGGCA------
TCTCAACTCGGATTACTCCTACGG-- 606
                | |    | | | |          | |  |  |    | | | | | | |  | | | | |     | |  |
Db       2445 GCCCCAACCCAAGAATTCAGGTATAACATTTAATTTTCATCT-
GTAATGCATATATTGGA 2387

Qy        607 ------------TTTCGCCTACATC-CTGGCCTGGGTGG---CCT----------
TC--- 637
                               |  | |   |  | |  | | | |     | |  |   | | |              | |
Db       2386
AGGACAAAATATATATGCAAATAACACTGGAAAATGTTGTTTCCTATACAAGTGATCAAG 2327

Qy        638 -----------------------CCCCTGGCCCTTC----------------------
TCA 653
                                        | | |  | | |  | |                               |
 |
Db       2326
AAAAAAACAAAGAAAAAGAAAACCCATAGCACTAAGTTTGCTGTAGTGAAAATATGGTTA 2267

Qy        654 GCGGTGTCAT----------CTATGT---------
GATCT-------------------- 674
                | | | | |  | |            |  | | |         |  | | |
Db       2266
ACGGTGCCGTGCAAAATTAGATTTGTTGAAAAGTAGTTCTATTACAGGGAGCAAAAGCAA 2207

Qy        675 ---TGC---------GGAAACGCGAATGAGGCG---------------
CCCAGACGG--- 704
                    | |         | | | | |  | | | | | | | |                   | |    |   |
Db       2206
AGAAGCAAGTTTGTGGGCAACTCGGAAGAGGGGATCATATTCTCATTTCCTTAATTGTAA 2147

Qy        705 -------------------------TCTGTCTGAGGC-----TCTGAGCGT------
AC 727
                                          | | |  | | |     | |      | | |    |  |
 | |
Db       2146
TTTAAATAATCATTCTCCATAATTTCTCTTTCTAGAGCTTTCTTCTTTGTATGCTATCAC 2087

Qy        728 ATAGGGAAG--------------
GGAGGAAGGGAAAACAGAAAGCAGACAAAGAAAAA-- 771
                | |  | |  | |                | |  | || || |||  |   |||  | ||||  |
Db       2086
GTAAGGTAGTACTATTTCACCTTAAAAAATGGAAAGACAAATTTCAGCCTAAGAATGATG 2027

Qy        772 -----AGAGCTAGCCCAAAATCCCAAACTC-----------
AAACCAAACCAAACAGAAA 815
                     | | |  | | |    | |  | |  |  | |    |              | | |  | |  |  | | | | |
 | | |
Db       2026 TATTCTGAGTTGGC---
AATTACTTAAAACAATGAGAGAGTAAAACACATCAAACTTAAA 1970

Qy        816 G--------------
CAGTGGAGGTGGGGGTTGCTGTTGATTGAAGATGTATATAATAT 860
```

```
                  |                 ||  |   |       ||  |  |  |  |   |||   |||||
||
Db     1969 GTGTTTACTTTTTGAACA-TTAAAATAAATGT--
CAGGTAAATACAGAAAAATATATAAT 1913

Qy      861 CTC----------CGGTTTATAAAACCTATTTATAACACTTTTTACA------
TATATGT 904
                  | |          |  |||||  ||  ||  |||  |  |  ||| ||   |          |
||||
Db     1912 CACTAGTTCTCAGCATTTTATCAATCC-
CTTTGTTTCTCTTCTTCTAGAAGATTCTATGA 1854

Qy      905 ACATAGTATTG-----------------TTTGCTTTTTATGTTGACCATC--
AGCCTCGT 945
                     |||  | |||              |  || ||  |  |||||| |||  ||
Db     1853 GCATTATGTTGCTCCGATCAAAAGTAACCTCACTACTCAAAT--
ACCATCATAGCTTC-- 1798

Qy      946 GTTGAGCCTTAAAGAAGTAGCTAAGGAACTTTAC------
ATCCTAACAGTATAATCCA- 998
                     || || |||| ||   |  |  || |  ||  ||       ||| |  |||| ||  |
||
Db     1797 AATGTGCATTATAGTGATTTC--
AGTAGATTCACACTCAAATCTTTTCAGTGTCATACAT 1740

Qy      999 --GCTCAGTATTTTTGTTTTGTT---------TTTTGTTTGTTTGTTTTG------
TTTT 1041
                       | ||    |    ||| ||         |  ||| |  |   |  | ||
Db     1739 TTATTAAGCCATAAAGTTATGAAACCCTCAGCTCTTG-
TGGAGAGATCTGGGCAGAATTT 1681

Qy     1042 ACCCAGAAATAAGATAACTCCATCTC----
GCCCCTTCCCTTTCATCTGAAAGAAGATAC 1097
                     |  ||  || ||| | |  |||        |  | | |   |  || |   ||||
Db     1680 ATACAAGAAGAAGTTTAATTTATCACTTAAAAATCATCTCATAATTGTGGTAACAGATTT 1621

Qy     1098 CT-------CCCT-----------------------CCC---------
AGTCCAC------ 1113
                     |       ||||                     |||          |||  |||
Db     1620 TTAAAGTAACCCTTTGGAAAAAATTTTACGTGATACCCAAAGGCACTAGTTCACATAAGG 1561

Qy     1114 -------CTCATTTAG------
AAAACCAAAGTGTGGGTA-------------------- 1140
                     || |   ||    ||| |||  |||| |||
Db     1560 GGTGTGGCTGAAAAAGCAAAACAAAGCCATTGTGTAAGTAAAGAGCACACAAAAAAAGGA 1501

Qy     1141 ---------GAAACCCCAAATG------------TCCAAAA---
GCCCTTTTCTGGTGGG 1176
                     ||||||     | |           ||  ||||   || ||||||   ||
Db     1500 TATTAAAAGGAAACCTGTTAAGCTTTAAAGTTATTCTAAAAATGGCACTTTTCACGTTGG 1441

Qy     1177 TGAC-----CCAGTGCATCCAACAGAA------------------
ACAGCCGCTGCCCGA 1213
                     |          ||||| |  |   |||                |  ||| | |
```

```
|
Db        1440
TATAAAATGAAAGTGCTTTAAGATGAAATTTTTATGTATTTTTTTAAAGCTGATTTTTAA 1381

Qy        1214 ACCTCTGTGTGAAG-----CTTTACGCGCACACGGA------CAAAAT------
GCCCA 1255
                 || |||      ||         | ||  | |||| ||       | || |         ||
Db        1380
CCCCCTGAAAATAGGGGGTTATAACAAGAACACTGATAGACTCTAACTCATAGCGGCAAT 1321

Qy        1256 AACTGGAG-----
CCCTTGCAAAAACACGGCTTGTGGC--------------------- 1288
                || | | |        | ||   ||| | | |  |||| |
Db        1320 AAGTAGTGGATGTCACT--
AAAATGCTCTGTGTGTGTGTCTTTATTTTTTAGTATTTTTAAT 1263

Qy        1289 ATTGGCATACTTGCCCTTACAGGTGGAGTATC---------------------
TTC--- 1323
                 ||| | | |||||| |  | |       | |||||                     |||
Db        1262
GTTGATAGACTTGCTTTATCTATCTGTGTATCATTAGTGAGATTTGCTTTTCAATTCTTT 1203

Qy        1324 --------GTCACA---CATCTAAA-----TGAGAAAT------------------
CAGT 1349
                      || |||   ||| ||||      || ||||
|||
Db        1202
ACTAGAAAGTTACAGCTCATTTAAAATAGCTGGTAAATACAGAAAGCATAAATATACAGT 1143

Qy        1350 GA-------------------------CAACAAGTCTTTG--------------
AAATG 1369
                 |                       |||||| |   |
|||||
Db        1142
AAGTTTAAACACTGATTGTACTAAATGCAACAATACAAAGAAGCAAATGGAACACAAATG 1083

Qy        1370 ---------------------------GTGCTATGGAT-
TTACCATTCCTTATTATCACT 1401
                                           |||||    || |||| || | |||| ||
|
Db        1082
GTAACACAATAAAACTGTATTACATTTGTGCTTCAAATATTACAATACATTATATACAAT 1023

Qy        1402 AATC--ATCTAAACAACTCA------------------------CTGG-----
AAATCC 1429
                 | ||  |   |||||| ||||                        | |
||||||
Db        1022
AGTCCAAAATAAACATCTCATGCCAAGTGACACAAAAACGAATAGCAAGCAAAAAAATCC 963

Qy        1430 A-----------ATTA----------------------------------------
ACAAT 1439
                 |            ||||
||||
Db         962
AGCCATATGTACATTACTTTTTTCTTTAATAATAAACATTCAACTCTGAACTGGGGCAAT 903

Qy        1440 TTTACAACATA-AGATAGA----------------ATGGAG-------
ACCTGAATAATT 1475
                 || || ||||| |||| |                 || |          |||   ||
```

```
|
Db        902
TTCACTACATACAGATGCAGTCCGCCTTTTATTCCATATAACCATCCTGCCTTCCTATAT 843

Qy       1476 CTGTGTAATATAAATGGTT----TATAACTGCTTTTGTACCT----
AGCTAGGC------ 1521
              ||  |  || |   ||||    | | | ||| ||||| |   ||| |
Db        842
CTACGCTATTCAGTAGGTTCCTGTGTCAATTCTTATGTACATGTGGAGCAAAAAAGATAA 783

Qy       1522 ----------
TGCTATTATTACTATAATGAG---------------------------- 1542
                        |||| |   | || ||||| |
Db        782 AAGAATGTAGTGCTCTGTATTCT-
TAATGGGGTGATGTTGATAGATCAGCGAACCTGGGG 724

Qy       1543 ----------TAAATCATAAAGCCTTCATC--ACTCC--------------
CACATTTTT 1576
                        |   |||| || ||||| ||  | |||           || ||
||
Db        723
TGCATAACCTTCTTTCATTAAACCTTCCTCGTAGTCCGTCTGGCAAAGGATCATGTTATT 664

Qy       1577 CTTACGG-----------------TCGGAGCATCAGA-----------
ACAAGC------ 1602
                        ||| ||             |   |   || ||         ||| ||
Db        663
CTTTAGGAAAAATTTGTCTCCAACACAAAATCTCTGATTACAAAGCTGACATGCAAAGCA 604

Qy       1603 GTC-------TAGAC----TCCTTGGGAC-CGTGA--
GTTCCTAGAGCTTGGCTGGG--- 1645
                        |||       || ||   ||||||| || | |   |  | |  ||  || || |
Db        603
GTCCAGGTGGTAAACATTGTCCTTGGCACGCATCACCATCTCAAAGGCAGGGATGAGCTT 544

Qy       1646 --TCTAGGCTG-------TTCTGTGCCTCCAAGGA--CT------GTCT----
GGCAATG 1684
                        |  |||| |       | | | |  |||| ||  ||      ||||   | |||
Db        543
ACTACAGGCAGCGCAGTTTCCCGTTACACCAAAGAGCCTCAGATAGTCTCTGCGACAAAG 484

Qy       1685 ACT--------------TGTATTGG-------CCAC----------
CAACTGT------- 1706
                        |            |||| ||   ||||          | || ||
Db        483
GATAAGATTAGCTTTAGTGTACAGGGTGGAGCCCACCTCCCCCAAGCGACAGTCACAGCA 424

Qy       1707 -----------AGATGTATATATG--------------GTGCCCTT--------
CTGATG 1733
                        |  || | |||             |||| ||           | |
Db        423
GGCACACTTCAGGCAGTCTTCATGCCAGTATTTGTCCAGTGCCTTTAGAAGATACCGGTC 364

Qy       1734 CTAAGACT-----------CCAG----ACCTTTTGTTTT--
TGCTTTGCATTTTCTGA-- 1774
                        ||    ||    ||||   |||||| | || || | || |   ||||
Db        363 CTTGATCTTTCGGTTGCAGCCAGCACAACCTTTCGGCTTGGTGTCTGGC-
TGGACTGAGA 305
```

```
Qy      1775 ----TTTTATACCAA----------------CTGTGTG--------------
GACTAAG 1799
                  || ||||||||                |||  ||              | ||
||
Db       304
GCATTTGTATACCAAAACTTTTCTCCTTTTTCTGCATGAGTTGACTTAGGCGTGTCTGAG 245

Qy      1800 ATGCA------TTAAAATAAACATCAGAGTAACTC 1828
                  ||||        |  | | | || ||    ||| |
Db       244 TTGCAGCAGCTTCGCATTGAGCACCA----AACCC 214


RESULT 7
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match            38.9%;  Score 4221.5;  DB 1;  Length 2120;
  Best Local Similarity   44.1%;  Pred. No. 9e-277;
  Matches  990;  Conservative   0;  Mismatches  705;  Indels  549;
Gaps  134;

Qy         1 CAGTTACAG-GGAGCACCACCAG--GGAACATCT-
CGGGGAGCCTGGTTGGAAGCTGCAG 56
                 |  ||| |  | |   | |      || | ||| ||| |    || | |   |||
|
Db         5 CCTGTACGGAAGTGTTACTTCTGCTCTAAAAGCTGCGGAATTCC---
TCGAGCACTGTTG 61

Qy        57 GCTTAGTCTGTCG-GCTGCGG--GTCTCTGAC-TGCCCTGTG--
GGGAGGGTCTTGCCTT 110
                 || || ||| | |||| |  | | | ||| ||||| |||   || | ||  | | |
Db        62 GCCTA--
CTGGAGTGCTGAAGTAGGCGCGGACGTGCCCGGTGCCTGGCGCGTGGTAGC-A 118

Qy       111
AACATCCCTTGCATTTGGCTGCAAAGAAATCTGCTTGGAAGAAGGGGTTACGCTGTTTGG 170
                 |  || |||   | | ||||||     || || | |  | | | || || |
||
Db       119 GGCGCCCGGTGCCCCGGCCGGCGAAGACCCATGGCGTTCATGGTGAAG--
```

```
ACCATGGTGGG 176

Qy         171 CCGGGCAGAAACTCCGCTGAGCAGAACTTGCCGCC-AGAATGCTCC-----
TCCTGTTGC 224
                   ||| |||       | |  | |   ||| | ||| | | ||  |      |  |
|
Db         177 -CGGCCAG-----
CTGAAGAACCTCACTGGGAGCCTGGGAGGCGGCGAGGATAAGGGAGA 230

Qy         225 TGAGTATCA-TCGTCCTCCACGTCGCGGTGCTGGTGC----TGCTGTTCG-------
TCT 272
                   || | |  | |||| |  ||    | | ||  | ||      |  || ||
||
Db         231
TGGGGACAAGTCGGCAGCCGAAGCTCAGGGCATGAGCCGGGAGGAGTACGAGGAGTATCA 290

Qy         273 ----CCACGATCGT----CAGCCAATGGATCGTGG-GCAATGGACACGCAACTGAT--
CT 321
                   | ||  ||       ||  ||||| || ||||  |   | || |   ||
|
Db         291 GAAGCAAC--
TCGTGGAAGAGAAGATGGAGCGGGATGCACAGTTCACACAGAGGAAGGCA 348

Qy         322 ---CTGGCAGAACTGTAGCACCTCTTCC---TCAGGAAATGTCCACC----
ACTGTTTCT 371
                   | |||   |||| |  | || |||||    ||  |  | | |||     |  |
|
Db         349
GAGCGGGCCACACTGCGGAGCCACTTCCGAGACAAATACCGGCTACCCAAGAACGAGACA 408

Qy         372 CATCATCACCAAA--CGAATGGC---TGCAGT-------CTGTC-------
CAGGCCACC 412
                   || |  ||| |  | ||||| |||| || |          ||| |        | |||||
Db         409
GATGAGAGCCAGATCCAGATGGCAGGTGGAGACGTGGAGCTGCCCCGGGAGCTGGCCAAG 468

Qy         413 ATGATCCTGTCGATCATCTTCAGC-----------
ATTCTGTCTCTGTTCCTGTTCTTCT 461
                   ||||||| | ||   |||        |    | ||| || | ||  |
||
Db         469 ATGATCGAGGAGGACA----
CAGAGGAGGAGGAGGAGGAAGGCCTCAGTCCTTGGGCAGCT 524

Qy         462 -GCCAACTCTTC---------ACC----CTCAC-CAAGG----
GGGGCAGGTTTTACATC 502
                   |||| | ||||         |||   |||||| |||||    || ||||     |
|
Db         525 GGCCAGC-CTTCCTGGCTTGAACCTGGGCTCACTCAAGGACAAGGCCCAGG-----
CCAC 578

Qy         503 ACT--GGAATCTTCCAAATTCTTGCTGGTCTGTG---CGTGATGAGT--
GCTGC-----G 550
                   ||| || |||  | ||    |||   ||| ||| |     || |
|
Db         579 ACTGGGGGGATCTCAAGCAATC-
AGCTGAGAAGTGTCACGTCATGTGACCACTTCCCCGGG 637

Qy         551 GCCATCTACACGGTGAGGCACCCGGAGTGGC-------ATCTCAACT--CGG-----
ATT 596
                   | | | || ||  ||| ||| |||   |    | |||||| | |
```

```
|
Db        638
GTTACCCACTGGGCTGGGCCCCCATGAGGGCTAAGAGTGTGTCAACTTCCAGGGACCCAT 697

Qy        597 ACTCC-TACG-------GTTTCGC---CTACATCCTGG--CCTGGG---
TGGCCTTC--- 637
             ||||| |  |        ||||| |   |  |||||| | ||  |    |  || ||
Db        698
ACTCCATTTGGGGCTTTGTTTCCCTTGCCCCATCCTAGTTCCAAGACCTTTCCCATCCAT 757

Qy        638 -CCCCTGGCC----------------CTTCTCAGC--GGTG-----------
TCATCTAT 667
              ||||  |||              | ||||| || || |         || ||
|
Db        758
GCCCCAAGCCTATCTTCTGGTTTCTTCCTCTCCGCTGGGAGTAAAGTCCCCATCTTCACT 817

Qy        668 GTGATCTTGCGGAAACGC------------GAATGAGG----
CGCCCA------------ 699
              |  ||| ||| | |          |  || ||  | ||||
Db        818
CTACCCTTCAGGACCCTCCCCACCAGCTCAGCCTGTGGAGGCCTCCCAAGATTGTAGGAA 877

Qy        700 ---GACGGTCTGTCTGAGGCTCTGAGC----
GTACATAGGGAAGGGAGGAAGGGAAAACA 752
                | |  || ||| ||| || |   || | |    |  |||| |
|||
Db        878 TAGGCCCCATCCCTCTCTGGCCATGGCCCCAAGTTCCTGCACACAGGAGCA----
CCCACA 933

Qy        753 GAAAG-CAGACAAAGAAAAAAGAG---CTAGC----------CCAAAATCC-
CAAACTCA 797
              || || ||| ||| || | | |     || ||         || || || || ||
||
Db        934
GAGAGACACACACAGGACACAAAACCCCTGGCACGTTCAGAGACAGAAGCCACAGACACA 993

Qy        798 AACCAAACCAAACAGAAAGCAGTGGAGGTGGGGGTTGCTG-
TTGATTGAAGATGTATATA 856
              ||    || ||||| | ||   ||||        | |  |||      || |
|
Db        994 TCCCGGCACAGACAGACA-CACACGAGGC--------CAGCTCCCTTGC----
GTGTCCA 1040

Qy        857 ATATCTCCGGTTTATAAAACCTATTTATAACACT----------
TTTTACATATATGTAC 906
              ||||  | | ||| |  ||| ||                | || |
|
Db        1041 GCCCCTCCAG---
ACACCACCACTCAGAAACTCTGAGAGAGAGCATGGGCAGACACCCTC 1097

Qy        907 ATAGTATTGTTTGCTTTTTATGTTGACCA---
TCAGCCTCGTGTTGAGCCTTAAAGAAGT 963
              |   |   |    |   ||| |||   ||  || ||| | ||| | | ||||
Db        1098 AGCAGACAGGAGGC---CTGAGTT--CCAGTCTCCACCTT-
TATTGTTCTTGAAAGCCCC 1151

Qy        964 AGCT---AAGGAACTTTACATCCT-AACAGTATAAT---
CCAGCTCAGTATTTTTGTTTT 1016
              |||        || | ||| || | ||| |   |||        |  | | ||   |  |
```

```
Db       1152
TGCTCTCTCTGAGCCTTATTTCATCATCTGTAAAATGGGAATGTCCTGAATGACTTCTAA 1211

Qy       1017
GTTTTTTGTTTGTTTGTTTTGTTTTACCCAGAAATAAGATAACTCCATCTCGCCCCTT-- 1074
         |  | || | ||| |  ||| |||     |||| |||     ||| || | ||||
Db       1212 GGCTCTTTCTGGCTTGAACTGT------CAGAGCCAAGC-----
CCACATCCCTCCTTGG 1260

Qy       1075 CCCTTTCATCTGAAAGAAGATACCTC--CCTCC--CAGT--CCAC------
CTCATTTAG 1122
              |   ||  |   || | | |  |||||| | |  ||||       |||
|
Db       1261 GCAGGGCAGC----AGCTGCTGCCACAGCCTCCAGCGGCTGCCACTGTGGGCTC----
TG 1312

Qy       1123 AAAACCAAA--------GTGTG---
GGTAGAAACCCCAAATGTCCAAAAGCCCTTTTCTG 1171
              | || |     |||||  || |||   || |        || ||   |
|
Db       1313
GGAGCCGGAGCGATGCTGTGTGAGAGGCAGAGTGCCAAGGATGAAGCTGGCACTGAACAG 1372

Qy       1172 GTGGGTGACCCAGTGCATCCAACAGAAACA--GCCGCTGCCCGAACCTCTGTG-
TGAAGC 1228
              |  |  |||| || |  ||||     |   ||  ||| | |||  || | |||  ||
|
Db       1373 TAAGCGGCTCCAG-GCCTCCTCTGGGCCCAGGGCC-CAGCC--
AATTTCTGTTCTGTTCC 1428

Qy       1229 TTTA-
CGCGCACACGGACAAAATGCCCAAACTGGAGCCCTTGCAAAAACACGGCTTGTGG 1287
              | || |||| | |   ||| || |||||        || | | || |
|
Db       1429 TGTAGAACGCTCTCTG----GATTCCATAGCTGG-----------
AATCTCCTCTCTTAG 1473

Qy       1288 CATTG-GCATACTTGCCCTTACAGGTGGAGTATCTT-
CGTCACACATCTAAATGAGAAAT 1345
              |  | | | | | |     | || |||| || | | | ||| ||| ||| | || |
Db       1474 CTCAGTGAAAAATAAAAATCCCAAATGGTGTGCCTACCTTCCCACTTCTTACTG-
GCTTC 1532

Qy       1346 CAGTGACAACAAGTCTTTGA---AATGGTGCTATGGATTTACCAT---------
TCCTTA 1393
              |||       |||||| ||   || |  |   | || |            ||||
Db       1533 CAG-------
GAGTCTTGGAGTTCATAGCCCCCGAGCCTGCCTTAAAGGGGTGTCCT-- 1583

Qy       1394 TTATCACTAATCATCTAAACAAC-TCACTGGA----------AATCCAAT--------
TA 1434
                |||    || ||  ||| | |||| |||           |||||| |
Db       1584 ---CCACCCCCCACCT--
ACAGCTTCACAGGAGGGGAGAGGGCATCCAGTGCTAGGAGTA 1638

Qy       1435 ACAATTTTACAACATAAGATAGAATGGAGACCTGAATAAT-------TCTG-------
TG 1480
              | | | | |  | |    ||| | |||| | |        ||||
||
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```
Db        1639
GAAGTGTCTCCAGCTCTGTTCTCTTGGGGCCCTGGGTGAAGGTGGGGTCTGGGGCTTATG 1698

Qy        1481 TAATATAAATGGTTTAT-----------AACTGC----TTTTGT------------
ACCT 1513
               ||||     |||  | |            |  |  ||    || |||
Db        1699
AAATAGGTCTGGGCTTTGAGGAGGATGGAGCAGCCTCATTATGTGGGGAAGATGGGGCCT 1758

Qy        1514 --------------------------------
AGCTAGGCTGCTATTATTACTATAATG 1540
                                            |||  |  |  ||         || |
Db        1759 CTGGGGCGTCACTGAGACCACAGGTGGGGCCGGGGCTGGACCGC------
AGCTGTCTTG 1812

Qy        1541 AGTAAATCATAAAGCCTTCATCACTCC-
CACATTTTTCTTACGGTCGGAGCATCAGAACA 1599
               ||   |       |||| || | |||| |||      | ||  | |||| || |
Db        1813 GGTGCCT----GTGCCTGCACCCCTCCTCAC------CCTAGAGACGGAAGAT--
GTGCA 1860

Qy        1600 AGCGTCTAGACTCCTTGGGACCGTGAGTTCCTAGAGCTTGGCTG---GGTCT---
AGGCT 1653
               |    |||      || | || |||| ||  | |   |||   | ||    ||
Db        1861 AAAAGAAAGAAGGAAGGGCAAC-TGCATTCC-
AGCCCCACACTGTGATGACTTTGAGCCT 1918

Qy        1654 GTTCTGTGCCTCCAAG-GACTGTCTGGC-------------AATGACTTGT---
ATTGGC 1696
               || || | |||||  | | |||||| ||            |||||   ||      |
Db        1919
GTCCTTTCCCTCCTTGAGCCTGTCTTGCTTGTCCCCTGTAAAATGAACAGTCCCCCTCTC 1978

Qy        1697 CACCAACT-------GTAGATGTAT-ATATGGTGCCC--TTCTGATGC-TAAGAC--
TCC 1743
               | |||| |        || |||| | | ||| ||  || || | | || || |||
Db        1979
CCCCAAATAGTAATAATACATGTTTCAAAGGGTGACCATTTATAAAGCATATGACAAACC 2038

Qy        1744 AGACCTTTTGTTTTTGCTTTGCATTTTCTGATTTTATACCAACTGTGTGGACTAAGATGC 1803
               | | |  | | |   || |  || ||||  |  | ||       || | |
Db        2039 ATATCAATAAATGTAACT---CA--
TTCTTTTAAAAAAAAAAAAAAAAAGGCCACATGTGC 2093

Qy        1804 ATTAAAATAAACATCAGAGTAACT 1827
               | |  | |  |  ||   |  ||
Db        2094 -TCGAGCTGCAGGTCGCGGCCGCT 2116


RESULT 8
US-10-478-914-20
; Sequence 20, Application US/10478914
```

  Query Match   38.8%; Score 4214; DB 1; Length 2495;
  Best Local Similarity   42.5%; Pred. No. 7.8e-276;
  Matches 1079; Conservative   0; Mismatches 682; Indels 776;
Gaps 146;

Qy   1 CAGT-----TACAGGGAGC-ACCACCAGG-----GAACATCTCGGGGAG-------
CCTG 42
            | || ||| | || || | |||| | || | ||| ||
Db   3 CTGTTGGCCTACTG---
GCTACTATCAGGATCGTGGCTATTTGAAGAGCTGATCACCAT 59

Qy   43 GTTGGAAGCTGCA----GGCTTAGTC---------------
TGTCGGCTG---------- 73
            ||||||||| ||| | ||| | ||| |||
Db   60
GTTGGAAGCAGCACTGGGACTTGAGCGAGCTCACATGGGAATGTTTACTGAATTAGCTAT 119

Qy   74 -CGGGTCTCTGACT----GCC-------CTGTGG--------GGAG-------
GGTCTTG 106
            | |||| | | ||| || || |||| |||||
|
Db   120
TCTATACTCTAAATTTAAGCCTCAGAAAATGAGGGAGCACCTGGAGCTGTTCTGGTCTAG 179

Qy   107 CCTTAACA-TCCCT---TGCATTTGGCTGCAAAGAAA--TCTGCTT--
GGAAGAAGGGGT 158
            | || | |||| ||| |||||| | || || ||| || ||||
|||
Db   180
AGTGAATATTCCCAAGGTGCTAAGAGCTGCAGAACAAGCTCATCTTTGGGCAGAACTGGT 239

Qy   159 TACGCTGTTTG--------------------------------GCCGGGCAGAAAC-
TCC 185
            ||| || || | ||| |
|||
Db   240
GTTTTTGTATGACAAGTATGAAGAATATGATAATGCCATAATTACCATGATGAATCATCC 299

Qy   186 -GCTGA----------------GCAGAAC----------TTGCC------

```
GCCAGAATGCT 213
            ||||                   ||| |         || ||      |||| ||
Db        300
AACTGATGCCTGGAAAGAAGGGCAATTCAAAGATATCATTACCAAGGTTGCCAATGTGGA 359


Qy        214 CCTCCTGTTGCTGAGTATCATCGTCCTC---------
CACGTCGCGG------------- 251
              || | | | ||| | ||| | |         || | | | |
Db        360 ACT-
ATACTACAGAGCAATACAGTTCTACTTAGAATTCAAGCCTCTGTTGTTAAATGATT 418


Qy        252 TGCTGGTGCTGCTGTTCGTCTCCACG-----------ATCGT-
CAGCCAATGGATCGTGG 299
              ||||| |||| || |||| ||||||||||          |||| ||| |||| | |
Db        419 TGCTGATGGTGCT----GTCTCCACGGTTGGATCACACTCGTGCAGTCAATTATT--
TCA 472


Qy        300 GCAATGGACACGCAACTGATCTCTGGCAGAACTGTA---GCACCTCTTCC--
TCAGGA-A 353
              |||| || | || || | | |||||   ||| ||| ||   | ||| |||| |
Db        473 GCAA-GGTTAAACAGCT-ACCACTGGTGAAACCGTATTTGCG----
TTCAGTTCAGAACC 526


Qy        354 ATGTCCACCA--CTGTTTCT-CATCATC-ACCAAACGAATGGCTGCAG----------
TC 399
              || | || | |||| | ||||| | ||| | |    | | |||
||
Db        527
ATAACAACAAATCTGTGAATGAATCATTGAACAATCTTTTTATTACAGAAGAAGATTATC 586


Qy        400 TGTCCAGGCCACCAT-----GATCCTGTCGATCATCTTCAGCATTCTGTCTC-
TGTTC-- 451
              | |   || | |||    ||| ||  || || ||| ||  || | | || | || ||
Db        587 AGGCTCTGCGAACATCAATAGATGCTTATGA-
CAACTTTGACAATATCTCGCTTGCTCAG 645


Qy        452 ------------------CT------GTTC--------TTCTGC-
CAACTCTTC------ 472
                                || |    ||||      | |||| | ||||||
Db        646
CGTTTGGAAAAACATGAACTCATTGAGTTCAGGAGAATTGCTGCTTATCTCTTCAAAGGC 705


Qy        473 -ACCCTCAC----------------------CAAGGGGGGCAGGTTTTACAT-----
CA 503
              || || |                        |||| | ||| ||||||
||
Db        706
AACAATCGCTGGAAACAGAGTGTAGAGCTGTGCAAGAAAGACAGCCTTTACAAGGATGCA 765


Qy        504 CTGGAATCTTC--CAAATTCT-----TGCTGGTCTGTGCGTGATGAG-
TGCTGCGGCCAT 555
              || | | | | | | |||      | ||| || || ||| || | |||| |
|
Db        766 ATGCAGTATGCTTCTGAATCTAAAGATACTGAATTG-GC-
TGAAGAACTCCTGCAGTGGT 823


Qy        556 CTACACGGTGAGGCACCCGGAGTG-GCATCTCAAC---TCGGATTA-
CTCCTACGGTTTC 610
              |  | | ||| | |   ||| | || |  | |  || | ||| || |||| |
|
```

```
Db        824 TTTTGCAG-
GAAGAAAAAAGAGAGTGCTTTGGAGCTTGTCTGTTTACCTGTTACGATCTT 882

Qy        611 -----GCCT----ACATCCTGG--CCTG---GGTGGCC-------------
TTCCCCCTG 643
                  |||      | |||| |   |||   || |||          || ||
                                                                       ||
Db        883
TTAAGGCCAGATGTCGTCCTAGAAACTGCATGGAGGCACAATATCATGGATTTTGCCATG 942

Qy        644 GCCCTTCTCAGCGGTGTCATCTATGTGATCTTG------------------------
CG 678
                  || | |||| |   ||||| | | | ||||
                                                                       |
Db        943
CCCTATTTCATCCAGGTCATGAAGGAGTACTTGACAAAGGTGGATAAATTAGATGCTTCA 1002

Qy        679 GAAACGCGAATGAGGCGCCCAGACGGTCTGTCT---
GAGGCTCTGAGCGTACATAGGGAA 735
                  ||| | |  ||||      ||| | | || ||| | |    | |   | |
Db       1003 GAATCAC---
TGAGAAAAGAAGAAGAACAAGCTACAGAGACACAACCCATTGTTTATGGT 1059

Qy        736 GGGAGGAAGGGAAAACAGAAAGCA-
GACAAAGAAAAAAGAGCTAGCCCAAAATCCCAAAC 794
                  |    ||   |  | || |||| |||  ||      ||   |||       ||||
                                                                       |
Db       1060 CAGCCCCAGTTGATGCTGACAGCAGGACCCAGTGT----TGCCGTCCCTC---
CCCAGGC 1112

Qy        795 TC--------------AAACCAAACCA-------AACAGAAAGCAG--
TGGAGGTGGGG 830
                  |              | ||| |||      |||| | || || |||
                                                                       ||||
Db       1113 ACCTTTTGGTTATGGTTATACCGCACCACCGTATGGACAGCCA-
CAGCCTGGCTTTGGGT 1171

Qy        831 GTTGC-TGTTGATTGAA--GATGTATATAATATCTCCGGTTT-----
ATAAAACCTATTT 882
                  || |||    |||| | ||    | || || |||      | |||| |
Db       1172
ACAGCATGTGAGATGAAGCGCTGATCCTGTAGTCACCTATTTTCGTACTGAAACATCGTC 1231

Qy        883 ATAACACTTTTTACA---TAT-ATG-------------
TACATAGTATTGTTTGCTTTTT 925
                  | ||| | || || ||| |||         || | | |||| |||| |
                                                                       |
Db       1232
TTTACCCACTTCTCAGTTTATAATGGGGGAAAACAGGCAACGTGTTCTTGTAACCTTTAT 1291

Qy        926
ATGTTGACCATCAGCCTCGTGTTGAGCCTTAAAGAAGTAGCTAAGGAACTTTACATCCTA 985
                  | ||| | | | |||| | | |  |||| | | || |  | ||| |
                                                                       |||
Db       1292
TTCATGAAGGACTTCTTTTTGTTTCTAACTATAAACTTGGATCACCTATGTTAAAACCTT 1351

Qy        986 ACAGTATAATCCAGCTCAGTATTTTTGTTTTGTTTTTTGTTTG---TTTGTTT---
TGTT 1039
```

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                        |    |  | |||| ||  ||||| | ||  |||| |   |    | ||||
            ||||
Db      1352 ATTTCACATTCCACATC---
ATTTTAGAATTTATTTTCGAAGGGGAATAGTTTCAATGTT 1408

Qy      1040 TTACCCA---GAAATAAGATAACTCCATCTCGCCC---------CTTCCC----
TTTCAT 1083
                        |||| ||    |    |    |  ||| ||| |      || | |     ||
            ||
Db      1409
TTATTCACTTGGGCTTTTTTTCTTCCCCCTCTTTCTTTAAAGAACTGCTCAATATTCAAT 1468

Qy      1084 CTG-AAAGAAGATACCT------CCCTC-----------------CCAGTCCAC-
CTCAT 1118
                        |||   ||||| ||||     | |||                || |   || ||
            ||
Db      1469 CTGTTGTGAAGA-
ACCTGATTTGCACTCTGTAGTGTTTAAAGAAACAAAGAAACTCTAAT 1527

Qy      1119 TTAGAAAAACC------AAAGTGTGGGTAGAAACC--CCAAA-------
TGTCCAAAAGCC 1163
                          | |||   |       ||||| ||| | | |   ||||        |||| |||
            ||
Db      1528
ATTGAATCTCTTAAATTTAGTGTATGTAAACAGCTTACAAATACGTATTGTCTAAATGCA 1587

Qy      1164 -------CTTTT-----------------------------
CTGGTGGGTGACC------ 1181
                               || ||                          ||||     |||||
Db      1588
TTTAAATCTGTTTTATTCAAAGAAAAGCTAAAGCAAAAACACTGGCATATGACCATGCAA 1647

Qy      1182 ------CAGTGCATCCAACAGAAACAGC----CGCTGCCCGAAC---CTCTG---
TGTGA 1225
                             ||||| |||||| | ||| |     | | ||| |  | ||| | |   ||
Db      1648 GACTGTCAGTG---CCAACAAAGACAACACTAATCAGCAC-
ATCGTACACTGGATTGCAG 1703

Qy      1226 AGCTTTAC--------GCGCAC----ACGGACAAAATGCCCAA-----
ACTGGAGCCCTT 1268
                            |||| |       | |    || ||||| |||| |    |   ||||
Db      1704
TGCTTCCCAGATTATTGAAAAATGTTACAGACAACTTGCCTGATTTTTAAATGAGC---- 1759

Qy      1269 GCAAAAACACGGCTTGTGGCATTGGCATACTTGCCC---TTACAGGTGG--------
AGT 1317
                          | ||||   | | | | | || |  ||| | || ||| |   | || | |
            |||
Db      1760 GTAAAAG---
GCCCTCTAACCTATGCAGGTTTCCCCATTATGCATATAGAAAATGCTAGT 1816

Qy      1318 ATCTTCGTCACACATCTAAATGAGAAATCAGTGACAACAAGT----
CTTTGAAATGGTGC 1373
                          || ||   | ||| ||  || | ||   ||| | ||    || |      |
            ||||
Db      1817 ATGTTTTGCTCACTTC---ATATGTAACAGGTGCCCTTATGTTGTGCTGTATCCT-
GTGC 1872

Qy      1374 TATGGATTT---ACCATTCCTT---------
ATTATCACTAATCATCTAAAC-------- 1413
```

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                |  |    |  |   ||||||||  |          |   |  |||  |    ||  ||  |
Db      1873
TTTTTCTGTGGGACCATTCCATTCAGGAGCAAAGAGCACCATGATTCCAATCTTGTGTGT 1932

Qy      1414 -------AAC---TCACTGGAAAT----CCAATTAACCAATT-------------
TTAC-- 1444
                        |||  || |||    |       ||   |||          | ||
Db      1933
GTTTACTAACCCTTCCCTGAGGTTTGTGTATGTTGGATATTGTGGTGTTTTAGATCACTG 1992

Qy      1445 ----AACATAAGATAGAATGGAGACCTGAATAATTCTGT------
GTAATATAAATGG-- 1492
                        |||  |||| ||||      | |  ||||  ||||    ||  | |   |||
Db      1993
AGTGTACAGAAGAGAGAAATTCAAACAAAATATTGCTGTTCTTCAGTTTTGTTTGTGGAA 2052

Qy      1493 TTTATAACTGCT----TTT---GTACCTAGCTAGGCTGCTATTATTAC-TATAAT--
GAG 1542
                       |||  || | ||     |||     ||  |  ||||  |     || ||  |  ||
Db      2053
TTTGAAATTACTCAAATTTAAAATAAATTACTGGACTGTGGAAATAACATAGAATTGAAG 2112

Qy      1543 TAAATCATAAAGCCTTCATCACTCCCAC---------------------
ATTTTTCT--- 1578
                       |     |||| |    ||||| ||                     | |||| |
Db      2113 TTTTAATTAAATAC-----
CACTCAAACGAAAAGAACAGTAGTTTTTGTAGTTTTATATT 2167

Qy      1579 ---TACGG------TCGG--AGCATCAGAACAAGCGTCTAGACTCCTTGGGACC-
GTGAG 1626
                        ||| |      | ||   |||| | |  ||| |     ||     ||| |||
Db      2168 GGATACTGAGGCATTAGGGAGGCATGAAAGGAAGAGGAATGA-
GGATTGAGACATGTGAA 2226

Qy      1627 TTCCTAGAGCTTGGCTGGGTC--TAGGCTGTTCTGTGCCTC-----
CAAGGACTGTCTGG 1679
                         | | | | |    | | ||   ||||  ||||     ||    |||||      |
Db      2227 GACATTGTGCAT---TATATCAATGTGCATTCCTGTAGTTCATTAACAAGGT---
ACATG 2280

Qy      1680 CAAT-GACTTGTATTGGCCA-----CCAACTGTAGATG--------
TATATATGGTGCCC 1725
                        |||| | ||    |    |||        | ||| |||  |       |   || ||
Db      2281 CAATAGTCT--
AAAGAACCAGAGTCACTACTATAGTGGCTTAACATTTAATCTGTCTCCA 2338

Qy      1726 TTCTGAT-GCTAA--GACTCCAGACCTTTTGTTTTTGCTTTGCATTT-----------
TC 1771
                         | |  |  | ||    |  |     |||| |    || || || ||
Db      2339 ATATTTTAACCAAGTGACACCGGGGTTTTTATCGAAGCATTTCACTTAAATGAACAAATC 2398

Qy      1772 T--GATTTTATACCAACTGTGTGGACTAAGATGCATTAAAA----
TAAACATCAGAGTAA 1825
                        | |  ||||| | ||||    || | ||| ||  ||| |||     |||| |  | |
```

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||
Db      2399 ATGGCTGTTATATTAACT---
TGAAATAAAATATATTTAAACATGTAAAAAAAAAAAAAA 2455

Qy      1826 --------------CTC 1828
                           |||
Db      2456 AAAGGCCACATGTGCTC 2472


RESULT 9
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match            38.8%;  Score 4211;  DB 1;  Length 2120;
  Best Local Similarity  43.9%;  Pred. No. 4.9e-276;
  Matches  994;  Conservative   0;  Mismatches  669;  Indels  602;
Gaps  139;

Qy         5 TACAGGGAGCACCACCAGGGAACATCTCGGGGA------
GCCTGGTT------------- 45
             |  || | | || |  ||| |    || |||| | |      |||| ||
Db      2119 TCTAGCGGCCGCGACCTG----
CAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTAA 2064

Qy        46 --GGA--AGCTGCA------GGCTTAGTCTGTCGGCTGCGGGTCTCTGACTG----
CCCT 91
              |  |  || | ||     |  | || ||| ||| |||  | | | | ||
||||
Db      2063 AAGAATGAGTTACATTTATTGATATGGTTTGTCATATGC---
TTTATAAATGGTCACCCT 2007

Qy        92 GTGGGGAGGGTCTTGCCTTAACATCCCTTGC-
ATTTGGCTGCAAAGAAATCTG------- 143
             |     |   | || |||  || | |||||| | | |     |||
Db      2006 TT-----GAAACATGTATTA-------
TTACTATTTGGGGGAGAGGGGGACTGTTCATTT 1959

Qy       144 ---------CTTGGAAGAAGGGGTTACGCT--GTTTGGCCGGGCAGAAACTC--
CGCTGA 190
                       |  | |||| || | | |    |   || | ||| ||| || | |
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```
                |
                Db        1958
                TACAGGGGACAAGCAAGACAGGCTCAAGGAGGGAAAGGACAGGCTCAAAGTCATCACAGT 1899

                Qy         191 GCAGAACTTGCCGCCAGAATGCTCCTCCTG-----
                TTGCTGAGTATCATCGTCCTCCACG 245
                               |  |  || |   ||| ||| | |||     ||  ||   ||| ||   ||| |
                |
                Db        1898 GTGGGGCTGGAATGCAG-
                TTGCCCTTCCTTCTTTCTTTTTGCACATCTTCCGTCTCTAGG 1840

                Qy         246 TCGCGGTGCTGGTGCTGCTGTTC-
                GTCTCCACGATCGTCAGCCAATGGATCGTGGGCAAT 304
                               | ||| |  ||||| |  | | ||    |  | ||    || |     ||
                Db        1839 GTGAGGAG-GGGTGCAG--GCACAGGCACCCAAGACAGCTGC----GGTCC---
                AGCCCC 1790

                Qy         305 GGACACGCAACTGATCTC--TGGCAGAACTGTAGCACC-
                TCTTCCTCAGGAAATG----- 356
                               || | | |   || ||||  || |     |  | || || ||||| ||    ||||
                Db        1789 GGCCCCACCTGTGGTCTCAGTGACGCCCCAGAGGCCCCATCTTCCCCACATAATGAGGCT 1730

                Qy         357 ------TCCACCACTG----------
                TTTCTCATCATCACCAAACGAATGGCTGCAGTCT 400
                                     ||| || |          | | |||| | | ||| ||       |  |
                ||
                Db        1729 GCTCCATCCTCCTCAAAGCCCAGACCTATTTCATAAGCCCCAGAC-----
                CCCACCTTC- 1676

                Qy         401 GTCCAGGCCACCA--TGATC----CTGTCGA-TCATCTTC----AGCATT-----
                CTGTC 444
                                 |||||| ||| ||| |    |||  ||  | ||| |    ||||| |        |
                ||
                Db        1675 ACCCAGGGCCCCAAGAGAACAGAGCTGGAGACACTTCTACTCCTAGCACTGGATGCCCTC 1616

                Qy         445 TCTGTTCCTGTTCTTCT------------------
                GCCAACTCTT---------------- 471
                                 ||   ||||||    ||                 | ||| |||
                Db        1615 TCCCCTCCTGTGAAGCTGTAGGTGGGGGGTGGAGGACACCCCTTTAAGGCAGGCTCGGGG 1556

                Qy         472 ---------CACC----CTC------ACCA-----AGGGGGGCAGGTT-TTACATCA-
                CT 505
                                         | ||   |||        |||    | | ||| ||||    ||| ||
                |
                Db        1555 GGCTATGAACTCCAAGACTCCTGGAAGCCAGTAAGAAGTGGGAAGGTAGGCACACCATTT 1496

                Qy         506 GGAATCTTCCAAATTCTTGCTGGTCTGTGCGTGATGAGTGCTGC---GG---
                CCA----- 554
                                 || || ||   |||   ||| || | ||  || | | ||   ||   |||
                Db        1495 GGGATTTTTATTTTTC--
                ACTGAGCTAAGAGAGGAGATTCCAGCTATGGAATCCAGAGAG 1438

                Qy         555 ---TCTACACGGTGAGGCACCCGGAGTGGC----
                ATCTCAACTCGGATTACTCCTACGGT 607
                                   |||||| ||    | ||     | ||||      ||   | | ||   |  |||
                ||
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```
Db      1437 CGTTCTACA-GGAACAGAACAGAAATTGGCTGGGCCCTGGGCCCAGAGGAGGCCT--
GGA 1381

Qy       608 TTCGCCTAC--ATCCTGGCCTGGGTGGCCTTCC-CCCTGGCCCT-----TCTCA-
GCGGT 658
                 ||| |||   ||   ||| |       |||| || |||| ||     ||||| |
|
Db      1380 GCCGCTTACTGTTCAGTGCCAG------
CTTCATCCTTGGCACTCTGCCTCTCACACAG- 1328

Qy       659 GTCATCTATGTGATCTTGCGGAAACGCGAATGAGGC-GCC-CAGACGGTCTGT--
CTGAG 714
                 ||||  |  |   || | ||  | |  | ||| ||| | |  || |||| | |
Db      1327 --CATCGCTCCGG-CTCCCAGAGCC-C-ACAGTGGCAGCCGCTGGAGG-
CTGTGGCAGCA 1274

Qy       715 GCT-CTGAGCGTACATAGGGAAGGGAGGAAGG----------------
GAAAACAGAAAG 757
                 ||| |||   |   |   ||| ||||| | ||                    ||
||||||
Db      1273 GCTGCTGCCCTGCCCAAGG--
AGGGATGTGGGCTTGGCTCTGACAGTTCAAGCCAGAAAG 1216

Qy       758 CAGACAAAGA----
AAAAAGAGCTAGCCCAAAATCCCAAACTCAAACCAAACCAAACAGA 813
                 || | |||    |   || |  |||| | | |      || ||  | |
|||
Db      1215 -
AGCCTTAGAAGTCATTCAGGACATTCCCATTTTACAGATGATGAAATAAGGCTACAGATA 1157

Qy       814
AAGCAGTGGAGGTGGGGGTTGCTGTTGATTGAAGATGTATATAATATCTCCGGTTTATAA 873
                 ||||| ||  |   |  |  | || || | |  |||| || |
Db      1156 GAGCAGGGGCTTTCAAGAACAATAAAGGTGGAGACTGGAACTCAGGCCTCCTGTCTGCTG 1097

Qy       874 A--------
ACCTATTTATAACACTTTTTACATATATGTACATAGTATTGTTTGCTTTTT 925
                 |       |  || ||      | | |   | | | |   | || ||| ||
Db      1096 AGGGTGTCTGCCCAT-----
GCTCTCTCTCAGAGTTTCTGAGTGGTGGTGTCTGGAGGGG 1042

Qy       926 ATGTTGACCATCA---------GCCTCGTGT---------
TGAGCCTTAAAGAAGTAGCT 967
                 || ||| ||      |||||||||        || |||     || ||
||
Db      1041 CTG--GACACGCAAGGGAGCTGGCCTCGTGTGTGTCTGTCTGTGCC---
GGGATGTGTCT 987

Qy       968 AAGGAACTTTACATCCTAACAGTATAATCCAGCTCAGTATTTTTGTTTTGTTTTTTGTTT 1027
                 ||  |||      || | | |  | | | ||  ||| ||||| |||  | |||
|
Db       986 GTGG--CTT------CTGTC--TCTGAACGTGC-CAGGGGTTTTG---
TGTCCTGTGTGT 941

Qy      1028 GTTTGTTT-TGTTTTTACCCAGAAATAAGATAACT-----
CCATCTC-------------G 1068
                 || | | | || |  || |    || |     || ||||     |||| |
|
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```
Db         940 GTCTCTCTGTGTGGGTGCTCCTGTGTGCAGG-
AACTTGGGGCCATGGCCAGAGAGGGATGGG 882

Qy        1069 CCCCTTCC--CTTTCAT---------------------------------
CTGAA-- 1088
               ||  ||||  |  ||                              ||||
Db         881
CCTATTCCTACAATCTTGGGAGGCCTCCACAGGCTGAGCTGGTGGGGAGGGTCCTGAAGG 822

Qy        1089 ------AGAAGAT----ACCTCCCTCCCAG-------------
TCCA------------- 1112
                    ||||||   || |  |||||||           |||
Db         821
GTAGAGTGAAGATGGGGACTTTACTCCCAGCGGAGAGGAAGAAACCAGAAGATAGGCTTG 762

Qy        1113 ---CCTCATTTAGAA---------AACCAAAGTGTGGGTAG-------
AAACCCCAAATG 1153
                  |  |   |  |||           |||  |  || ||  ||         ||
                ||||||||||
Db         761
GGGCATGGATGGGAAAGGTCTTGGAACTAGGATGGGGCAAGGGAAACAAAGCCCCAAATG 702

Qy        1154 TC-CAAAAGCCCTTTTCTGGTGGGTGACCCAGTGCAT--
CCAACAGAAACAGCCGCTGCC 1210
                |   | |     ||||  | |||| | ||| | | | |  || ||      ||| |
                |||
Db         701 GAGTATGGGTCC----CTGGAAGTTGACACACT-CTTAGCCCTCATGGG-GGCC-
CAGCC 649

Qy        1211 CG------AACCTCTGTGT----
GAAGCTTTACGCGCACACGGACAAAATGCCCAAACTG 1260
                |       |||| | |  ||     |   |  | ||| | ||||        | | | |
                ||
Db         648 CAGTGGGTAACCCCGGGGAAGTGGTCACATGACGTG-ACAC--------TTCTC-
AGCT- 600

Qy        1261
GAGCCCTTGCAAAAACACGGCTTGTGGCATTGGCATACTTGCCCTTACAGGTGGAGTATC 1320
               ||  ||||  |    |  |  | ||||| |  ||  |  | | |||          ||||
Db         599 GATTGCTTGAGATCCCCCAG--TGTGGCCTGGGC---CTTGTCCTT-------
GAGTG-- 554

Qy        1321
TTCGTCACACATCTAAATGAGAAATCAGTGACAACAAGTCTTTGAAATGGTGCTATGGAT 1380
                 | |      || ||   |||  | | || |  |  || | |  | | ||  || |
                |
Db         553 --AGCCCAGGTTCAAGCCAGGAAGGCTG-GCCAGC-TGCCCAAGGACTGAGGCCTT--
CT 500

Qy        1381 TTACC-ATTCCT---TATTATCACTAATCATC-TAAACAACTCACTGG--
AAATCCAATT 1433
                ||   ||||   |  | |     |||||| |   || ||||  |  | |   | ||||
                |
Db         499
CCTCCTCCTCCTCTGTGTCCTCCTCGATCATCTTGGCCAGCTCCCGGGGCAGCTCCACGT 440

Qy        1434
AACAATTTTACAACATAAGATAGAATGGAGACCTGAATAATTCTGTGTAATATAAATGGT 1493
                 | |  | | || |  | | |  |         | |||  | |||| |        ||
                |||
```

```
Db        439 CTCCACCTGCCATCTGGATCTGGCTC--TCATCTGTCTCGTTCTTGG----
GTAGCCGGT 386

Qy       1494 TTATAACT--GCTTTTGTACCTAGC----TAGGCTGCTAT-
TATTACTATAATGAGTAAA 1546
                  | |  || |   |  || ||   | | |||  |  || ||   || ||    || ||
||
Db        385 ATTTGTCTCGGAAGTGGCTCC--GCAGTGTGGCCCGCTCTGCCTTCCT---
CTGTGTGAA 331

Qy       1547
TCATAAAGCCTTCATCACTCCCACATTTTTCTTACGGTCGGAGCATCAGAACAAGCGTCT 1606
                   |  | ||      | |||| |  || |||| |   |  || ||  |   |  |
||
Db        330 CTGTGCATCC-----CGCTCCATC--TTCTCTTCCACGAGTTGCTTCTG---
ATACTCCT 281

Qy       1607 AG-ACTCCTTGGGAC-CGTGAGTTCCTAGAGCTT-GGCTG-
GGTCTAGGC---------- 1652
                   |  |||||||  |  | | ||    ||  ||||||| |||||  | || |  |
Db        280 CGTACTCCTCCCGGCTCATG----
CCCTGAGCTTCGGCTGCCGACTTGTCCCCATCTCCC 225

Qy       1653 ---TGTTCTGTGCCTCCAAGGACTGTCTGGCAATGA----
CTTGTATTGGCCACCAACTG 1705
                   |  ||  |||||| |||   || || |||   |||     ||||| || ||
Db        224 TTATCCTCGCCGCCTCCCAGG-----
CTCCCAGTGAGGTTCTTCAGCTGGCCGCCCACCA 170

Qy       1706 TAG--------ATGTAT-ATATGGT--------GCC-----------
CTTCTGATGCTA- 1736
                   | |       ||| |  |||||      |||        |  ||| | |
Db        169
TGGTCTTCACCATGAACGCCATGGTCTTCGCCGGCCGGGGCACCGGGCGCCTGCTACCAC 110

Qy       1737 -----AGACTCCAGAC-CTTTTGTTTTTGCTT-
TGCATTTTCTGATTTTATACCAACTGT 1789
                   || | ||  | | |  |   | ||| ||| | | |    ||  |||||
Db        109 GCGCCAGGCACCGGGCACGTCCGCGCCTACTTCAGCA-CTCCAG----
TAGGCCAACAGT 55

Qy       1790 GT-----GGACTAAGATGCATTAAAATAAACATCAG-AGTAACTC 1828
                   |     | | |  |  || ||      |  ||| |||||| |
Db         54 GCTCGAGGAATTCCGCAGCTTTTAG------AGCAGAAGTAACAC 16


RESULT 10
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
```

```
  Query Match              38.6%;  Score 4192;  DB 1;  Length 2198;
  Best Local Similarity   44.3%;  Pred. No. 1.3e-274;
  Matches 1028;  Conservative   0;  Mismatches  655;  Indels  640;
Gaps  141;


Qy        3 GTTACAGGGAGCAC---CACCAGGGAAC--------------------
ATCTCGGGGAGC 39
            |  ||  |  ||| |   |||  |  |  |                       |  |    ||
            ||
Db     2198
GCGACCTGCAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTTTATGGTGC 2139


Qy       40 CTGGTTGGAAGCTGCAGGCTTAGTCTGTCGGC--TGCGGGT--
CTCTGACTGCCCTGTG- 94
            |   ||  ||  ||        |  ||  |  |   |||   |   |  || ||    |
            |||
Db     2138 CAATTTTAAA-----TAGTTTTATTT-
AAGACATTGCATTTTCCACTTACAATACAGTGT 2085


Qy       95 ---------GGGAGGGTCTTGCCTTAACATCCCT-
TGCATTTGGCTGCAAAGAAATCTGC 144
                     |  | |  | ||  ||||       |||| ||||| ||  | |  |    | ||
Db     2084 TTATAAAGTGCAATGTTATTTCCTTC----CCCTGTGCATATG--TTCCA--
TATTCAAG 2033


Qy      145
TTGGAAGAAGGGGTTACGCTGTTTGGCCGGGCAGAAACTCCGCTGAGCAGAACTTGCCGC 204
            |      ||||                  |||   ||| ||||     |||||  ||| |
Db     2032 TATTGAGAA---------------TGCC---CAGTAACTTACTATAGCAG--
CTTAACTT 1993


Qy      205 CAGAATGCTCCTCCTG---TTGCTGAGTATCATCGTCCTCCACG-----
TCGCGGTGCTG 256
               ||  || |  | |   |||||  | ||    |||||  ||        |    |||
               ||
Db     1992 TTTAAAACTGCCACAGAATTTGCTACGAATTTAGGTCCTTCAAATGTTTTAAATGTG-
TG 1934


Qy      257 GTGC--TGCTGTTCGTCTCCAC--GATCG------TCAGCCAATG-
GATCGTGGGCAATG 305
            |   |  ||| |  | ||| |||  | | |         ||| ||  |   || ||||||
            ||
Db     1933 GAACAATGC--
TACATCTACACTTGGTTGGCTTAATCAACCTCTTCAATGGTGGGCCCTG 1876


Qy      306
GACACGCAACTGATCTCTGGCAGAACTGTAGCACCTCTTCCTCAGGAAATGTCCACCACT 365
               |  |||       |  |   |  |  |  | ||| || |   |  ||||||| |||  |||
```

```
Db      1875 AGGAAGCAC-----CACCAGAGGGA--GGAGCTCCAC--CACCAGGAAA--
TCCCCCAGG 1827

Qy       366
GTTTCTCATCATCACCAAACGAATGGCTGCAGTCTGTCCAGGCCACCATGATCCTGT--- 422
              |||       | | |  ||| | | | || |   || || | ||  ||
Db      1826 CATTC-------CTCCTGGC--ATGCCTCCTG-
CACTCTGGTACAGCTTGGTGATGATGG 1777

Qy       423 -----CGATC-ATCTTCAGCATTCTGTCTCTGTTCCTGTTC---
TTCTGCCAACTCTTC- 472
              | | | |||  ||| || |  | ||||||  |||||   |||| || | |||
Db      1776 GGTTGCAAACTTTCTCCAGC--TC--
TTTCTGTTGATGTTCAAATTCTTCCTTCTCAGCA 1721

Qy       473 -----ACCCTCACCAAGGGGGGCAGGTT-----TTACAT--
CACTGGAATCTTCCAAATT 520
              |  || | ||| |     || |||     || ||| |||| |    |||| |
Db      1720 GTCTGATTCTTATCAA-----GCCAGTTGATAATTTCATTACACTTG-----
TCCAGAAT 1671

Qy       521 CTTGCTGGT----CTGTGCGTGATGAGTGC--TGCGG----CCATCTAC-
ACGGTGAGGC 569
              ||| ||| |   || | ||| |   ||| || |   ||||| | || ||
Db      1670 CTT-
CTGTTTGTCCTCATCGTTAATCTTGCCTTGAAGTTTCTCATCTTCAACAGTTGCTT 1612

Qy       570 ACCCGGAG-TGGCAT----CTCAA-------CTCGGATTACTCCT------
ACGGTTTCG 611
                | | | ||||| |    ||||| |      || |||| || |||      | |
|||
Db      1611 TCATGTTGAAGGCATAGGACTCAAGTGAATTCTTGGATGACACCTTGTCCCTCTGCTTCT 1552

Qy       612 C--------------------CTACATCCTGGCCTGGGTG------GCCTTCC---
CCCT 642
              |                    | | |||||| |     | | |||||
|
Db      1551 CATCTTCAGCTTTGTACTTCTCAGCTTCCTGGACCATACGTTCAATGTCTTCCTTGCTCA 1492

Qy       643 ---GGCCCTTCTCAGCGG------------TGTCATCTAT----GTGATCTTG----
CGG 679
                 |||||||| |||  |           ||| ||| |   || |||||    |
|
Db      1491 AACGGCCCTTGTCATTAGTGATAGTAATCTTGTTCTCTTTTCCCGTACTCTTGTCCACAG 1432

Qy       680 AAACGCGAATGAGGCGCCCA--GACGGTC--TGTC---TGAGGC-----TCTGA-
GCGTA 726
              | | |||  | | |  |||| ||  ||||  | | |    ||||| |
Db      1431 CAGAGACATTGAGTATACCATTGGC-
ATCAATGTCAAAAGTGACTTCAATCTGAGGAACA 1373

Qy       727 CATAGGGAAG--GGAGGAA-----GGGAAAACAGA------AAGCAG--------
ACAAA 765
              | | ||| | | ||||| |    | || || |       ||||||
|
```

```
Db        1372
CCTCGGGGTGCAGGAGGTATGCCTGTGAGTTCAAACTTGCCAAGCAGGTTGTTATCCTTT 1313

Qy         766 GAAAAAAGA-GCTAGCC--CAAAATCCCAAACTCAAACCAAACCAAACAGAAAG-
CAG-- 819
               |   |     | ||| |||  || || ||  ||    || || |||| | |   | |||
Db        1312 GTCATGGCACGCTCGCCTTCATAAACCTGAA---
TAAGCACACCAGGCTGGTTGTCAGAA 1256

Qy         820 -TGGAGGTGGGGGTTGCTGT---
TGATTGAAGATGTATATAATATCTCCGGTTTATAAAA 875
               || ||| ||| |||| |||   |  ||||| | ||| | || || || |
Db        1255 TAGGTAGTGAAGGT--CTGTGTCTGCTTGGTAGGAATGGTGGTAT-
TACGCTTGATGAGG 1199

Qy         876 CCTATTTATAACAC---------TTTTTACATATATGTACATAGTATTGTT-------
TG 919
               | | | || || |        |||  | |   | | | | || | ||
Db        1198 AC-
AGTCATGACTCCACCAGCAGTTTCAATACCAAGGGAAAGAGGAGTGACATCCAAGAG 1140

Qy         920 CTTTTTATGTTGACCA---
TCAGCCTCGTGTTGAGCCTTAAAGAAGTAGCTAAGGAACTT 976
               |     || ||||| ||   |||| || | ||  || || ||   |||| |   |||
||
Db        1139 CAGCAAATCTTGAACATTCTCAGACTTGTCTCCAGAC---AAGATG--GCT----
GCCTG 1089

Qy         977 TACATCCTAACAGTATAATCCAGC----
TCAGTATTTTTGTTTTGTTTTTTGTTTGTTTG 1032
               ||| |   || ||   |||| |||| ||||  || || | | ||   |||
Db        1088 GACAGCTGCACCATAAGCAACAGCTTCATCAGGGTTGATGCTCT-
TATTCAGTT------ 1036

Qy        1033 TTTTGTTTTACCCAGAAATAAGATAACTCCATCTCGCCCCTTCCCTTTCAT----
CTGAA 1088
               ||| ||  || ||| | |  |    |||| | || |     |
Db        1035 -----CTTTTCCATTGAAGAAGT------
CTTGGAGAAGCTTCTGAATCTTGGGGATACG 987

Qy        1089
AGAAGATACCTCCCTCCCAGTCCACCTCATTTAGAAAACCAAAGTGTGGGTAGAAACCCC 1148
               || ||| ||| || || | | |   |||| |        || || | |  | |
Db         986 AGTAGA-
ACCACCAACCAGGACAATATCATGAATCTGTGACTTGTCTAGTTTGGCATCTC 928

Qy        1149 AAATGTCCAAAAGCCCTTTTCTGG----TGGGTGACC-----------------
CAGTGC 1187
               || | |     || | |||||     ||||| |                    ||||
Db         927 GAAGGGCTTT-----
CTCTACTGGGTCCAGGGTGCCACGGAACAGGTCAGCATTCAGTTC 873

Qy        1188 ATCCAA-CAGAAAC------------------AGCCGCTGCC--------------
CGAA 1214
               || || | ||  ||                    || || | ||
Db         872
```

```
TTCAAATCGGGCACGGGTAATGGAGGTATAGAAGTCGATTCCTTCATAGAGAGAATCGAT 813


Qy      1215 C------CT---CTGTGTG-------------AAGCTTTACGCG--CAC-------
ACG 1242
                |        ||   ||| |||              | |||| | || |||
|||
Db       812
CTCAATACTGGCCTGGGTGCTGGAAGAGAGGGTACGCTTAGCACGTTCACAAGCAGTACG 753


Qy      1243 GA-----CAAAATGC--------CCAAACTGGAGCCCTTGCAAAAACACG-
GCTTGT--- 1285
                ||      || | || |    | |||| |||| | |   |   | ||||
Db       752 GAGGCGTCTTACAGCTCTCTTGTTCTCACTGATGTCCTT-
CTTATGCTTGCGCTTAAACT 694


Qy      1286 -GGCATTGGCATACTTGCCCTTACAGGTGG-AGTATCTTCGTCACACA--------
TCTA 1335
                 ||| |   ||  ||| || | | || |   |||||| ||| ||
|||
Db       693
CAGCAATAAAATGGTTGACCATTCGGTTGTCAAAATCTTCTCCACCCAAGTGGGTGTCTC 634


Qy      1336 AATGAGAAATCAGTGACAACAAGTCTTTGA-----
AATGGTGCTATGGATTTACCATTCC 1390
                | | | |||| ||| || |   ||| |||    ||||| ||
||
Db       633 CAGCTGTAGACT-TGACCTCAAAGATTCCATCCTCAATAGTG---
AGGATTGACACATCA 578


Qy      1391 TTATTATCACTAATCA--TC-----TAAACA----
ACTCACTGGAAATCCAATTAACAAT 1439
                | | ||| || || | | || ||  ||  |||   |||| | |
|
Db       577 AAAGTGCCACCTCCCAGGTCAAAGATGAGCACGTTTCTTTCTG---CTCCA---
ACCTTT 524


Qy      1440 TTTACAA---CATAAG--ATAG-------
AATGGAGACCTGAATAATTCTGTGTAATAT- 1486
                || | | | |||| |||     | | |  | | ||||||||| |||
|
Db       523
TTGTCTAAGCCGTAAGCAATAGCAGCAGCAGTTGGCTCATTAATAATTCTAAGTACATTG 464


Qy      1487 -------AAATGGTTTATAACTGCTTTTGTA-CCTAGCTAGGCTGCTA-
TTATTACTATA 1537
                |||| || | | |||| ||| ||| |   |||| | | ||||
||
Db       463 AGACCAGCAATAG-TTCCAGCATCTTTGGTAGCCTGAC---
GCTGAGAGTCATTAAAGTA 408


Qy      1538 A----------TGAGTAAATCAT-----AAAGCCTTCATCA------
CTCCCACATTTTT 1576
                |           ||| | | |||    | || |||| |    || | | ||
|||
Db       407
AGCTGGCACTGTGACCACAGCATTGGTAACAGTCTTCCCAAGGTAGGCTTCTGCAATTTC 348


Qy      1577 CTTAC----GGTCGGAGCATCAGAACAAGCGTC-------TAGACTCCTTGGG-----
AC 1620
                |||        ||| || |   |||| | | ||       |||| | || ||
```

```
|
Db       347
CTTCATCTTTGTCAGAACCATAGAAGACACCTCCTCTGGATAGAAGCTTTTGGTCTCTCC 288

Qy      1621 CGTGAGTTCCTAGAGCTTGG--CTGGGTCTAGGCTG-TTCTGT-GCCTCC---
AAGGACT 1673
             |  ||  |||      |||||  || || | | | |  ||  | || ||   ||||
|
Db       287 CTTGTATTC----
TACTTGGACCTTGGGCCTGCCAGCATCATTCACCACCATAAAGGGC- 233

Qy      1674 GTCTGGCAATGACTTGTATTGGCC--
ACCAACTGTAGATGTATATATGGTGCCCTTCTGA 1731
             |||||| |  ||| | |   |||| | |     | || ||   || ||
||
Db       232 ------
CAATGTTTCATATCAGACTGGACAACAGCATCATCAAATCTGCGTCCAATCAGA 179

Qy      1732 TGCTAAGACTCCAGACCTTTTGTTTTTG-----
CTTTGCATTTTCTGATTTTATAC---- 1782
             | |  |  || | | ||||| ||     |  | ||||| |  ||||| | |
Db       178 CGTTTGGCATCAAAAAC-TGTGTTGGTGGGGTTCATTGCAACT--
TGATTCTTTGCGGCA 122

Qy      1783 --------CAACTGT---GTG-----------
GACTAAGAT------------------ 1801
             |||| ||  |||          ||| || |
Db       121
TCACCGATCAACCGTTCAGTGTCCGTAAAGGCGACATAGCTTGGAGTGGTTCGGTTTCCC 62

Qy      1802 ---------GCATTAAAATAAACAT-------CAGAGTAACTC 1828
             ||| |  |  | || |        | |   ||| | |
Db        61 TGATCATTGGCAATTATCTCGACTTTTCCGTGCTGGAAAACAC 19


RESULT 11
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;  LENGTH: 2495
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match         38.1%;  Score 4134;  DB 1;  Length 2495;
```

```
  Best Local Similarity   42.4%;  Pred. No. 3.1e-270;
  Matches 1084;  Conservative   0;  Mismatches  672;  Indels  798;
Gaps  158;

Qy         1 CAGTTACAGGGAGCAC---
CACCAGGGAAC----------------------------- 27
             | |  ||  | ||| |   ||| | | |
Db      2488
CCGCGACCTGCAGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTACATGTTTAAATA 2429

Qy        28 ------ATCTCGGGG---------AGCC-TGGTTGG-------
AAGCTGCAGGCTTAGTC 64
               || || |          |||| || || |     |||   | |||| |
Db      2428
TATTTTATTTCAAGTTAATATAACAGCCATGATTTGTTCATTTAAGTGAAATGCTTCG-A 2370

Qy        65 TGTCGGCTGCGG-GTCTCT--------------GACTG--------------
CCCT-- 91
             |     |  ||| ||| ||              ||| |            | ||
Db      2369
TAAAAACCCCGGTGTCACTTGGTTAAAATATTGGAGACAGATTAAATGTTAAGCCACTAT 2310

Qy        92 -GTGGGGA----GGGTCTT--GCCT-TAACA--TCCCTTGCATTTG-
GCTGCAAAGAAAT 140
              || | ||    || |||| | || ||  || | |||||     ||  || | | |||
Db      2309 AGTAGTGACTCTGGTTCTTTAGACTATTGCATGTACCTTGTTAATGAACTAC-
AGGAATG 2251

Qy       141 CTGCTTGGAAGAAGGGGTTACGCTGT-TTGGCCGGGCAGAAAC-----
TCCGCTGAGCAG 194
             |    ||| | | |     || ||| ||  | | | || |     ||| ||    |
Db      2250 CACATTGATATAATG---CACAATGTCTTCACATGTCTCAATCCTCATTCCTCT--
TCCT 2196

Qy       195 AACTTGCCGCCAGAATGC-------TC--------------------
CTCCTGTTGC---- 224
              | |||| || ||||||        ||                   || ||||| |
Db      2195 TTCATGCCTCCCTAATGCCTCAGTATCCAATATAAAACTACAAAAACTACTGTT-
CTTTT 2137

Qy       225 ----TGAGT------------ATCATCG--TC--------CTCCAC-
GTCGCGGTGCTG 256
                 |||||            | | ||   ||        ||||| ||| | ||
Db      2136 CGTTTGAGTGGTATTTAATTAAAACTTCAATTCTATGTTATTTCCACAGTC-
CAGTAATT 2078

Qy       257 GTGCTGCTGTTCG-------TC----TCCACGATC----------
GTCAGCCAATGGATC 295
             |    || |        ||     ||||| | |           ||| ||||
Db      2077 TATTTTAAATTTGAGTAATTTCAAATTCCACAAACAAAACTGAAGAACAG-
CAATATTTT 2019

Qy       296
GTGGGCAATGGACACGCAACTGATCTCTGGCAGAACTGTAGCACCTC------------- 342
             || | | |  | |  || ||| | ||   || ||  | |||| |
Db      2018 GTTTGAATT--
TCTCTCTTCTGTACACTCAGTGATCTAAAACACCACAATATCCAACATA 1961
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```
Qy        343 ----TTCCTCAGGAAA-------TGTCCAC-CAC-
TGTTTCTCATCAT-----------C 378
                  |||||||| ||        |   ||| |||   | ||    |||||
|
Db      1960
CACAAACCTCAGGGAAGGGTTAGTAAACACACACAAGATTGGAATCATGGTGCTCTTTGC 1901

Qy        379 ACC--AAACGAATGG--CTGCAG-------TCTG--TCCAGGCCCACCAT----
GATCCTG 421
                 ||  ||  |||||| |  |||         | |  | ||| || |||    |
||||
Db      1900
TCCTGAATGGAATGGTCCCACAGAAAAAGCACAGGATACAGCACAACATAAGGGCACCTG 1841

Qy        422 TCGATCATCTTCAG---------CATTCTG------TCTCTGTTCCTGTT-----
CTTCT 461
                  |   ||| |  ||          ||| ||     ||| | ||| | |
||
Db      1840 T--
TACATATGAAGTGAGCAAAACATACTAGCATTTTCTATATGCATAATGGGGAAACCT 1783

Qy        462 GCCAA----------CTCTTCACCCTCA---
CCAAGGGGGGCAGGTTTTACATCACTGGA 508
                  || |          |  || || ||||     ||    |||| ||| |   | ||
|
Db      1782
GCATAGGTTAGAGGGCCTTTTACGCTCATTTAAAAATCAGGCAAGTTGTCTGTAAC---A 1726

Qy        509 ATCTTCCAAATTCTTG------CTG--GTC---TGTGCG------
TGATGAGTGCTG--- 548
                 | |||| | ||| |        ||| ||  ||| ||     |||| |||| ||
Db      1725
TTTTTCAATAATCTGGGAAGCACTGCAATCCAGTGTACGATGTGCTGATTAGTGTTGTCT 1666

Qy        549 ---------CGGCCA-TC-TACACGGTGAGGCACCCGGAGTG-----GCAT---
CTCAAC 589
                         | | ||| | | | | ||         ||| |   ||
|
Db      1665 TTGTTGGCACTGACAGTCTTGCATGGTCATATGCC---
AGTGTTTTTGCTTTAGCTTTTC 1609

Qy        590 TCGGATTACTCCTACGGTTTCGCCTACATCCTGGC-------
CTGGGTGGCCTTCCCCCT 642
                 |  || ||   || | ||   | |||  | |        |   || |   ||
|
Db      1608 TTTGAATA---
AAACAGATTTAAATGCATTTAGACAATACGTATTTGTAAGCTGTTTACA 1552

Qy        643 GGCCCT---TCTCAGCGGTGTCA-----------
TCTATGTGATCTTGCGGAAACGCGAA 688
                 | ||    | || | | ||           ||| |||    ||||   |||| |
|
Db      1551 TACACTAAATTTAAGAGAT-TCAATATTAGAGTTTCTTTGT-TTCTT---
TAAACACTAC 1497

Qy        689 TGAGGCGCCCAGACGGT---------CTGTCTGAGGCTCTGAGC-
GTACATAGGGAAGGG 738
                 || ||  |   |||        | |  |||   | |||||| || |  |      |
|
Db      1496 AGA-GTGCAAATCAGGTTCTTCACAACAGATTGAATAT-
```

```
TGAGCAGTTCTTTAAAGAAAG 1439


Qy        739 AGGAAGGGAAAACAGAAAGCAGACAAAGAAAAAAGAGC-
TAGCCCAAAATCCCAAACTCA 797
              |||  ||||| | | ||||| | ||| || | | | |    | |||| |
|
Db       1438 AGG--GGGAAGAAAAAAAGC---
CCAAGTGAATAAAACATTGAAACTATTCCCCTTCGAA 1384


Qy        798 AACCAAACCAAACAGAAAGCAGTGGAG-GTGGGGGTTGCTGTTG--
ATTGAAGAT----G 850
              || || ||| || ||  || | ||||| |||     | | ||  || | |||
|
Db       1383 AATAAATTCTAA---
AATGATGTGGAATGTGAAATAAGGTTTTAACATAGGTGATCCAAG 1327


Qy        851 TATATAAT----ATC---------TCC-------------GGTTTATAAAA-------
CC 877
              | |||| |    | |         |||          |||| | ||
||
Db       1326
TTTATAGTTAGAAACAAAAAGAAGTCCTTCATGAAATAAAGGTTACAAGAACACGTTGCC 1267


Qy        878 TATTTATAACACTTTTTACA----------------------TATATGTAC----
ATAG 910
              | ||| | | | || || |                      | |  ||||
||||
Db       1266 TGTTT-
TCCCCCATTATAAACTGAGAAGTGGGTAAAGACGATGTTTCAGTACGAAAATAG 1208


Qy        911 -----TATTGTTT----GCTTTTT-----ATGTTG-ACCATCAGCC------------
TC 943
                   || | | |||| |  ||| || ||| ||||
||
Db       1207 GTGACTACAGGATCAGCGCTTCATCTCACATGCTGTACCCAAAGCCAGGCTGTGGCTGTC 1148


Qy        944 ------GTGTTGAG------CCTTA---AAGAAGTAGCTAAGG---------
AACTTT-- 977
              ||| || |      || ||  || | ||  || ||         ||| |
Db       1147 CATACGGTGGTGCGGTATAACCATAACCAAAAGGTGCCTGGGGAGGGACGGCAACACTGG 1088


Qy        978 -ACATCCTAACAGTATAATC-----CAGCTCAGTATTTTTGTTTTGT-TTTTTGT---
TT 1027
               | | || ||| || | |      || | || |    || |||| | | |||
||
Db       1087 GTCCTGCTGTCAGCATCAACTGGGGCTGACCATAAACAATGGGTTGTGTCTCTGTAGCTT 1028


Qy       1028 GTTTGTTTTGTTTTACCCAGAAATAAGATAACTCC--ATCTCGCC-
CCTT---------C 1075
              ||| | || |||| | ||| ||  || |    | | | ||  | || ||||
|
Db       1027 GTTCTTCTTCTTTT-
CTCAGTGATTCTGAAGCATCTAATTTATCCACCTTTGTCAAGTAC 969


Qy       1076 CCTTTCAT---CTGAAAGAA--------------------GATA-----
CCTCCC---- 1102
              | |||||  ||| | |||                      ||||     |||||
```

```
Db        968
TCCTTCATGACCTGGATGAAATAGGGCATGGCAAAATCCATGATATTGTGCCTCCATGCA 909

Qy       1103 ---TCCCAGTCCACCTC----------------------ATTTAGAAAA---
CCAAAG 1132
                   ||    | | || ||                  |    ||| ||
              ||||||
Db        908
GTTTCTAGGACGACATCTGGCCTTAAAAGATCGTAACAGGTAAACAGACAAGCTCCAAAG 849

Qy       1133 --------------TGTGGGTAGAAACCC---CAAATGTCCAAAAGCC----------
CT 1165
                             |    | | ||||| || ||| | ||||
              ||
Db        848
CACTCTCTTTTTTCTTCCTGCAAAAACCACTGCAGGAGTTCTTCAGCCAATTCAGTATCT 789

Qy       1166 T----TTCTGGTGGGTGACCCAGTGCATCCAACAGAAACAGC-----------
CGCTGCC 1210
                  |   ||| |  |   || ||||||| | || ||          | |
              ||
Db        788 TTAGATTCAGAAGCATACTGCATTGCATCCT--
TGTAAAGGCTGTCTTTCTTGCACAGCT 731

Qy       1211 CGAACCTCTGTGTGAAGC-----------
TTTACGCGCACACGGACAAAATGCCCAAACT 1259
                | |  |||||| | |||       || | |  |    ||| |   ||
              ||||
Db        730
CTACACTCTGTTTCCAGCGATTGTTGCCTTTGAAGAGATAAGCAGCAATTCTCCTGAACT 671

Qy       1260 ---GGAGCCCTTG------CAAAAACACGGCTT--
GTGGCATTGGCATACTTGCCCT--- 1305
                   ||| | ||       |||| |   || |  | | |||| || | ||| | |
Db        670
CAATGAGTTCATGTTTTTCCAAACGCTGAGCAAGCGAGATATTGTCAAAGTTGTCATAAG 611

Qy       1306 ----TACAGGTG------------
GAGTATCTTCGTCACACATCTAAATGAGAAATCAGT 1349
                    || | ||             || ||||||| ||    || ||| ||    |||
              |
Db        610 CATCTATTGATGTTCGCAGAGCCTGATAATCTTCTTCGTAAT-
AAAAAGATTGTTCAAT 552

Qy       1350 GA--CA---ACAAGTCT-TTGAAATGGTGC---------------
TATGGATTTACCA-- 1386
                || ||  ||| |   ||| | ||| ||||| |          || || || ||||
Db        551
GATTCATTCACAGATTTGTTGTTATGGTTCTGAACTGAACGCAAATACGGTTTCACCAGT 492

Qy       1387 --TTCCTTATTATC--------ACTAATCATCTAAAC-------AACTCACTG----
GAA 1425
                | || ||| |        | |||| || || | | || |
              ||
Db        491
GGTAGCTGTTTAACCTTGCTGAAATAATTGACTGCACGAGTGTGATCCAACCGTGGAGAC 432

Qy       1426 ATC-CAATTAACA----ATTTTACAACATAAGATAGAAT-----
GGAGACCTGAATAATT 1475
                | | ||| || ||    |||| ||||||| | | ||||    | ||| ||| ||
```

```
|
Db        431 AGCACCATCAGCAAATCATTTAACAACAGAGGCTTGAATTCTAAGTAGAACTG--
TATTG 374

Qy       1476 CTGTGTAATATAAATGGTTTATAACTGCTTTTGTAC--CTAGCTAGGC--
TGCTATTATT 1531
              || |||| |||| |      |   |  | || |||   || || |   ||| ||
||
Db        373
CTCTGTAGTATAGTTCCACATTGGCAACCTTGGTAATGATATCTTTGAATTGCCCTTCTT 314

Qy       1532 AC------TATAATGAGTAAATCAT-AAAGCCTTCAT--
CACTCCCACATTTTTCTTAC- 1581
              |       |     || | | |||| |  |  | || || |  || ||| |||
|||
Db        313
TCCAGGCATCAGTTGGATGATTCATCATGGTAATTATGGCATTATCATATTCTTCATACT 254

Qy       1582 GGTCGGAGCATCAGAACAAGCGTCTAGACTCCTTGGGACCGTGAGTTCC-
TAGAGCTTGG 1640
              |         ||| | ||  |  || |  |||      ||  |   |  | |||| || |||
|
Db        253 TGTCATA-CAAAAACACCAGT-TCTG---
CCCAAAGATGAGCTTGTTCTGCAGCTCTTAG 199

Qy       1641 C----TGGG---------TCTAGGCTGTTCTGTGC--
CTCCAAGGACTGTCT-------- 1677
              |    ||||       ||||| | | | ||||| |  || ||
Db        198 CACCTTGGGAATATTCACTCTAGAC----
CAGAACAGCTCCAGGTGCTCCCTCATTTTCT 143

Qy       1678 --GGCAATGACTT---
GTATTGGCCACCAACTGTAGATGTATATATGGTGCCCTTCTGAT 1732
                 |||   | || |||| |   | | ||     ||| | |   | ||| |
              |||
Db        142 GAGGCTTAAATTTAGAGTATAG---AATAGCTAATTCAGTAAACA---
TTCCCATGTGA- 90

Qy       1733
GCTAAGACTCCAGACCTTTTGTTTTTGCTTTGCATTTTCTGATTTTATACCAACTGTGTG 1792
              |||   ||| ||| ||   ||   ||||| |  | |||| |   | |  |
              |
Db         89 GCTC--GCTCAAGTCCCAGTG---CTGCTTCCAACATGGTGATCAGCT--
CTTCAAAATA 37

Qy       1793 GACTAAGATGCATTAAAATAAACATCAGAGTAAC 1826
              | | | ||| | | | ||  || ||   |||
Db         36 GCC--ACGAT-CCTGATAGTAGCCAGTAGGCCAAC 5


RESULT 12
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
```

  Query Match   37.7%; Score 4097; DB 1; Length 2198;
  Best Local Similarity   45.1%; Pred. No. 5.9e-268;
  Matches 1026; Conservative   0; Mismatches 664; Indels 586;
Gaps 150;

Qy   1 CAGTTACAGGGAG------CACCACCAGGGAACATCTCGGGG----AGCC--
TGGTT--G 46
             | | | | | | | ||| || |||| | ||| | ||| || |
             |
Db   5 CTGGTCTTGTGTGGGTGTTTTCCAGCACGGAAAAG-
TCGAGATAATTGCCAATGATCAGG 63

Qy   47 GAAGCTG---CAGGCTTAG-TCTGTCGGC--TGCGGGTCTCTGAC----
TGCCCTGTGGG 96
             ||| | | || | || | |||| | | | || | |||| || | |||
Db   64 GAAACCGAACCACTCCAAGCTATGTCGCCTTTAC-
GGACACTGAACGGTTGATCGGTGAT 122

Qy   97 G------AGGGTC---TTGCCTT-AACATCCCTTGCA----
TTTGGCTGCAAAGAAATCT 142
             | || || |||| | ||| | | || ||| | ||| || |
             |||
Db   123 GCCGCAAAGAATCAAGTTGCAATGAACCCCACCAACACAGTTTTTGATGCCAA-
ACGTCT 181

Qy   143 GCTTGGAAGAAGG---GGTTACGCTGTTTGGCCGGGC-----AGAAACT-----
CC---- 185
             | ||||| | || | | |||| ||| || | | ||||| ||
Db   182 GATTGGACGCAGATTTGATGATGCTG-
TTGTCCAGTCTGATATGAAACATTGGCCCTTTA 240

Qy   186 --------------GCTGAGCAGAACTTG---CC--------------------
GCCAGAA 209
                           |||| |||| | | || | |
             ||
Db   241 TGGTGGTGAATGATGCTG-
GCAGGCCCAAGGTCCAAGTAGAATACAAGGGAGAGACCAAA 299

Qy   210 TGCTCC--TCCTGTTGCTGAGTATCATC----GTCCT--
CCACGTCGCGGTGCTGGTGCT 261
             ||| | ||| | | || |||| || || || | | | | | | | |
             |||
Db   300 AGCTTCTATCCAGAGG--AGGTGTCTTCTATGGTTCTGACAAAGATGAAG-
GAAATTGCA 356

Qy   262 GCTGTTCGTCTCCACGATCGTCAG---

```
CCAATGGATCGTGGGCAATGGACACGC------ 312
           |  |   |    |   |  |    |  |  ||||||    |||| ||   |    |   ||
Db        357 GAAG--CCTACCTTGGGAAGACTGTTACCAATG--
CTGTGGTCACAGTGCCAGCTTACTT 412

Qy        313 AACTGA-TCTCTG------------------GC-AGAACTGTAGCACCTCT-----
TCCT 347
              | |||  |||| |                  ||  ||||| |  ||    |||     |
Db        413
TAATGACTCTCAGCGTCAGGCTACCAAAGATGCTGGAACTATTGCTGGTCTCAATGTACT 472

Qy        348 CAGGA-----AATGT-CCACC-------ACTGTTTCT--
CATCATCACCAAACGAATGGC 392
              |   | |     ||||  ||| |     ||  || |  ||    | |    ||||    |
Db        473
TAGAATTATTAATGAGCCAACTGCTGCTGCTATTGCTTACGGCTTAGACAAAAAGGTTGG 532

Qy        393 TGCAGTCTG-TCCAGGC-CACCATGATCCT-----GTCGATCATCTTCAG---
CATTCTG 442
              ||||    |    |  | || || |    |||     || |  | | |    |   ||  ||
Db        533
AGCAGAAAGAAACGTGCTCATCTTTGACCTGGGAGGTGGCACTTTTGATGTGTCAATCC- 591

Qy        443 TCTCTGTTCCTGTT--CTTCT-----GCCAACTCTTC--------
ACCCTCACCAAGG-G 486
              || || ||     | |  |      |||      | ||| ||| |        || | ||| ||
Db        592
TCACTATTGAGGATGGAATCTTTGAGGTCAAGTCTACAGCTGGAGACACCCACTTGGGTG 651

Qy        487 GGGCAGGTTTT-ACATC--ACTGGAATCTTCCAAATTCTTGCTG-
GTCTGTGCGTGATGA 542
              |  ||| |||| |    |    | ||| || | | ||| | |  |  |   |  | |  ||| |
Db        652 GAGAAGATTTTGACAACCGAATGG--TCAACCATTTTATTGCTGAGTTTAAGCGC-
AAGC 708

Qy        543 GTGCTGCGGCCATCTACACGGTGAGGCACCCGGAGTG--
GCATCTCAACTCGGATTACTC 600
              |        |   ||| |||    | ||||| | |  ||| | |  || | |    |  ||| |
||||
Db        709 ATAAGAAGGACAT-----CAGTGAG--AACAAGAGAGCTGTAAGACGCCTCCG--
TACTG 759

Qy        601 CT-----ACG-
GTTTCGCCTACATCCTGGCCTGGGTGGCCTTCCCCCTGGCCCTTCTC-- 652
              ||    ||| | |  ||| ||| ||  ||| | || |   || | |||| |||| | |
Db        760 CTTGTGAACGTGCTAAGCGTAC--CCTCTCTT------
CCAGCACCCAGGCCAGTATTGA 811

Qy        653 -AGCGGTGTCATCTATGTGATCTTGCGGAAACG-CGAATGAGGCGCCCAGAC----
GGTC 706
              | | | ||| ||| ||||    |||| || |    |   | ||    ||    ||
Db        812 GATCGAT-TC-TCTCTATGA-----
AGGAATCGACTTCTATACCTCCATTACCCGTGCCC 864

Qy        707 TGTCTGAGGCTCTGA--
```

```
GCGTACATAGGGAAGGGAGGAAGGGAAAACAGAAAGCAGACAA 764
   | ||| |  |||| | |||| ||  | | |      || |  | |       |||
Db        865 GATTTGAAGAACTGAATGCTGACCT--------GTTCCGTGGCACCCTG------
GACCC 910

Qy        765 AGAAAAAAGAGCTAGCC--
CAAAATCCCAAACTCAAACCAAACCAAACAGAAAGCAGTGG 822
   | | ||| ||| |||   || | | |  |||||| | ||  |    |||||   ||
Db        911 AGTAGAGAAAGC---CCTTCGAGATGCCAAACT-AGACAAGTC---ACAGATT-
CA---- 958

Qy        823 AGGTGGGGGTTGCTGT--TGATTGAAGATGTATATAATATCTCC-
GGTTTATAAAACCTA 879
             | |  |||  || ||| | |         |  |||| ||  | || || |
|
Db        959 -------
TGATATTGTCCTGGTTGGTGGTTCTACTCGTATCCCCAAGATTCAGAAGCTTC 1011

Qy        880
TTTATAACACTTTTTACATATATGTACATAGTATTGTTTGCTTTTTATGTTGACCATCAG 939
             |   |  || |     | | | ||||| | ||                      ||
|||||
Db       1012 TCCAAGAC------TTCTTCAATGGA-AAAGAACTGAAT----------
AAGAGCATCAA 1054

Qy        940 CCTCGTGTTGAGCCT-----TAAAGAAGTAGCT----
AAGGAACTTTACATCCTAACAGT 990
             || |  || ||| ||     | | | |||| |    | | |  |||| |  |
|
Db       1055 CC-C-TGATGAAGCTGTTGCTTATGGTGCAGCTGTCCAGGCAGC----
CATCTTGTCTGG 1108

Qy        991 ATAATCCAG-CTCAGTATTTT--TGTTTTGTT--
TTTTGTTTGTTTGTTTTGTTTTACCC 1045
            | |  | || | || |  | |  ||||| | ||| ||| | | |||
|||
Db       1109 AGA--CAAGTCTGAGAATGTTCAAGATTTGCTGCTCTTGGATGTCACTCCTCTTT--
CCC 1164

Qy       1046 AGAAATAAGATAACTCCATCTCGCCCCTTCCCTTTCATCTGAAAG-
AAGATACCTCCCT- 1103
            || |||| |    | | | | || || || |   |||    ||||| ||
|
Db       1165 TTGGTATTGA-
AACTGCTGGTGGAGTCATGACTGTCCTCATCAAGCGTAATACCACCATT 1223

Qy       1104 ------------CCCAGTCCACCTC-----
ATTTAGAAAACCAAAGTGTGGGTAGAAAC 1145
             | ||| ||  |    ||| || |||| || || |   |
Db       1224 CCTACCAAGCAGACACAGACCTTCACTACCTATTCTGACAACC--
AGCCTGGTGTGCTTA 1281

Qy       1146 CCCAAATGTCCAAAAGC-------CCTTTTCTGGTGGGTGAC--CCAGT---
GC------ 1187
             || |  |||| |  | |  | | || | |   ||
Db       1282 TTCAGGTTTATGAAGGCGAGCGTGCCATGAC-
AAAGGATAACAACCTGCTTGGCAAGTTT 1340

Qy       1188 -ATCCAACAG--AAACAGCC-GCTGCCCCGA-----ACCTCTGTGTGAAG---
CTTTACGC 1235
```

```
              | |  |||| | || || ||  |||||      |||| |  ||||| |  ||||
|
Db      1341
GAACTCACAGGCATACCTCCTGCACCCCGAGGTGTTCCTCAGATTGAAGTCACTTTTGAC 1400

Qy      1236 ------GCACACGG---
ACAAAATGCCCAAACTGGAGCCCTTGCAAAAACACGGCTTGTG 1286
              || | ||  || |||| |  ||| |       ||| | ||||
|
Db      1401 ATTGATGCCAATGGTATACTCAATGTCTCTGCTGTGG-----
ACAAGAGTACGGGAAAAG 1455

Qy      1287 -GCATTGGCATACTTGCCCTTA---------CAGGTGGAGTATCTTCGTCA---
CACATC 1333
              | |   | |||| |||        | | |||| |   | ||    ||
|
Db      1456
AGAACAAGATTACTATCACTAATGACAAGGGCCGTTTGAGCAAGGAAGACATTGAACGTA 1515

Qy      1334 TAAATGAGAAATCAGTGAC-AACAAGTCT-TTGAAATGGTGCTATGG----
ATTTACCAT 1387
              |     || || | | ||   |||| ||   ||   | || ||    | |
||
Db      1516
TGGTCCAGGAAGCTGAGAAGTACAAAGCTGAAGATGAGAAGCAGAGGGACAAGGTGTCA- 1574

Qy      1388 TCCTTATTATCACTAATCATCTAAACAACTCACTGGAAATC--
CAATTAACAAT-----T 1440
              |||  ||||| |||  | |    || |||| | | || | ||
Db      1575
TCCAAGAATTCACTTGAGTCCTATGCCTTCAACATGAAAGCAACTGTTGAAGATGAGAAA 1634

Qy      1441 TTACAACATAAGATAGA--ATGGAGAC---CTGAATAATTCT------
GTGTAATATAAA 1489
              | ||| |||| | ||| ||| |   ||| ||||      |||||||
||
Db      1635 CTTCAAGGCAAGATTAACGATGAGGACAAACAGAA-
GATTCTGGACAAGTGTAATGAAA- 1692

Qy      1490 TGGTTTATAACTGCTTTTGTACCTAGCTAGGCTGCT-----------
ATTATTACTATAA 1538
              ||  ||||| || ||   | | || |||||         ||| ||
Db      1693 ---TTATCAACTGGCTTGATAAGAATC-
AGACTGCTGAGAAGGAAGAATTTGAACATCAA 1748

Qy      1539 TGAGTAAATC---
ATAAAGCCTTCATCACTCCCACATTTTTCTTACGGTCGGAGCATCAG 1595
              | |  | |||| |||| |   ||||  |   | | ||     |
Db      1749 CAGAAAGAGCTGGAGAAAGTTTGCAAC---CCCATCATCACCAAGCTGT----
ACCAGAG 1801

Qy      1596 AACAAGCGTCTAGACT---------
CCTTGGGACCGTGAGTTCCTAGAGCTTGGCTGGGT 1646
              || | | || |   |||       || | ||||| |    ||| |||
||
Db      1802 TGCAGGAGGCATGCCAGGAGGAATGCCTGGGG-----GATTTCCTGG----TGG-
TGGAG 1851

Qy      1647 CTAGGCTGTTCT----GTGCCTCC-AAGGACTGTCTGGCAATGAC----
```

```
TTGTATTGGCC 1697
            ||   |   |||    |||| |||  ||| |   |   || |||    ||| |
|||
Db      1852 CTCCTCC-CTCTGGTGGTGCTTCCTCAGGGC---
CCACCATTGAAGAGGTTGATTAAGCC 1907


Qy      1698 -ACCAACTGTAGATGTATATATGGTGCC------------CTTCTGATG---
CTAA---- 1737
             ||||| |||||||||| || || ||            | | ||| |   ||||
Db      1908 AACCAAGTGTAGATGTA-
GCATTGTTCCACACATTAAAACATTTGAAGGACCTAAATTC 1966


Qy      1738 GACTCCAGACCTTT---TGTTTT------------TGCTTT-------------
GCATTT 1769
             |   | |  || |   |||||            |||| |
|||||
Db      1967
GTAGCAAATTCTGTGGCAGTTTTAAAAAGTTAAGCTGCTATAGTAAGTTACTGGGCATTC 2026


Qy      1770 TC------TGAT----------------------------------------
TTTATACCA 1784
             ||     |||                                    ||||||
Db      2027
TCAATACTTGAATATGGAACATATGCACAGGGGAAGGAAATAACATTGCACTTTATAAAC 2086


Qy      1785 ACTGT-------GTGGACTAAG--ATGCATTAAAATAAAC---ATCAGAGTAACTC
1828
             |||||       ||||| | | ||| ||||| ||||   | | | | ||
Db      2087 ACTGTATTGTAAGTGGAAAATGCAATGTCTTAAATAAAACTATTTAAAATTGGCAC
2142


RESULT 13
US-10-478-914-57
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;    LENGTH: 2336
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match             37.7%;  Score 4092;  DB 1;  Length 2336;
  Best Local Similarity   43.0%;  Pred. No. 1.9e-267;
  Matches 1042;  Conservative    0;  Mismatches  682;  Indels  698;
Gaps  138;
```

```
Qy           3 GTTACAGGGAGCACCACCAG----GGAACATCTCGGGGA------
GCCTGGTTGGAAGCT 52
               |||||    || | |  ||||   |||| |||| | |   |||| |||||
|
Db          11 GTTACT-TCTGCTCTAAAAGCTGCGGAATTCCTCGAGCACTGTTGGCCT-
ACTGGAA--T 66

Qy          53 GCAGGCTTAGTCTGTC--GGCTGC--GGGTCTCTGACTGC---------
CCTGTGGGGAG 99
               || ||| || | |  ||||||  ||  |||| | ||          |||
Db          67 GCGAGCTGAG-CAGACAGGGCTGCAAGGAAATCTGGC-
GCGGTTCAATACCT------- 116

Qy         100 GGTCTTGCCT---------TAACATCCCTTGCATTTG-----GCTG-
CAAAGAAA----T 140
                |||| ||||        || |     ||  ||||     ||| ||||   |
|
Db         117
CGTCTAGCCTGGGTTCCAGTATCTAATTTTTTTTTTGTTTTAACTGACAAACTCATTTCT 176

Qy         141 CTGCTTGGAAGAAGGGGTTACGCTGTTTGG-----CCG-------GGC-
AGAAACTCCGC 187
               || || |||  | | | | ||||  |||      ||         || |||| |
|
Db         177 CTACTGGGAC-
AGGATGCTGTGCTGGCTGGAAGTTCCATTTCTACAGCAAGAATCCTATC 235

Qy         188 TG----AGCAGAACTTG-CC----GCCAGA-ATGCTCCTCCT------------
GTTGCT 225
               ||        ||||| ||| |    |||| |  |||| |  ||
||||||
Db         236
TGGAAACACAGAAGTTGTCCTCTAGCCACAGCAGCTCGAACTTTTTTGATTGTCGTTGCT 295

Qy         226 GAGT------ATCATCGTCCTCC--------------------------------
ACGT 246
               |  |       |||| |  | |||
||||
Db         296
GCTTTCTCCCATCACCCCCATCCCCTTTTGACAAAGATCCAACTGTAAAAAGTCTTACGT 355

Qy         247 CGCGGTGCTGG--TGCTGCTGTTC---------
GTCTCCACGATC--------------- 280
                | || ||| | || |  ||       ||   ||| ||
Db         356
AACAGTTCAGGACTACTTCGGTTCTTTTACTGGGTAAGCACTTTCAATTTTTTTTTTTTA 415

Qy         281 ---GTCAGCC--------AATGGATC-GT----
GGGCAATGGACACGCAACT-------- 316
                  ||||      | || ||| |  |||||  | |||     | ||
Db         416 ACTAAAAGCCATTTTAAAATTGAATCTGTTGAGGGGC--
TTGACTAAAATCTTTTAAGTA 473

Qy         317 ------------GATCTCTGGCAG------------------AACTGTA---
GCACCTCT 343
                          ||  ||| |||                  ||| |   || |||
|
Db         474
ATTTGTGTAATGGAATACTGTCAGTGGATTTTTTCGTCTCATTTCTGCACGTGCTCCTTT 533
```

```
Qy       344 –TCCTCAGGAAATGTCCACCACTGTTTCTCATCATCACCAAACGAA––
TGG–––––––C 392
             | ||||| |       |    || || |  |||| | |||| | |||
Db       534 GTTCTCAGAA–––––
CAGAAGCTTTTATACACATCCCATAACGCAGCTGGAGAGAGTTA 588

Qy       393 TGCAGTCTG––––––TCCAGGCCACCATGAT––CCTGTCGATCAT–––
CTTCAGCATTCT 441
             || |||| |        |        || || |    ||| |  ||| || |
                                                           |
Db       589 TGAAGTCAGTTATTATAAGGAACACAAAGGTTGCTTTCCATTCTTTGCCTTTAG–
ATAAT 647

Qy       442 GTCTCTGTTCCTGTTCTT––––––––––––––––––CTGCCAACTCTTCACCC–––––
TC 478
                 |  | || | ||||                    |  |    |||||
Db       648 TAATTTTTTGTTTTCTTAAAATGGAGTATTTAAAGAAGGAAGAAAATTCACAAGAAATAA 707

Qy       479 ACCAAGGGGG–––––––––––––––GCAGGTTTTAC––––––––––
ATCACTGGAATCTT 513
                  ||    || |        | || |||||     ||| || | |
                                                                  |
Db       708 ACTGTTGGAGAATTTAGAAAAGTTTGAAGTTTTTACCACCTTTTCTATCTCTAGTTTTGT 767

Qy       514 ––––CCAAATTCTTGCTG––GTCTGTGCGTGATGAGTGCTGCGGCCATC–
TACACGGTGA 566
                 |||||  |||| ||  | ||| | | ||| | |  | ||| | ||| | || | |
                                                        ||
Db       768 GTGGCCAAACACTTG–TGCCGCCTGGG–
GCGGTGGGGGTAGAGGCAAGCATAGACAGAGA 825

Qy       567 GGCACCCGGAGTGGCAT–CTCAA–––CTCG–GATTACTCCT–ACGGTTTCGCCT––
ACAT 618
               || ||  | || | |  | |  || |  |  | ||  |         |
                                                                   |
Db       826 GGAACTAAGCCAGACATGGACAAAGGCACGAGCCAAAACCAGACAGT––––
CCTGGCCGT 881

Qy       619 CC–––TGGCC–––––TGGGTG––––––––––GCCTTCCCCCTGGCCCTTCTC–––––
AGC 655
                 |   ||||      ||||||         ||| |  | || |      |
                                                                  ||
Db       882 TCGATAGGCCAGCAGTGGGTGAGACAGGTCAGCCAGCTGCAGGGGCGGGAGCGGGGGGGC 941

Qy       656 G––––GTGTCATCTAT–––––––GTGATCTTGCG–––––––GAAACGCGA––
ATGAGGCG 695
             |   | | ||| ||       ||| || |||| |      | | || |   |||
                                                                   |
Db       942 GGGTAGGGACATGGATGTGTGAGGTGCTCATGCGTGCGATCGTGACTAGATTCTGAAACT 1001

Qy       696 CCCAGACGGTCTGTCTGAG––GCTCTGAGCGTACATAGGGAAGG––––––––––
GAGGAA 743
               |||| | | | |  | |     ||| || ||  | | ||||| |          || |
                                                                  |
Db      1002
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```
GCCAGCCATTTTCCCAGCTCCGCTTTGTGCAATCTAAAGGAATGCATCCCCTCTGAAGCA 1061

Qy         744 GGGAAAACAGAAAGCAGACAAAGAAAAAAG------
AGCTAGCCCAAAATCCCAAACTCA 797
               |    ||||  ||  |  || |||     |  || | ||| ||    ||
|||
Db        1062 GTCTTGCCAGAGCCTAGTGAGGGAGAGAAGTATGGTAAATACCACAACATATGGAA-
TCA 1120

Qy         798 AACCAAACC--AAAC---------------
AGAAAGCAGTGGAGGTGG------------ 828
               |  |  ||||   ||| |           ||| |||| ||  ||||
Db        1121 GAAAATACCGGGAACTGGAGTGGGCAAGGGGGAATGCAGAGGGTGTGGAAATTTTTTAGT 1180

Qy         829 -----GGGTTGCTGTTGATTGA----
AGATGTATATAATATCTCCGGTTTATAAAACCTA 879
                    || || |||||| |||   |  ||    |   ||||||            |||
                                                                           |
Db        1181 GATCTGGAATG-TGTTGAGTGACAGGAAGTGCCCCAAGCTTCTCC-------
CCCACCAA 1232

Qy         880 TTTATAACA----------CTTTTTACATA-------
TATGTACATAGTATTGTTT---- 918
               |  |  ||          ||||| | |       || |||| | || || ||
Db        1233 CTCTTCTCAGTCGCGCCTGCTTTTGTCTAACTCTTGTAATCTACACACTACTGCTTACAA 1292

Qy         919 -GCTTTTTATGTT---GACCATCAG---CCTCGTGTTGAGCCTTA--
AAGAAGTAGCT-- 967
               ||| | | |||  ||| | ||  |  |     | |||||      |||| ||
Db        1293 AGCTGTCTGAGTTTAAGACAAAAAGAAACCTAAAAGT-
CTCCTTACTTCATAGTACCTGT 1351

Qy         968 -------
AAGGAACTTTACATCCTAACAGTATAATCCAGCTCAGTATTTTTGTTTTGTTT 1020
                       ||||||  | | | ||  | | | |    |  |   |  ||| ||  |
                                                                           |
Db        1352 GATATGGAAGGAATGTAAAAGCATGACCCTTTAAGC---
CTATGGACATTTTTTCAGGTA 1408

Qy        1021 TT----TGTTTGTTTGTTTTGTTTTACCCAGAAATAAGATAACTC-----
CATCTCGCCC 1071
               |    |    | |     |  |||| | ||||||| || || |      || | |
                                                                           |
Db        1409 TACAGGAGAAAGATAAAATAATTTTCCACAGAAAAATGAGAATTATGAATTATATAGTTC 1468

Qy        1072 C--TTCCCTTTC-
ATCTGAAAGAAGATACCTCCCTCCCAGTCCACCTCATTTAGAAAACC 1128
                 ||||    ||  | |    | |||| |||  | |    | | | |||
               ||
Db        1469 AGGTTCCAAATCTAATTTTTAAAAGAATTCTGATTC----TGCTACACTTT------
ACA 1518

Qy        1129 
AAAGTGTGGGTAGAAAACCCCAAATGTCCAAAAGCCCTTTTCTGGTGGGTGACCCAGTGCA 1188
               || |  ||| | ||  ||  ||  |||||| ||  |  | | | |||      |
               ||||
Db        1519 AATGCTTAGGTTGGTTCCTAATTTG--AAGGAGACTTGTTTTATTTGGT----
```

```
TAATGCA 1572


Qy      1189 TC-CAACAGAAACAG---
CCGCTGCCCGAACCTCTGTGTGAAGCTTTACGCGCACACGGA 1244
             |  ||  ||| |  |  |    |     | |   | || | |||| | | | |
             |
Db      1573 TTGCATTTGAACTTGTTTCTATTTTCTTTGCATAAATTTGGA-
CTTTGGGAGAAAAATGC 1631


Qy      1245 CAA-----------AATGCCC--------AAACTGGAG-------
CCCTT---------- 1268
             ||         ||||| |     ||| ||||    |||||
Db      1632
AAAGTAATAAGTAGAATGCACTTGGGGGAAAAAAGGAGGATTTTTCCCTTCATGGGTTGG 1691


Qy      1269 ---GCAAAAACACGGCTTGTGGCATTG-----
GCATACTTGCCCTTACAGGTGGAGTATC 1320
                | |      | || ||||    |||       ||  ||  | |||||        |
                ||
Db      1692 AAAGTATTTTAAAGGGTTGTTTCTTGAAAAAACAAGCTCTCTCTTAC--------
TTTC 1743


Qy      1321 TTCGTC---------------ACACATC-----TAAATG------AGAAATC-----
AGT 1349
             | | ||                ||   |     ||||||    ||||| |
             ||
Db      1744
TGCATCTATGCTATAAAGATAACTATGCTATAATAAATGTAAGGTAGAAAACTTTAAAGA 1803


Qy      1350 GACAACA--AGTCTT-----
TGAAATGGTGCTATGGGATTTACCATTCCTTATTATCACTA 1402
             || || |  ||| |     ||||| | | ||  | |||| ||    |     |||| 
Db      1804 GAAAATAACAGTGTTCTAAGTGAAAAGCTACTTAGCATTTTCCCAAAC------
TCACAC 1857


Qy      1403 ATCATCTAAACA-ACTCACTGGAAAT--------------
CCAATTAACAATTTTACAA- 1446
             || ||| ||||  |  |||| ||||           |||| ||| | | | 
Db      1858 ATTATC--
AACAGAAACACTAAAAATTAAGAGAAAAGCGGCCAACTAATTAAATAGCTAG 1915


Qy      1447 -CATAAGATAGAATGGAGACCTGAATAATTCTGTGTAATATAAATGGT--
TTATAACTGC 1503
              | ||   | |        |   | | |||| |||| | ||||| | || 
              ||
Db      1916
CCTTATTTTGGGGGTATGGGATAGAAAATTAAGTGTGAATAAAATGATACTTGGGAATGT 1975


Qy      1504 TT-----
TTGTACCTAGCTAGGCTGCTATTATTACTATAATGAGTAAATCAT-------- 1550
             ||    | ||||| |   ||| || || |   | |||| |||| | 
Db      1976 TTCTCCCTCGTACC-
ACAAAGGATGTTAGTGGTCAGCCTACGAGTTAATCCTTCCTAGCA 2034


Qy      1551 ------AAAGCCTTCAT--CACTCCCACATTTTTC---TTACGG-
TCGGAGCATCAGAAC 1598
                   ||||||||  |   || || |||  | ||| ||| |   ||
                |
Db      2035
```

TGGCTCTGAGCCTTCATGCCGAGCAGACGTTATTCACATGACGATTCGAAAAGTCCATTC 2094

Qy   1599 AAGCGTCTAGACTCCTTGGGACCGTGAGTTCCTAGAGCTTGGCTGGGTCTAGGCT---
GT 1655
                | ||| | || ||| ||| | | | | || || || ||
||
Db   2095 ATATATCTCG-CTACCTGGATT--TGAAT---AGAAACCAGACAG---
CAATTCTTTAGT 2145

Qy   1656 TCTGTGCCTCCAAG-GACTGTCTGG-CAATGAC-TTGTATTGGC-------
CACCAACTG 1705
                || ||| ||| | | |||| |||| | | || || | |||
|||
Db   2146 TCC-
AGCCACCATTCGCCCCACTGGACAATAGCGATTTGTTAGCACAGAGTCACAGGCTG 2204

Qy   1706 TAGATGTATATATGGTGCCCTTCTGATGCTAAGA-
CTCCAGACCTTTTGTTTTTGCT--- 1761
                ||| | | | ||| || || |||| | | | |
Db   2205 ------------TGGGACAC----
AAAGCTTGGAGCTGCAGAAAGATGGGGGATTCAGAG 2248

Qy   1762 ---TTGCATTTTCTGATTTTATAC-CAACTGTGTGGACTAAG-
ATGCATTAAAATAAACA 1816
                | | || | | | | || | ||| | || || || || |||| |||
|
Db   2249
AACAGGAAATTACAGGCTCGATGCACTCCTGGCAGCTCTGAGAATACAAAAAAAAAAAA 2308

Qy   1817 TCAGAGTA----------ACTC 1828
                | | | |||
Db   2309 AAAAAAAAGGCCACATGTGCTC 2330

RESULT 14
US-10-478-914-57/c
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match   37.4%; Score 4064.5; DB 1; Length 2336;
  Best Local Similarity 42.4%; Pred. No. 1.6e-265;

```
  Matches 1021; Conservative   0;  Mismatches  680;  Indels  707;
Gaps  136;

Qy        12 AGCAC---CACCAGGGAAC----------------------ATCTCGGGG-
AGCCTGG 43
             ||| |   ||| | | |                       |||| | | |||
|
Db      2335
AGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTGTATTCTCAGAGCTGCCAG- 2277


Qy        44 TTGGAAGCTGCAGGCTTAGTCTGTCGGCTGCGGGTCTCTGACTGCC----
CTGTGGGGAG 99
             |   || | ||    ||||    | | |||||||| | ||    || | |
||
Db      2276 --GAGTGCATCGAGC-----
CTGTAATTTCCTGTTCTCTGAATCCCCCATCTTTCTGCAG 2224


Qy       100 GGTCTTGCCTTAACATCCCTTGCATTTGGC----TGCAAAGAAATCTGC--
TTGGAAGAA 153
             |  || ||    ||    || | | | |    ||| | |||||| ||   |||
Db      2223 CTCCAAGCTTTGTGTCCCACAGCCTGTGACTCGTGCTAACAAATC-
GCTATTGTCCAGT 2165


Qy       154
GGGGTTACGCTGTTTGGCCGGGCAGAAACTCCGCTGAGCAGAACTTGCCGCCAGAATGCT 213
             ||||         |  |||    ||| | ||||         |  | |||| | | |   |
||
Db      2164 GGGG------CGAATGGT--GGCTGGAACT--------
AAAGAATTGCTGTCTGGTTTCT 2121


Qy       214 -----CCTCCTGTTGCTGAG---
TATCATCGTCCTCCACGTCGCGGTGCTGGTG-----C 260
                  ||| | |   ||| ||| | | ||   ||    || |    |  |||
|
Db      2120 ATTCAAATCCAGGTAGCGAGATATATGAATGGACTTTTCGAATCG--
TCATGTGAATAAC 2063


Qy       261 TGCTGTTCGTC-TCCACGATCGTCAGCCA-------ATGGA-----
TCGTGGGCAATGGA 307
                  ||| ||| | | | | | ||  |||||        | |||    |||| ||| ||
Db      2062 GTCTGCTCGGCATGAAGGCTCAG-AGCCATGCTAGGAAGGATTAACTCGTAGGC--
TGAC 2006


Qy       308 CACGCAACTGATCTCTGGCAGAAC--TGTAGCACCTCTTCC-----
TCAGGAAATGTCCA 360
             |||   |||   |||   | | | ||   | | | | | | ||      |||    ||
||
Db      2005 CAC-TAAC--
ATCCTTTGTGGTACGAGGGAGAAACATTCCCAAGTATCATTTTATTCACA 1949


Qy       361 CCACTGTTTC--TCATCATCACCAAACGAATGGCT-GCAGTCTGTCCA---
GGCCACCAT 414
             |       |||| ||      | || ||   | |||| || | |     |    |||| |
Db      1948
CTTAATTTTCTATCCCATACCCCCAAAATAAGGCTAGCTATTTAATTAGTTGGCCGCTTT 1889


Qy       415 GATC----------------CTGTCGATCATCT-TCAG--------CATTCT--
GTCTCT 447
             ||                  |||| ||| || | | ||        || || ||
```

```
    ||
Db        1888
TCTCTTAATTTTTAGTGTTTCTGTTGATAATGTGTGAGTTTGGGAAAATGCTAAGTAGCT 1829

Qy         448 GTTC----------CTGTTCT----
TCTGCCAACTCTTCACCCTCACCAAGGGGGGCAGG 493
                |||        ||||| |   ||| || | ||| ||| |         ||
Db        1828 TTTCACTTAGAACACTGTTATTTTCTCTTTAAAGTTTTCTACCTTA----------
CATT 1779

Qy         494 TTTTACATCACTGGAATCTTCCAA--ATTCTTGCTG---
GTCTGTGCGTGATGAGTGCTG 548
                | ||| || | ||||| | || ||| | || | | | |
|
Db        1778
TATTATAGCATAGTTATCTTTATAGCATAGATGCAGAAAGTAAGAGAGAGCTTGTTTTTT 1719

Qy         549 C-GGCCATCTACACGGTGAGGCACCCGGAGTGGCATCTCAACTC------
GGATTACTCC 601
                |  |  | | || | |           | | |||| |     ||| |
|||
Db        1718 CAAGAAAACAACCCTTTAAAATA----------
CTTTCCAACCCATGAAGGGAAAAATCC 1669

Qy         602 TACGGTTTCGCCTACATCCTGGCCTGGGTGGCCTTCCCCCTGGCCC---------
TTCTC 652
                | |  |||         ||| ||  || ||| ||| | |     |
|||||
Db        1668 TCCTTTTT--------TCC---CCCAAGT-
GCATTCTACTTATTACTTTGCATTTTCTC 1621

Qy         653 AGCGGTGTC---ATCTATG---TGATCTTGCGGAAACG----
CGAATGAGGCGC-----C 697
                |  ||| || |||| || | ||||| | |||| ||
|
Db        1620 C-CAAAGTCCAAATTTATGCAAAGAAAAT--
AGAAACAAGTTCAAATGCAATGCATTAAC 1564

Qy         698 CAGA------CGGTCTGTCTGAGGCTCTGAGCGTACATAGG-------
GAAGGGAGGAAG 744
                || |      |||| | | | || | || | |        ||| | |
||
Db        1563
CAAATAAAACAAGTCTCCTTCAAATTAGGAACCAACCTAAGCATTTGTAAAGTGTAGCAG 1504

Qy         745 GGAAAACAGAAAGCAGACAAA----------GAAAAAAGAGCTAGC-----
CCAAAATCC 789
                || ||||| |   ||| || ||   || ||| | ||
||
Db        1503 ---
AATCAGAATTCTTTTAAAAATTAGATTTGGAACCTGAACTATATAATTCATAATTCT 1447

Qy         790 CA----------------------AACTCAAACC---AAACCAAACAGAAAG--
CAGTGG 822
                ||                      | ||    || | ||| | ||| | ||
||
Db        1446
CATTTTTCTGTGGAAAATTATTTTATCTTTCTCCTGTATACCTGAAAAAATGTCCATAGG 1387

Qy         823 AGGTGGGGGT--TGCTGTTGATTGAAGATGTATATAATATCTCCGGTT--------
```

```
TATA 872
                    ||||  |||| ||      | ||   |  ||||| | |||              ||
Db      1386 CTTAAAGGGTCATGCTTTT------
ACATTCCTTCCATATCACAGGTACTATGAAGTAAG 1333

Qy       873 AAACCTATTTATAACACTTTTT-------------
ACATATATGTACATAGTATTGTTTG 919
                    |  || |||     ||||||          ||| | |||| |||| |||
                                                                          |
Db      1332 GAGACT-
TTTAGGTTTCTTTTTGTCTTAAACTCAGACAGCTTTGTAAGCAGTAGTGTGTA 1274

Qy       920 CTTTTTATG---TTGACCAT--CAGCCTCG--TGTTGAGCCT---
TAAAGAAGTAGCTAA 969
                    || | |  ||| |    ||| | ||  ||   |   |  | || ||||
Db      1273
GATTACAAGAGTTAGACAAAAGCAGGCGCGACTGAGAAGAGTTGGTGGGGGAGAAGCTTG 1214

Qy       970 GGAACTTTACATCCTAACAGTATAATCCAGCTCAGT----ATTTT----------
TGTTT 1015
                    ||    || |   |   || | |||| ||| |   | |||              ||
                                                                          |
Db      1213
GGGCACTTCCTGTCACTCAACACATTCCAGATCACTAAAAAATTTCCACACCCTCTGCAT 1154

Qy      1016 TGTTTTTTG------TTTGTT-----TGTTTTGTTTTACCCAGAAATAAGATAACT-
CCA 1063
                    |     |||       |||     | |||| | ||    | | || |
                    |||
Db      1153
TCCCCCTTGCCCACTCCAGTTCCCGGTATTTTCTGATTCCATATGTTGTGGTATTTACCA 1094

Qy      1064 TC--TCGCCCCTTCCCTTTCATCTGAAAGAAGATACCTCCCTCCCAG----
TCCACCTCA 1117
                    |   || | ||| |      |||| |   |||| |||| || | |   | |
                    ||
Db      1093 TACTTCTCTCCCTCACTAGGCTCTGGC--AAGA---CTGCTTCAGAGGGGATGCA-
TTCC 1040

Qy      1118 TTTAGAAAAC-CAAAGTG----TGGGTAGAAACC---------CCAAAT---
GTC----- 1155
                    ||||||   | |||||  |   |||| | |    |        |  ||| |||
Db      1039
TTTAGATTGCACAAAGCGGAGCTGGGAAAATGGCTGGCAGTTTCAGAATCTAGTCACGAT 980

Qy      1156 ------
CAAAAGCCCTTTTCTGGTGGGTGACCCAGTGCATCCAACAGAAACAGCCGCTGC 1209
                    || ||| | |   | |  | ||| | |  |  | ||  |  |||||
Db       979 CGCACGCATGAGCACCTCACACATCCATGTCCC---TAC--CCGCC-----
CCCCCGCT-C 930

Qy      1210 CCGAACCT----CTGTGTGAAGCTTTACGCGCACACGG--------
ACAAAATGCCCAAA 1257
                    ||| |||   ||| |||| | | | | | ||| |     | || |||
Db       929 CCGCCCCTGCAGCTGGCTGA--
CCTGTCTCACCCACTGCTGGCCTATCGAACGGCCAGGA 872

Qy      1258 CTG--------------GAGCCCTTGCAAAAACACGGCTTGTGGCAT---TGGC-
```

```
ATACT 1299
                   |||                  | ||| |||   |     ||||||   | |    || | ||
     ||
Db      871
CTGTCTGGTTTTGGCTCGTGCCTTTGTCCATGTCTGGCTTAGTTCCTCTCTGTCTATGCT 812


Qy      1300 TGCCCTTA------------CAGGTGG----AGTATCTTCGTCACAC--
ATCTAAATGAG 1341
             |||| ||                |||| ||   ||| | || | ||||| | ||| |
Db      811 TGCCTCTACCCCCACCGCCCCAGGCGGCACAAGTGT-
TTGGCCACACAAAACTAGAGATA 753


Qy      1342 AAATCAGTGACAACAAGTCTTTGAAATGGTGCTATGGATTTACC--------
ATTCCTTA 1393
                  ||  |||| || || |||  || | || ||| |||  ||         |||
     |||
Db      752 GAAAAGGTGGTAAAAA--CTTCAAACT-TTTCTA--
AATTCTCCAACAGTTTATTTCTTG 698


Qy      1394 T-TATCACTAATCATC-TAAACAACTCACT----
GGAAATCCAATTAACAATTTTACAAC 1447
              | || ||  | ||| | ||  |||| |    |||| | ||  ||  | || |
     |
Db      697 TGAATTTCTTC-
CTTCTTTAAATACTCCATTTTAAGAAAACAAAAAAATTAATTATCTAA 639


Qy      1448 A---TAAGATAGAATGGAGACCTGAATAATTCTGTGTAATATAAATGG-
TTTATAA---- 1499
             |   |||| | | | |||| | |   ||  |||| || || ||||
Db      638 AGGCAAAGAATGGAAAGCAACCTTTGTGTTCCT---
TATAATAACTGACTTCATAACTCT 582


Qy      1500 ------CTGCTTT------
TGTACCTAGCTAGGCTGCTATTAT----------------- 1530
                   |||| ||      || |   | ||| || ||
Db      581 CTCCAGCTGCGTTATGGGATGTGTATA-
AAAAGCTTCTGTTCTGAGAACAAAGGAGCACG 523


Qy      1531 TACTATAATGAG-----
TAAATCATAAAGCCTTCATCACTCCCACATTTTTCTTAC---- 1581
             | |  ||||||        ||| |     | | ||  |  |||| || ||||
Db      522 TGCAGAAATGAGACGAAAAAATCCACTGACAGTATTCCATTACACAAATTACTTAAAAGA 463


Qy      1582 ----GGTCGGAGCATCAGAACA----------------
AGCGTCTAG------------- 1608
                 ||| ||| | ||||                  || | |||
Db      462 TTTTAGTC-
AAGCCCCTCAACAGATTCAATTTTAAAATGGCTTTTAGTTAAAAAAAAAAA 404


Qy      1609 ---------ACT--CCTTG-----GGACCG---------TGA---GTTCC-
TAGAGCTT- 1638
                           || || |    | |||          |||   ||| | ||
     |||
Db      403
ATTGAAAGTGCTTACCCAGTAAAAGAACCGAAGTAGTCCTGAACTGTTACGTAAGACTTT 344


Qy      1639 ----GGCTGGGTCT----------------AGGCTGTTCTGTGC---
CTCCAAGGACTGT 1675
                 | ||| |||                || || | |    |  ||| |||
```

```
|
Db        343
TTACAGTTGGATCTTTGTCAAAAGGGGATGGGGGTGATGGGAGAAAGCAGCAACGACAAT 284


Qy       1676 CTG-------------
GCAATGACTTGTATTGGCCACCAACTG----------------- 1705
              |                |   ||  || | |    || || |  |||
Db        283 CAAAAAAGTTCGAGCTGCTGTGGCTAG---
AGGACAACTTCTGTGTTTCCAGATAGGATT 227


Qy       1706 -TAGATGTATATATGGTGC--
CCTTCTGATGCTAAGACTCCAGACCT------------ 1749
               | | |||| | |||| |  || |     ||  ||  ||| | ||
Db        226 CTTGCTGTAGAAATGGAACTTCCAGC--
CAGCACAGCATCCTGTCCCAGTAGAGAAATGA 169


Qy       1750 -TTTGTTTTT--------------------------------GCTTTGC---
ATTTT- 1770
               |||||   |                            |||    |    |
||
Db        168
GTTTGTCAGTTAAAACAAAAAAAAAATTAGATACTGGAACCCAGGCTAGACGAGGTATTG 109


Qy       1771 --------CTGATTTTATACCAACTGTGTGGGACTAAGAT-GCATTAAAATA-
AACATCAG 1820
                      | |||||  |  || |  |||   || || | |||||  | ||   ||
|||
Db        108
AACCGCGCCAGATTTCCTTGCAGCCCTGTCTGCTGCTCAGCTCGCATTCCAGTAGGCCAACAG 49


Qy       1821 AGTAACTC 1828
               |   |||
Db         48 TG---CTC 44


RESULT 15
US-10-478-914-62
; Sequence 62, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 1946
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-62

  Query Match          36.7%;  Score 3982;  DB 1;  Length 1946;
```

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  Best Local Similarity   44.6%;  Pred. No. 3.3e-260;
  Matches  949;  Conservative    0;  Mismatches  680;  Indels  498;
Gaps  121;

Qy         1 CAGTTACAGGG----------AGCACCACCAG----
GGAACATCTCGGGGAGCCTGGTTG 46
             |   ||| |             || | |  ||    |||| |  ||| |  ||||
||||
Db         2 CCTGTACGGAAGTGTTACTTCTGCTCTAAAAGCTGCGGAATTCCTC---
GAGCACTGTTG 58

Qy        47 GAAGCTGCAGGCTTAGTC-TGTC-
GGCTGCGGGTCTCTGACTGCCCTGTGGGGAGGGTCT 104
             |   || | |||| || | | || | |   |   ||  || |  ||||| | | | ||
|
Db        59 GC--CTACTGGCTGAGGCTTATCTGACATC---TCATTGTC--
CCCTGGTGTGTGTGTGT 111

Qy       105 -
TGCCTTAACATCCCTTGCATTTGGCTGCAAAGAAATCTGCTTGGAAGAAGGGGTTACGC 163
                |   ||  |      |    || | ||| |   ||      ||   || ||| |||
||
Db       112 GTGTGTGGTGTTTTTGTGTGTGTGG--GGTGTGAGTGTGGCAGAGAGGAAAGGG--
GAGC 167

Qy       164 TGTTTGGCCGGGCAGAAACTCCGCTGAGCAGAACTTGCCGCCAGAATGCTCCTCCTGT-T 222
             ||||||   | | ||           || | |||   | ||    ||||
Db       168 TGTTTGATT---CTGTAGTTCC-----------
TTTTCTGCCTTCTTCCTTTCTCTGTAA 213

Qy       223 GCTGAGTATCATCGTCC----TCC--ACGTCGCGGTG---CTGGTGCTGCTG---
TTCGT 270
                || | || |  |||      | |  ||| |     ||   |   ||| | || |
||
Db       214 ACTTTGGATACTTATCCAAATTACTAACGGCAGATTGAGCCCTATGCAGATGGCATGTGT 273

Qy       271 CTCCACGATCGTCAGC---
CAATGGATCGTGGGCAATGGACACGCAACTGATCTCTGGCA 327
                ||   |   | || |   | |  || ||||| ||   || | ||  ||| |||
||
Db       274 CTGTGACAACCTCTGCTCTCCACATCTCTTGGGC-CTGTTTAC----CTGCGCTCC--
CA 326

Qy       328 GAACTGTAGCACCTCTTCCTCAGGAAATGTCCACCACTGTTTCTCATCATCACCAAACGA 387
             || |    || |   || | ||| |||  ||| ||| | | | |||||| | |   || ||
Db       327 GAGCCTCCGC-CAGCATCC-CAG--AATCTCCATCCCCATCTCTCA-
CTTATACACACAT 381

Qy       388 ATGGCTGCAGTCTGTCCA--GGC--CACCATGATCCT--
GTCGATCATCTTCAGCATTCT 441
             | | | || | |||| || | |||    | |   |||| | | |   | | | |
||
Db       382 CAGTCATCGGT-TATCCATTAGCTAAACCGCCTTCCTTAATAGCTTTAC-
ACTGTTTGCT 439

Qy       442 GTCTCTGTTCCTGTTCTTCTGCCAACTCTTCA-----CC----
CTCACCAAGGGGGGCA- 491
```

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                  |||||    |    |  ||   |   ||   ||||      |      |  ||| || |   |
Db        440 TTCTCTGGAAC--
ATTTTTAGTTAAAATTTCATAATGCAGTTGCACACAAATGAAGACAC 497

Qy        492 GGTT--
TTACATCACTGGAATCTTCCAAATTCTTGCTGGTCTGTGCGTGATGAGTGCTGC 549
                  |  |    |  ||||   |  ||||||    || | ||
Db        498 AGATGGCTGCATCCTCCGTCTCTTCCCCTCGTTTACAGG--------------
AAGCTGC 543

Qy        550 GGCCATCTACACGGTGAGGCACCCGGAGTGGCATCTCAACTCGGATTACTCCTACGGTTT 609
                  ||  ------- |  | |||||    || ||          |  ||  ||||  |   |  |||
Db        544 GG-------ATCAGGGAGG-----GGTGT-----------
TAGGGTTACCCACATGGTAA 580

Qy        610 CGCCTACATCCTGGCCTGGGTGGCCTTCCCCCTGGCCCTTCTCAGCGGTGTCATCTATGT 669
                  |  |    |  |    ||  ||  ||   |  ||  |  || | |     |   |||||
Db        581 GGGCAGAGACAAG----AGGGGACC--
CCAGTTTTCCATGCTGCACATGGTCATTGCTGG 634

Qy        670 GATCTTGCGGAAACGCGAATGAGGCGCCCAGACGGTCTGTCTGAGGCTCTGAGCGTACAT 729
                  |  | ||||    ||   ||  |   | |||  |   ||||    |||     | |  |
Db        635 GGAC-TGAGGTTT-GCACAT----CACCCTGCC---CTGTT-----CTC----
CCTCCGC 676

Qy        730 AGGGAAGGGAGGAAGGGA--AAACAGAAAGCAG-----
ACAAAGAAAAAAGAGCTAGCCC 782
                  ||| ||  ||  ||||| |  || |   ||||      |   | ||| || || |
Db        677 TGGGGAGAAAGTCAGGGATGGAGCAAGCTGCAGCATCTTCTGAAAAAGAAAAGGTGGCCT 736

Qy        783 AAAATCCCAAACTCAAACCAA-
ACCAAACAGAAAGCAGTGGAGGTGGGGGTTGCTG---- 837
                  ||| ||| ||| ||| |  |     |||       ||  || |||
Db        737 TGTCTCCAGGTCTCCCCTCAAGTCCCACCTTCCCATAGT-----------
TTTCTGCCAC 785

Qy        838 -----TTGATTGAAGATGTATATAATATCTCCGGTTTATAAAACCTATTT---
ATAACAC 889
                  |||||     |  |  | | ||||  | ||  |     ||| | ||  |    |
Db        786 TTCTCTTGATTTTC-CTCTCTGCCACTTCTCTTGATTTT----
CCTCTCTGCCACTTCTC 840

Qy        890 TT--TTTACATATATG----TACATAGTATT--
GTTTGCTTTTTATGTTGACCATCAGCC 941
                  ||  ||| || || |    |   |  |  |||| ||    ||| || ||
Db        841 TTGATTTTCCTCTCTGCAGCTGCTTTGAGGTGGGTTTTCTCCAGATGCACACTTTC--
CC 898

Qy        942 TCGTGTTGAG--CCTTAAAGAAGTAG---------CTAAGGAACTTTA--------
CATCC 983
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                 |   ||| |  |||||     ||||        |||| |  |  |||
Db        899
CTGCTTTGCGTCCTTATTCTGGTAGAAGCACAATCTAAAGCTCATTAAGGGAACTAATCA 958

Qy        984 TAACAGTATA---ATCCAGCTCAGTATTTTT--------
GTTTTGTTTTTTGTTTGTTTG 1032
                   |  ||  |     |  |||||||| |  |          |     |  || |    ||
                                                                       |
Db        959
ATTCTGTGCATGGCGCTAGCTCAGCAGATCACCACACAGGCAGCACTATTAGCAAGTCGG 1018

Qy        1033 TTTTGTTTTACCCA--GAAATAAGATAACTCCATCT--
CGCCC----------------- 1071
                     || || ||| ||   | | |   || | ||| |   ||||
Db        1019 ---
TGCTTAACACATGGCACTTCCATGAATCGATATGGAGCCCGTGTAGAACAAGGCATG 1075

Qy        1072 -----------CTTCCCTTTCATCTGAAAGA-AGATACC------
TCCCTCCCAGTCCAC 1113
                       |||||| ||| |  |||| |  ||| ||       |  || |||
Db        1076 GGTTTTTTTCTCTTCCCATTAA---
GAAAAACTGATGCCAAAAATAACTTCTCAGATATT 1132

Qy        1114 CTCATTTAGAAAACCAAAGTGTGGGTAGAAACCCCAAATGTC--
CAAAAGCCCTTTTCTG 1171
                     ||| | |  | ||     || || |||| |      ||| |||||| |     |||
                                                                       |
Db        1133 TTCAAGT--
ATGACTTTTATGAAGGGAAAAAGCATTTTTGTTTGCAAAATCATGCTTCAG 1190

Qy        1172 -GTGGGTGACCCAGT--------------GC-----
ATCCAACAGAAACAGCCGCTGCCC 1211
                     |  || |  |||||              ||       | | | |   | |    ||
Db        1191 TGCAGG----
CCAGTTGTGAATTGTGATGGCTTTTATTTCTCCTGGGGCTGTAACTTTAA 1246

Qy        1212 --------------GAACCTCTG---
TGTGAAGCTTTACGCGCACACGGACAAAATGCCC 1254
                         ||||| | |    |   || | | || | |||| |||        |
Db        1247 GGGTTTAGAATTTGGAACCACAGCCTAGCTAATCATGACACACACACACACA-----
CAC 1301

Qy        1255 AAACTGG--AGCCCTTGCAAAAACAC--GGCTTGTGGCATTGGCATAC---
TTGCCC--- 1304
                     | || |    |   | || | |||| ||| |   |  ||||| |||  |
Db        1302
ACACATGCACACACACATACACATACACAAAGCATCACGAAGAACCATACAAATTGTACATT 1361

Qy        1305 ---
TTACAGGTGGAGTATCTTCGTCACACATCTAAATGAGAAATCAGTGACAACAAGTCT 1361
                     |||||  ||||    | | |||   ||| | || |   || |
Db        1362 ATTTTACACATGGA--------GGCTCAC-
TCTAAAATAGATACCATTTTAAATATTAAC 1412

Qy        1362 TTGAAATGGTGCT-ATGGATTTACCATTC--------CTTATT-----
ATCACTAATC-A 1406
                     |  || | ||||| || |  |   |||||        || |||      ||||   ||
Db        1413
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TAAAACTTGTGCTCATTGTATGTTCATTCTATATGTACTGATTTGTTATTCACATTTCTT 1472

Qy       1407 TCTAAA-----CAACTCACTGGAAATC--CAATTAACAATT--------
TTACAACATAA 1451
              || |||     ||| | || |     |  ||||||| |||      || | |||
Db       1473
TCAAAATCGTTCAAATTTCTAGCCCACATCAATTAAATATTAATAGTACTTTCTACA--- 1529

Qy       1452 GATAGAATG-GAGACCTGAAT------AATTCTGTGTAATATAAATGGT-TTAT---
AAC 1500
                  |  ||| | |  |||      || ||| | |    | |||| ||||
||
Db       1530 ---AACATGAGCGCACAAAATAAATTCAAATCTAT-
TTTTCCCACTGGTGTTATCAATAC 1585

Qy       1501 TGCT-----TTTGTACCTAGCTAGG------
CTGCTATTATTACTATAATGAGTAAATCA 1549
              ||||     |||||  || ||| |      || | ||| || |||||    |
Db       1586 TGCTCATACTTTGTCAGTAACTAAGTATCACATGATCTTAAAAC--
TAATGTCACATACT 1643

Qy       1550 TAAAGCCTTC-------------------ATCACTC--
CCACATTTTCTTACGGTCGGA 1588
                  ||| ||||                   | | ||| |  |||| ||||   || |
Db       1644
AAAAAGCTTCTGAGGCAAATTGTAGAAAGAACTCTCAACATCATTGTTCTACTGGAC--- 1700

Qy       1589
GCATCAGAACAAGCGTCTAGACTCCTTGGGACCGTGAGTTCCTAGAGCTTGGCTGGGTCT 1648
                       |||| |  | | | ||          || | | | || |
|
Db       1701 -------AACATAC--ATAAAATTATT-----------TTAC-
AGTGATGGGAGAGAAAT 1739

Qy       1649 AGGCTGTTCTGTGC------CTCCAAGGACTGTCTGGCAATGACTTGTATTGGC----
CA 1698
              |||||  || | |        || | ||| |  | || || | ||| |||||
|
Db       1740 AGGCTCCTC-ATCCTAAAAGCTGCGAAGACAG--
TAGCGGTGCCGTGTTTGGCGTTACT 1796

Qy       1699 CCAACTGTAGATGTATATATGGTGCCCTTCTGATGCTAAGA---
CTCCAGACCTTTTGTT 1755
              || |||| |||  ||||||||||| |     ||   |||| |  ||||
Db       1797 CC--CCTGTGGAT------------CCCAGC-
GACGGGTGGATTTCTCCTGTGCTTTATCA 1842

Qy       1756 TTTG-CTTTGCATTTTCTGATTTTATACCAACT------GTGT---
GGACTAAGATGC-- 1803
              | | |    ||  |     ||  |   | | |     |||| |||| ||| ||
Db       1843
TCAGACACAAAATGGACCAAAATGGACCAAAATGGACGAGTGTGAGGGACACAGAGGCTG 1902

Qy       1804 --ATTAAAATAAACATCAGAGTAACTC 1828
                | |||| ||| | | |    | |
Db       1903 CTGTAAAAAAAAAAAAAAAAAGGCCAC 1929


Search completed: March  9, 2010, 15:52:21
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Job time : 10.2568 secs

                              GenCore version 6.3
                   Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:        March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                          (without alignments)
                                          1134.946 Million cell
updates/sec

Title:         US-10-572-905-29
Perfect score: 38331
Sequence:      1 cccagttgtctgcgggctgc..........taataaagcttgtttttctcc
6734

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:      834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      7335755.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES
                     %
Result          Query
   No.    Score  Match Length DB  ID                      Description

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     1  8423.5   22.0   3589  1   US-10-478-914-21         Sequence 21,
Appl
  c  2    8078   21.1   3589  1   US-10-478-914-21         Sequence 21,
Appl
     3  7966.5   20.8   3210  1   US-10-478-914-4          Sequence 4,
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Appli
     5  6088.5   15.9   2437  1   US-10-478-914-61         Sequence 61,
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     7    5811   15.2   2495  1   US-10-478-914-20         Sequence 20,
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c	8	5722	14.9	2495	1	US-10-478-914-20	Sequence 20, Appl
c	9	5407	14.1	2336	1	US-10-478-914-57	Sequence 57, Appl
	10	5370.5	14.0	2336	1	US-10-478-914-57	Sequence 57, Appl
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	12	5309	13.9	2120	1	US-10-478-914-64	Sequence 64, Appl
	13	5280.5	13.8	2198	1	US-10-478-914-17	Sequence 17, Appl
c	14	5272.5	13.8	2198	1	US-10-478-914-17	Sequence 17, Appl
c	15	4899.5	12.8	2083	1	US-10-478-914-3	Sequence 3, Appli
c	16	4797	12.5	2022	1	US-10-478-914-60	Sequence 60, Appl
	17	4790	12.5	1946	1	US-10-478-914-62	Sequence 62, Appl
	18	4750	12.4	2083	1	US-10-478-914-3	Sequence 3, Appli
	19	4621.5	12.1	2022	1	US-10-478-914-60	Sequence 60, Appl
c	20	4422	11.5	1946	1	US-10-478-914-62	Sequence 62, Appl
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	22	4142.5	10.8	1813	1	US-10-478-914-63	Sequence 63, Appl
c	23	2372.5	6.2	1020	1	US-10-478-914-68	Sequence 68, Appl
	24	2353.5	6.1	889	1	US-10-478-914-5	Sequence 5, Appli
	25	2291	6.0	867	1	US-10-478-914-6	Sequence 6, Appli
	26	2266	5.9	1020	1	US-10-478-914-68	Sequence 68, Appl
c	27	2243	5.9	867	1	US-10-478-914-6	Sequence 6, Appli
	28	2220	5.8	816	1	US-10-478-914-15	Sequence 15, Appl
c	29	2214	5.8	816	1	US-10-478-914-15	Sequence 15, Appl
	30	2193	5.7	938	1	US-10-478-914-69	Sequence 69, Appl
	31	2175.5	5.7	794	1	US-10-478-914-13	Sequence 13, Appl
	32	2173	5.7	717	1	US-10-478-914-42	Sequence 42, Appl
c	33	2172	5.7	938	1	US-10-478-914-69	Sequence 69, Appl
c	34	2171	5.7	889	1	US-10-478-914-5	Sequence 5, Appli
	35	2167.5	5.7	889	1	US-10-478-914-9	Sequence 9, Appli
c	36	2155.5	5.6	839	1	US-10-478-914-16	Sequence 16, Appl
c	37	2155	5.6	909	1	US-10-478-914-67	Sequence 67, Appl

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  c  38   2151.5    5.6    889   1  US-10-478-914-9        Sequence 9,
Appli
      39   2110      5.5    839   1  US-10-478-914-16       Sequence 16,
Appl
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Appl
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Appl
  c  42   2084.5    5.4    794   1  US-10-478-914-13       Sequence 13,
Appl
  c  43   2081.5    5.4    816   1  US-10-478-914-38       Sequence 38,
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Appl
  c  45   2062      5.4    820   1  US-10-478-914-39       Sequence 39,
Appl
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                              ALIGNMENTS

RESULT 1
US-10-478-914-21
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match   22.0%; Score 8423.5; DB 1; Length 3589;
  Best Local Similarity   37.0%; Pred. No. 0;
  Matches 2396; Conservative   0; Mismatches 1139; Indels 2937;
Gaps 331;

Qy   171 CCAAGTCCTGTGGTGCGCCAGATTGACAAGCAGTTTCTGATTTGCAGTATATGC-
CTGGA 229
                  || | ||| | | ||||| || |||||| | |||
Db   2 CC---TACTG-GATTCGCCA---------------TC-ATTTTGCA-------
CACTG-- 32

Qy   230 ACGGTACAAGAATCCCAAGGTTCTCCCCTGTCTGCACACTTTCTGCGAGAGGTGCCT-
GC 288
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Db          33 ---------------CGAGGGGCT-CCGTGTGTGCGCCCTGTCT--------
TGTCTGGC 68

Qy         289
AGAACTACATTCCTGCCCACAGTTTAACCCTCTCCTGCCCAGTGTGCCGCCAGACCTCCA 348
              |   ||  ||| |||  ||||          ||  |||   ||||||||| ||
           ||||
Db          69 CGTCCT-CATCCCTTCCCCCA------------CC--CCC----TGCCGCCA---
CTCCG 106

Qy         349
TCCTGCCCGAGAAAGGGGTGGCCGCGCTCCAGAACAATTTCTTCATCACAAACCTGATGG 408
                 ||  |   ||    ||    |||||  |  ||              |   |||
           ||
Db         107 ACCCGCTCCCAAA----GTGGCTTCACAATAG---------------TCGGTCCT--
CGG 145

Qy         409 ACGTGCT-
GCAGCGAACTCCAGGCAGCAACGCTGAGGAGTCTTCCATCCTGGAGACAGTC 467
                  |||   || |||  | |||||   |  || || | |         |||  ||||||
           |
Db         146 CGGTGTAGGCTGCG--CACCAGGT--CCACACTTAAGCG----
AAATCAAGGAGACC--C 195

Qy         468
ACTGCTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCACGATGGGAATGTGATGGAA 527
                 || ||             ||  | |||  |||                      ||||
Db         196 CCTTCT--------------ACTTCTACCTT-------------
TGGG------------ 216

Qy         528 TTTTACTGCCAGTC-
CTGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAGCACGC 586
                 ||| |||  || || |  ||||              ||||              ||
           |
Db         217 -TTTGGTGC---TCAATGCGAAGCTGC-------------TGCA------------
ACTC 247

Qy         587
AGAGCACCCCACAGTTCCACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTCCAGGT 646
                 ||| ||| ||  || || ||||| |            ||| | ||||
Db         248 AGA-CACGCCTAAG-TCAACTCATG------------CAGAAAAAGG----------
AGA 283

Qy         647
CCAGCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCAGTTCATCTC 706
                 || |   || || ||  ||  ||||                      |||||
Db         284 AAAGTT--TTG--GTATACAAA--------------------
TGCTC------------- 306

Qy         707
TGAAATCATTCATCAGTTAACCAACCAAAAGGCCAGCATCGTGGATGACATTCATTCCAC 766
                 |||||   ||| ||||  |
Db         307 ------------TCAGT---CCAGCCAGA------------------------
CAC 323

Qy         767
CTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTATGGAATTGGA 826
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```

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Db        324 C------AAGC--------------------
CGAAAGGTTGTGCTG-------------- 343

Qy        827
GGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGATACTCTGCTCCAGGG 886
                      ||   ||  ||  |||| |        |  || ||| ||
          |||
Db        344 -----GCTGCAACCGAAAGATCAAGGACC--------------GGTA-
TCTTCTAAAGGC 383

Qy        887
GCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCCTCAACCATGGCACGGA 946
               | |||                |||  |        |||||  |
|
Db        384 ACTGGA------------------CAAATAC--------------------
TGGCATGAA 405

Qy        947
GACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAGCTGGCCGACCA 1006
              ||| |   ||||    |||| ||| |   ||      ||      ||||
Db        406 GACTG----CCT---------GAAG----TGTGC------CT------
GCTG-------- 428

Qy        1007
GGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCATCGTGGAAACCGAGGG 1066
              ||||  | |||        ||| ||                        |
||
Db        429 TGACTGTCGCTT-------GGGGGA----------------------------
GGTGG 451

Qy        1067 GCTGAAGAAGTCCATCCACAAC-
CTCGGGACGATCTTAACCACCAACGCCGTTGCCTCAG 1125
                ||         |||| || | |   |  | |||||| ||           ||| |
          |||
Db        452 GC--------TCCACCCTGTACACTAAAGCTAATCTTATCCT---------
TTGTCGCAG 494

Qy        1126
AGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCAGCCCATGTCCGTCA 1185
              ||||  |              ||| |||    || | |||          |||
Db        495 AGACTAT----------------CTGAGGC------TCTTTGG--------
TGT------ 518

Qy        1186
CCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAACGCCTACCTCACCG 1245
                                          |||| | |||
          ||
Db        519 --------------------AACGGGAAACTG-------------------------
CG 532

Qy        1246
CCGAACTGAGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCCTGGACAACAAGAACG 1305
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CCTG------------- 539

Qy        1306
GCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTACCCTGTCTCTGAGAC 1365
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TAGTA---------------------------------------- 544


Qy      1366
TCTATGACCAGCACATCCGAGGCAGCCCGTTTAAGCTGAAAGTGATCCGATCCGCTGA-T 1424
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Db      545 ---------AGCTCATCC----CTGCC--TTTGAGATG---
GTGATGCGTGCCAAGGACA 586


Qy      1425
GTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGGAGCGGCCACGTC 1484
              ||| | |||||        ||
Db      587 ATGTTTACCACC----------
TG---------------------------------- 600


Qy      1485
AAGCAGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAACGAAAAGAGAAT 1544
                 || ||| |              |||||| ||||  || |
Db      601 -----GACTGCTTT--------------GCATGT-
CAGCTTTGTA-------------- 625


Qy      1545
CCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAAATAAAGGAGAGTTT 1604
                ||| |||         ||| | || |  |||              |
||| 
Db         626 ---ATCAGAGA----------TTTTGTGTTGGAGACAA------------------
ATTTT 655


Qy      1605 ACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGATATTAATTG-
CAGACAGTAA 1663
                 |   ||  ||               |||   | |||  |  ||| ||||| |
|
Db         656 TC----CTAAAG------------------AATAACATGATCCT--
TTGCCAGACGG--A 689


Qy      1664
CAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTCGTTTTGGCATACG 1723
                | ||         | || ||| ||||| |   |||
Db         690 CTAC--------GAGGAAGGTTT--
AATGAAAGAAGGTT--------------------- 718


Qy      1724
GGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTACATCCCAGTGGGGA 1783
                 | | | || ||  |||| | |  | | |||           || |||| |  |
|
Db         719 ---ATGCACCCCAGGTTCGCTG-ATCTATCAACA-----------
TCACCCCATTAAGAA 763


Qy      1784 CATA-
ATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCTCCGATGGGAAAT 1842
               | | | | |||| |   ||| |          ||     |||| | ||||    | |
|| 
Db         764 TACAGAGCACTAC--ATTCTTTTA---------TC----
TTTTTTGCTCCACATGTACAT 808


Qy      1843
TTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTTCTGTGGACCGCA 1902
               || ||||| ||||||            ||| | |  | ||| ||
Db         809 -------AAGAATTGACACAGGAA------------CCTACTGAATAGC-
GTAGATATAG 848
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```
Qy        1903
ATGGGCACATTATTGTTGTGGACAACAAGGCGTGCTGCGTGTTTATCTTCCAGCCAAACG 1962
                 ||||    |  |  |||| |  |||||| ||||     ||||
Db        849 GAAGGCAGGATGGTTATATGGAATAAAAGGCGGACTGC------
ATCT------------ 890


Qy        1963
GGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGTTTGCAGGTCCCC 2022
                 |  | ||||           |||||||||| ||||| |
||||
Db        891 -GTATGTAGT--------------------GAAATTG-------------------
CCCC 910


Qy        2023 ATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATTTCCATAAT---
CATT 2079
                 | ||  |||  | |||          |  |||||||||| |||      |||| ||
|
Db        911 AGTT--CAGAGTTGAAT-----------
GTTTATTATTAAAGAAAAAAGTAATGTACA-T 956


Qy        2080
CTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGGCTCAAATGGAGAAG 2139
                 || | | |||  |  |||| |||   ||||  ||| ||||  ||| | |||  |||
Db        957 ATGGCTGGATTTTTTTGCTTGC-----TATTC--GTT----
TTTGTGTCACTTGG----- 1000


Qy        2140 GAAATGGGCAGTTTAATGCTCCAACAGGTGTA-
GCAGTGGATTCAAATGGAAACATCATT 2198
                 ||| |  ||||| |  |  ||  ||||   | || |||       | || ||
||
Db        1001 --CATGAGATGTTTATT--TTGGACTATTGTATATAATGTATT------GTAATAT--
TT 1048


Qy        2199 GTGGCCGACTGGGGAAAACAGCAG-
GATCCAGGTTTTTGATGGGAGTGGATCATTTTTGTC 2257
                 |  ||       ||| | |||  |  ||| ||| |  ||        | |||||
|||
Db        1049 GAAGC-----------ACAAATGTAATACAGTTTTATTGTG-----
TTACCATTTGTGTT 1092


Qy        2258
CTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCCTGGCCCTAACTTCAGA 2317
                 |         ||| ||||       ||| ||
Db        1093 C----------CATTTGCT-------
TCTTTG-------------------------- 1107


Qy        2318 TGGTCATGTTGTGGTTGCAGACTCTGG--
AAATCACTGTTTCAAAGTCTATCGATACTTA 2375
                 | | |||||| | |  ||||| |||||                          |
|||||
Db        1108 ---------TATTGTTGCA---TTTAGTACAATCAGTGTTT------------
AAACTTA 1143


Qy        2376
CAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCACTATAAACTGGAATGGA 2435
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|
Db        1144 CTGTAT--------------ATTTATGCTTTC------------------------
TGTA 1165
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Qy        2436
TTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCGAGAAGGAATCATTGGTGA 2495
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||||
Db        1166 TTT-----------ACCAG-------CTA----TTTTA----------------
AATGA 1186

Qy        2496
ACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACTTATCCAATTTCTG 2555
              |        ||||||  |||  |||||   ||   ||  || ||
Db        1187 GC--------------------TGTAAC--TTTC--
TAGTAAAGAATT----------- 1210

Qy        2556
TATTTCACCTTTAGGGTTAAAAAAAAACTCTTCTACTGAATCTATAAAAACTGCAGTTTTA 2615
                     |  ||| |||  ||| ||  |
Db        1211 ---------------GAAAAGCAAATCTC-
ACTAATGATAC------------------- 1235

Qy        2616
CATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATTTTGCAAATCA 2675
                                       ||||       ||| ||||        ||||
||
Db        1236 -------------------------ACAG-------ATAGATAAA--------
GCAAGTCT 1256

Qy        2676
AACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGTGAATGGTAGC 2735
              | || ||| |||||||| |||  |  ||||| | |    | | || || |
|
Db        1257 ATCA-ACA-TTAAAAATACTA--
AAAAATAAAGACACACACAGAGCATTTTAGTGACATC 1312

Qy        2736
TTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAAATCTATTGTAGTTATATACTTCA 2795
                       ||| | | || |||   | | ||||| |||   |||
Db        1313 ----------CACTACTTATTGCCGCTATGAGTTAGAGTCTATCAGTGTT-----
CTTGT 1357

Qy        2796 TTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCTCACTTTTACAGTAGG-
TATTA 2854
              | |||||       |||          ||| ||| || ||
|
Db        1358 TATAACC------------CCCT--------------------
ATTTTCAGGGGGTTAAAA 1386

Qy        2855
CTCTTGTGACATTTTTTTGGTTATCAACAACTAAATATAAATTACTTTGGAAAAAGTAAG 2914
                     ||         |  || || ||| | ||||  || ||
|||
Db        1387 ATC---------------AGCTTTAAAAAAAATACATAAAAATTTCAT-------
CTTAAA 1424

Qy        2915
GCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCCCTCTGGAGTTCAGAACTTAAGT 2974
              ||  ||| ||  |||||    |  || ||| ||| ||  || |||  |  | ||||| |
Db        1425 GC--ACTTTCATTTT-ATACCAACG-TGAAAAG-TGCCATTTTTAG--
AATAACTTTA-A 1476

Qy        2975
```

```
ATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGATCCTTTTTTGTGTGTTCTTT 3034
           | |    || |||   ||||||              ||  ||||||||||| |||||  ||
|
Db     1477 AGCTTAACAGGTTT-----CCTTT-----------TAATATCCTTTTTT-
TGTGTGCTCT 1519


Qy      3035
TCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCTTCAGGGAAACCTGA 3094
           | ||    |  |  ||||   |||| |             | ||| |||||  | |||
Db     1520 TTACTTACACAATGGCT----TTGTTT------------
TGCTTTTTCAGCCACACC--- 1560


Qy      3095
AATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTTGGGAAACAAACT 3154
                        ||||                |   | | |  | || |||||| | ||
Db     1561 -----------CCTT--------------ATGTGAACTAGTGCC-
TTTGGGTATCA---- 1590


Qy      3155
GCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGTTAGTCATGTTTTAT 3214
                |||                       ||| |  || |  ||||
||||
Db     1591 ----CGTAA--------------------AATTTTTTCCAAAGGGTTA------
CTTTAA 1620


Qy      3215
GTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTTCCTGAAAGCGAAAGCTTTACCTC 3274
                | | |||| ||||            |  |  ||      | ||| || |  || |
||
Db     1621 AAATC-TGTTACCACA---------
ATTATGAGATGATTTTTAAGTGATAAATTAAACTT 1670


Qy      3275
CTGCAAATGTCAGCACATGTAGTAGGACACCAGTATCCTAGGACAGAGAGCCATAAGTAG 3334
              ||               |  | |||| |            || ||
|
Db     1671 CT------------TCTTGTATAA----------
ATTCT--------------------G 1688


Qy      3335
CCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGTGATTGATTAATGATTCCCCCTTA 3394
             |||     || ||             || |  || |                        | ||
Db     1689 CCC-----AGATCT------------------------------------
CTCC--- 1701


Qy      3395
GAAAGCAAGTGTTACCAAAGTTGTGTTATCTTGAAAGCATTACAGGTAAGGGCATGTTAT 3454
                             || | || || |         |    ||| ||
||||
Db     1702 -------------ACAAGAGCTGAG-------GGTTTCATAACT------------
TTAT 1729


Qy      3455
GGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGACTATGTATACATGATTA 3514
                || | || ||| |          |||| || |||
||||
Db     1730 GG--CTTAATAAATGTAT----------------------GACACTG---
AAAAGATTT 1761


Qy      3515
```

```
GGGTAAGATAGAATGTATTATATATATATATATATATACACACACACATATATATAGCTG 3574
              |  ||
||
Db     1762 GAGTG------------------------------------------------
TG 1768


Qy      3575
AATCTTTGGTGTATTGAAATAGGCAGCACTCTGAAAGACAGAAGCTTCGTCCAGCCACTC 3634
               |||||                         ||||||
||||
Db     1769 AATCT-----------------------ACTGAAA------------------
TCACTA 1786


Qy      3635
TTCAGCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGTGGAGCAAGCCCTAAAGCA 3694
         |  |||||                    || |||| |  |  | ||
Db     1787 TAATGCACA-----------------
TTGAAGCTATGATGGT------------------ 1811


Qy      3695
GATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCTTTTAGTCAGAAAATGGCCT 3754
          |||| | | |                      | ||| ||||| || ||
Db     1812 -ATTTGAGTAGT--------------------
GAGGTTACTTTTGATCGGA--------- 1841


Qy      3755
TCTGTGCTTTCAAAAAAAAAACAAAAAAAAAACCACACACACACATAAAAAACCCAACAG 3814
               ||            |||| ||                | |||| ||
Db     1842 -----GC------------AACATAAT-------------
GCTCATAGAA---------- 1861


Qy      3815
GTCAAAATAAAAGTTGAACTTGAGTTACATTTAATTTAAATATAAATGCATTTTGAGAAA 3874
                   ||    |    ||  |||
||||||
Db     1862 -TC----TTCTAGAAGAA------------------------------------
GAGAAA 1880


Qy      3875
TGTTAAGAACAATTTAGTCAATCGTTCATCTGTCATTGGTACTGTAAAATAAGCTGTGGT 3934
                                      ||  || | || |  | || | |||| |
Db     1881 --------------------------------CAAAGGGATTG-
ATAAAATGCTGAGAA 1906


Qy      3935 CTATTTCCACTGTTTAATTTTCTACTCAGT-
TCTACCAAATAGGATGTCATGTTTGACAT 3993
              ||| |   |  | | | ||||||      || | ||||
||||||
Db     1907 CTAGTG--ATTATATATTTTTCT-----GTATTTACC------------------
TGACAT 1942


Qy      3994
TTTTGATAGTGACTTTGGGGTCTTCTTCACTGAAAGCACCTTAGAACTGTACTATAAGAA 4053
               || |            |||                        | ||| | | |||
|
Db     1943 TTAT---------TTT----------------------------
AATGTTCAAAAAGTA 1964


Qy      4054
AACATTTCCCCTATGTATAATTATATGAATGTGATGTTTATTGCTTATTAATTTATAATT 4113
```

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                       ||||  ||                    |  |  ||||||  |  ||  ||    |  |||    |
                                                                                       ||
Db     1965 AACACTT-----------------TAAGTTTGATGTGTTTTACTCTCTCATTGTT--
TT 2004

Qy     4114
CAGTCATTCTCTATATAGGACTTCTTAAAATTTAGAAGGGAAATCTAGCTACTTCAAATT 4173
            |||  |||         || |  || | ||                          |||  |||
Db     2005 AAGTAATT----------GCCAACTCAGAA-------------------
TACATCA---- 2031

Qy     4174
GTCTGTTAAATTTATTATGCCCAAATCAACCTCTGAAAAAAGGTTTTTCCAGGAAGATTT 4233
                    || ||| |              ||||||  || ||||||
Db     2032 -----------TTCTTAGG-------------CTGAAATTT-
GTCTTTCCA--------- 2057

Qy     4234
ACATTTAGGTTTAATATTTTTTTAGTTAGGTAGAGTTTTAAAAAATACTTGAGCCTGTCC 4293
                        |||||||   ||||      ||| |  ||||     ||| |
Db     2058 -----------------TTTTTTA---AGGTG-------AAATAGTACT---ACCT-
TAC 2086

Qy     4294 GTGATAAAGCTATAAAATTCAATAACTTTTTAGAATGTTAAATGA-
AGACACTGTTTCCT 4352
            |||||  |||      |||      |  |  |  |||||  |  |||| |  || |  || |
                                                                              |
Db     2087 GTGAT--AGCATACAAAGAAGAAAGC--
TCTAGAAAGAGAAATTATGGAGAATGATTATT 2142

Qy     4353 AACATCAGTGAGATACATCTTTGAATTTAAACAT----
TCATATTTACTGAGTACCTACT 4408
             | ||           ||||  |  |  |  |  ||     ||    |  |  |  ||||  |
Db     2143 TAAAT-------
TACAATTAAGGAAATGAGAATATGATCCCCTCTTCCGAGTTGC---- 2190

Qy     4409 AGGTACCAAGTACT--
CTTTTAGGCACTGGAAATACAGTGATGGACAAAACAGGTAAAAA 4466
                      |||   |||   ||| |  ||  |
Db     2191 -----
CCACAAACTTGCTTCTTTGCTTT------------------------------- 2213

Qy     4467
ATCGCTGCCCCCTCAGAGCTGACATTCTGGGGTGGGAATTTCATTTTGCCACGTACTAAC 4526
                 |||  ||       ||| ||          ||| | ||||   ||  |
            ||||
Db     2214 -----TGCTCC-------CTGTAAT---------AGAACTACTTTTCAACAAAT-
CTAA- 2250

Qy     4527
GTTCTGCACAAAAGACAGGCTAGACTCTTGTCTAGATTGTTTAAAAGAAACTTTTCAAAT 4586
             || ||||||         ||| || |||  | |                         ||||||
Db     2251 -TTTTGCAC--------GGC---ACCGTTAACCATA---------------
TTTTCAC-- 2281

Qy     4587
TGGTTACATTAATTTTAGTTTATTTTCACAAGTAAAAATGGCTTTTTATTTAGATTCTTT 4646
                     ||||  ||  |||||                  |||| ||||   |||    ||
            |||
```

```
Db       2282  ----TACAGCAAACTTAGT--------------
GCTATGGGTTTTCTTTTTCTTTGTTT 2322

Qy       4647
CTGTCCCAGGCTGTTGATCTTAAAACTAGTTGATTTAAAGAGTTTTTTTGCACAACATTT 4706
                  |  ||       |||||    |||  ||   ||    ||
              |||||||||
Db       2323  TTTTC--------TTGATC-----ACTTGT--ATAGGAA------------
ACAACATTT 2355

Qy       4707  --CAATTATATTTGTGAACTTAGAAATTAACTTACAATCTAACCAGCCATCATAT-
CATA 4763
                    ||  |  ||||||    |  ||        ||  |  |  ||  |||  ||||
|||
Db       2356  TCCAGTGTTATTTG----CATA----------
TATATTTGTCCTTCCAATATATGCATT 2401

Qy       4764  TCCTATCAGGCTAGATATCTCAATAGTAGA-CTGAATAC-------
AAAGCTAATTTTTT 4815
                  |  ||       ||  |  |||  || |  ||||||| |          ||  ||    |
||
Db       2402  ACAGAT-------
GAAAATTAAATGTTATACCTGAATTCTTGGGTTGGGGCCAAAATATT 2454

Qy       4816  TTACATGTCAATATTGGCACAAACTGGAATGAAAGAATAGTTTGATTCAGACC--
TGCTC 4873
                  |  ||  ||||  ||        ||||  || |         |||| ||  |  |
|||
Db       2455  AAGC-TGAAAATAATG-------CTGGTGTGGA-------
TTTGTTTTAAAACAAAGCTT 2499

Qy       4874  CACTATGTGTTGCTAAAACACATGCTATGAGCA-
CTCGAGGAAACACTATATTTTTTCCA 4932
                  |  |||||         ||||||| ||| | | || |        | || |  |||||
Db       2500  TATTATG-----------AACATGC-ATGTGAATCTGGATATTGC-
CTCTTATTTTTAAG 2546

Qy       4933
AAAAATATGTGATTATATATGTTAAAGTATAGATAACATTTCACACTTGGATACATATGT 4992
              ||||       ||  ||  |       |||||                     ||
|||||||
Db       2547  AAAA-----TGGTTCTGTG---AAAAGT--------------------
GAATGATATGT 2577

Qy       4993  GCATTTAC-
TGTATTTCTTGGTAAGCATATTTTTGGGGGAAAGTGCTGCTGATATGATAC 5051
                  ||| |   |  ||| ||||  |                    ||| |||  |   | |  |
|
Db       2578  ATTTTTCCAAATGCTTCATGGTTAG---------------GAGT-CTTC----
AAGTTCC 2617

Qy       5052
AAGTAGACAAAATTTAAATGAAATTTTGTCACATTCTATGGAAAATGGTTTCTGGTAAAC 5111
                  |  ||    |  | ||||  |                          |  ||
||
Db       2618  ATGTTCCCCAGATTTGA----------------------------------
GATATAC 2641

Qy       5112  T-
GAGAAGGATATTAAAATAAGTGGCTTTTTTCTGGGCTACCATTATTGTTTGATTTCTC 5170
```

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                     |  |||| || ||| || |||| ||| |||   |||| |||  |   |      ||
|
Db      2642 TAAAGAAAGAAATTCAA--AAGTAGCTATTT--GGGGC--
CCACAAAAATAACTATTATT 2695

Qy      5171 TTTGTCAAGTGTATAGAACCTGTCA-
TACATTCATGATAAGTAGCACTGAAAAATTACTC 5229
                     || | |        |||| ||| || |  ||||||| || |      |  | || |
Db      2696 TTAGCC------TTAGAGCCTTACACTTGTTTCATGAAGAGAA------
AGGACTTGCAT 2743

Qy      5230 ATTCAAATTTCCC----
CTGGGCACGTAAGGCAAAATATTGCCGGTTGGGATTTCAAGGT 5285
                     |  |||| |  |    |  | ||| || ||||||| || |||      ||
|
Db      2744 AACCAAAATAAACAAAGCAAGACAAATTA---AAAATAT-----GTGGGGG---
AGAGAT 2792

Qy      5286
CAGTGACGACGCATTTCCTCCCAGTACAGACCCCCCAGCCCCCCTTGCTGGACATGGGGA 5345
                     |||||| |   ||| ||| |  | ||| |  |||||| ||     ||
Db      2793 CAGTGAAAAGTGGTTT--TCTTAATGCAGCCCTGCTGGTCCCCATT----
AAC------- 2839

Qy      5346
GGCAGAGAGTCACTTGACCATCCAGAAATACATGACTACAAGTCCTTTATGACTGTTTGC 5405
                     | | ||||| ||         ||||| | || |    |||| |
|||
Db      2840 -------AATTGCTTGAAATTC-------ACATGGATGTAA---AATTATAA----
TTGT 2878

Qy      5406
CATTTTTTTAATGGTACTTAGTATTTTGATCAAACTTTAGTCTCCAGAACTAAACAAGT 5465
                     ||         || |||| |  ||||| ||||     ||  |||
Db      2879 CA-----------GGATCTTATTCAGATGATCT---TTTA------
AGGTTTAA------ 2912

Qy      5466
CCCTAAGTTTCCTTATTTTAATTTACTGTGACTAGATTTGAAGCAAATAAATACTCCAGA 5525
                     ||   ||| ||| ||| || || || | | || | |      |   |||||
Db      2913 --CTGGTTTTGCTTTTGTTTATCTA-TATGTCAAAAT----- 2956

Qy      5526
TCCATGCAGCTAGAACACACACTTGCTTCCACTACTAAATATACAGGGTATGTCCTAACATG 5585
                     ||        ||||| ||||  ||   || |||
| |
Db      2957 ----TG-----GGAACAAACTTCTCTCAGCTTCT------------------------
TG 2983

Qy      5586
GAGTTAACTGGAATAGCAGTACACTAGCAAGTATCTGTGAATCCTTAGCACTGACGGGTT 5645
                     ||||                    |  || | |   ||||||| |||||  |
Db      2984 AAGTT-------------GTTC----------AACT----
ATCCTTGCCACTGGAAG--- 3013

Qy      5646
AACAGAAATGCTTTGGTAATACCTACTTAGTTAATTGGAGGAAGTAGTAAATAAACATTA 5705
                     |  || |  | |  | |||      |  || ||| |  | ||            ||||
|
```

```
Db       3014 ACCAAACAAGGTTT-----TCACTGCTTTTTCTTTT-----------------
ACATAA 3050

Qy       5706 GGTAATCTGCAGATTACTTCAAATGGGAAAAATCTTTTTG-
TAGACTCTATAGTACCCTC 5764
              ||  |||  |||| ||| |||        |||||| || | | | ||| |
|
Db       3051 --TATGCTGAGAATTATTTCTTATG--------
CTTTTTACTACAAACAAAATTACTCAC 3100

Qy       5765 TCTATTCACTAGCTTCTGAA--
AAGGGAGGAGTATTTTTAGTTTGACAATTTAATAATTT 5822
                     || | || |    | |||| | | |||||| || |
|||
Db       3101 --------CTGGATTAAAGATTAAGGCCTTAATCTGTTTAGATTATC----------
TTT 3142

Qy       5823
AAAAACAAGACATCTCCAGGTAGGAAAAAATGAAAGCTATTTCATGCAAACATTATCTAA 5882
              |             ||||||          |||||||        || ||
||
Db       3143 A----------ATCTCC------------ATGAAA------TCGTG------------
AA 3162

Qy       5883
TTTAGCTTAAAAGTGAAAGTGGTAATACTGTTGGTTTCTGTAAATGTTGCAGGGTTTTAA 5942
                    | ||    | ||| | |||| |    |||| ||
Db       3163 ATAAG---ACAAG-
AATAGTGTTTCAGCTGTAGG------------------------ 3192

Qy       5943
ACTTTATAATTACTTTAATATTTTTGATAACTAGAAATCTAGTATTGCCATAAAGGAAAC 6002
               | ||    |||||                                       |
|
Db       3193 CCATT----TTAC--------------------------------------------
AGC 3204

Qy       6003
TAAGTGCCCATCAAAGATTTGTTTGGTATAAATAAAGAATTATTTGTTTTGTTTTCAATG 6062
              |||| ||||||| ||    ||||             || ||| ||| ||
||
Db       3205 TAATTGCCCATAAA----TTGT-------------AGCATTTATTGACCTG-----
AAGT 3242

Qy       6063 ACAGTAAGCTACAAATCATGA-
TGCTTAAAAACTTTCTAAAGATGAATTGTGTGGCAGTG 6121
              ||  ||||||    || ||| | ||| |   |   |||||||| || ||
Db       3243 AC--TAAGCTAATTGTCTTGACTACTCAAAGCC---C-----CTGAATTGT-
TGTCA--- 3288

Qy       6122
ATTGGTCTGTTTGTGGAGAATGTATGAAAGCTATTAATATTCTAGAATAGATTAATAAAT 6181
              | |   | |||||| ||| | ||| | |                    | |
|
Db       3289 ACTTTCCCCTTTGTG----TTGTGT---AGCCCTAA-----------------
CGTCATT 3324

Qy       6182
TGGCTATGTTGTTCCAATGAATGTACAGCACTTCCATTAACTTTTGAAAGCAACACAGCC 6241
              | ||| ||||| ||  |||            | |||| ||            ||||
||
```

```
Db      3325 TAGCT-TGTTG-TCTGATG-----------CCTCCAGTAG-----------
GACACCTCC 3360

Qy      6242
TTAAACTCAATGCTTTTGCTTTATGACATGGGAATGTTCTGTCATCAATGGAGTGTATTC 6301
                    |     |||| ||| |||    | ||| | ||
Db      3361 GATGGAGC------
TTTGATTTCTGAGCAGCGAAAGCTC--------------------- 3393

Qy      6302
TTGTAATAGAATTCTTTATATCGTTCTCAATTCTATAGACTTTCAAGCCTATGTATGAAT 6361
                      ||| | | |  |||    |||| ||    |||||||
Db      3394 ---------CCTTCCTAAGATGCATCTCGC----ATAGGCT-----
GCCTATG------- 3428

Qy      6362
ATGAAGGGGTTTTTTTTTTTTTGCTTTGTTTTCTTTTTAGATTTTGTACATTCCATCTTT 6421
             |||||||           | || |          | || |||| |
Db      3429 ATGAAGG--------------ACCGTG----CACC----------
TCCACTCCAAC--- 3456

Qy      6422 ATAGGTCTGT-
TTCATATGTTTTATGTATAGAACACTAAGTCTTGCACTCTCTGACATTG 6480
             | || ||| || | ||        || || || ||| | | ||  ||
||
Db      3457 AGAGTGCTGAGTTTAAAAGTT----------GAC-CTGTGT-TTGTAATTTC--
ACTTTC 3502

Qy      6481 ATACTGATATATTCTCGTCATTTG--
TTCTTTTATGAATCAAAATGTTGACTGCCTATTT 6538
             || || | ||     || || |||||| |  || ||||           |
Db      3503 ATCTTGCTTAATAAATATCTGCTGGATTCTTTCAAAAAAAAAAA------------
AAAA 3550

Qy      6539 AAAGAAAAGAATGAACGCTGTGCATCAAAGTGTTTGTATGTTCGTAGCTACA 6590
             ||| |||| || || |    || ||        | || |||| |||| ||
Db      3551 AAAAAAAAAAAAAAAG----GCCACA---------TGTGCTCG-AGCTGCA 3588


RESULT 2
US-10-478-914-21/c
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;  LENGTH: 3589
;  TYPE: DNA
```

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  Query Match           21.1%;  Score 8078;  DB 1;  Length 3589;
  Best Local Similarity   41.5%;  Pred. No. 0;
  Matches 2220;  Conservative   0;  Mismatches 1291;  Indels 1844;
Gaps  297;

Qy       639
CTCCAGGTCCAGCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCAG 698
         || ||| || |||          ||| || ||    |  || | | ||
Db      3589 CTGCAGCTCGAGC-----------ACATGTGG---
CCTTTTTTTTTTTTTTTTTTTTTT 3545

Qy       699 TTCATCTCTGAAATCATTCATCAG---
TTAACCAACCAAAAGGCCAGCATCGTGGATGAC 755
         ||  | | ||||| || || |||  || |  || ||| | |  ||
|||
Db      3544 TTTTTTTTTGAAAGAATCCAGCAGATATTTATTAAGCAAGATGAAAG---------
TGAA 3494

Qy       756
ATTCATTCCACCTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTT 815
         |||      |||       || ||       ||||| ||  | |||       ||
||
Db      3493 ATTACAAACAC--------AGGTC-----AACTTTTAAACTCAGCA--------CT-
CTG 3456

Qy       816
ATGGAATTGGAGGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGATACT 875
         ||||  |||||| || |  ||| | || |   ||| |  || ||  ||
Db      3455 TTGGAG-TGGAGGTGCACGGT--CCTTCATCATAGG------
CAGCCTATGCGAGA---- 3409

Qy       876
CTGCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCCTCAAC 935
         ||| |  || ||| |||| ||  |||||| |  ||| | |||
|
Db      3408 -TGCATCTTAGGAAGG-GAGCTTT---CGCTGCTCAGAAATCAAAGC-----------
TC 3365

Qy       936
CATGGCACGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAG 995
         |||   ||||||    ||||||||||| | | |||    | | ||||| ||
||
Db      3364 CAT----CGGAGGT----GTCCTACTGGAG--GCATCAGA----
CAACAAGCTAAATGA- 3320

Qy       996
CTGGCCGACCAGGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCATCGTG 1055
         ||   ||| || | |   |||| |  |||| |   || |  | ||  | |||
Db      3319 -----CGT-TAGGGCTACAC--AACACAAAGGGGAAAGTTGACAAC---
AATTC------ 3277

Qy      1056 GAAACCGAGGGGC-
TGAAGAAGTCCATCCACAACCTCGGGACGATCTTAACCACCAACGC 1114
         |||||| |  || |||| |             ||| ||
Db      3276 -------AGGGGCTTTGAGTAGTCAA-------------
GACAAT-------------- 3252
```

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Qy        1115
CGTTGCCTCAGAGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCAGCC 1174
               | ||  |                              ||  | ||| ||  || ||
Db        3251 --TAGCTT--------------------------------AGTACTTCA--
GGTCAATA 3229


Qy        1175
CATGTCCGTCACCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAACGC 1234
               |||   |  ||    |         | ||  |||      |  |||||||  ||
||
Db        3228 AATG--CTACAATTT-------ATGGGCAA------TTAGCTGTAAAATG--------
GC 3192


Qy        1235
CTACCTCACCGCCGAACTGAGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCCTGGA 1294
               ||||            |  ||||   | |                        ||  ||
|
Db        3191 CTAC----------AGCTGA--AACACT------------------------
ATTCTTGT 3168


Qy        1295
CAACAAGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTACCCT 1354
               |                      || || || | ||       || || ||| |  |
Db        3167 C---------------------TTATTTCACGATTTC-------
ATGGAGATTAAA---- 3140


Qy        1355
GTCTCTGAGACTCTATGACCAGCACATCCGAGGCAGCCCGTTTAAGCTGAAAGTGATCCG 1414
               || |  ||||            | | |   || | |  |||| ||          |
|||
Db        3139 ------GATAATCTA----------AACAGATTAAGGCC--TTAATCT----
TTAATCC- 3103


Qy        1415
ATCCGCTGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGGAG 1474
                                       ||| ||  |           ||   ||
Db        3102 ---------------------------AGGTGAGTA-------
ATTTTGTT--------- 3086


Qy        1475 CGGCCACGTCAAGCAGAAAGC-
TGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAAC 1533
                               |  || |||   | |||    |  | | ||||| |    | |
|||||
Db        3085 --------TGTAGTAAAAAGCATAAGAAATAATTCTC-
AGCATATTATGTAAAAGAAAAA 3035


Qy        1534
GAAAAGAGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAAATA 1593
               |   || |||| | | |       | |||| || |
Db        3034 G--CAGTGAAAACCTT--------GTTTGGTCTTCC-
AGTGG-----------------C 3003


Qy        1594
AAGGAGAGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGATATTAATTG 1653
               ||||| |||| | | ||||     | ||||            || |||  ||
Db        3002 AAGGATAGTTGA-ACAACTTCA---AGAAGCT-------------
GAGAGAAGTT----- 2965


Qy        1654
CAGACAGTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTCGTT 1713
```

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                                       |||  |                    |||  ||  |  ||||
  ||
Db      2964  -------------------TGTTC-------------------CCAATTTACAAGT-
ATT 2944

Qy      1714
TTGGCATACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTACATC 1773
             |||  ||||  |||            |  |    |||   |            |  ||   |
  |
Db      2943  TTGACATATAGATA-------------AACAAAAGCAAAAC----------
CAGTTAAAC 2907

Qy      1774
CCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCTCCG 1833
                      |          |  |  |||||  |  ||  |||   |  |        |  |  |||||  |
  |||
Db      2906  CTT------AAAAGATCAT--CTGAATAAGATCCTGAC--AATTATAATTTT-
ACATCC- 2859

Qy      1834
ATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTTCTG 1893
             |||  |||  |||            |  |  |||||   |||
Db      2858  ATGTGAATTTCAAG----CAATT-----------
GTTAATGGGGACCA------------ 2826

Qy      1894  TGGACCGCAATGGGC-
ACATTATTGTTGTGGACAACAAGGCGTGCTGCGTGTTTATCTTC 1952
                      |||   ||||   |||||          ||  |||  |
Db      2825  ------GCA--GGGCTGCATTA-------AGAAAACCA------------------
CTTT 2799

Qy      1953
CAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGTTT 2012
                      |  |  |           ||  ||
Db      2798  TCACTGATC----------
TCTCCC--------------------------------- 2784

Qy      2013
GCAGGTCCCCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATTTCCAT 2072
                      ||  |||  |             ||  |||    |  |      |  |  |
  ||
Db      2783  ------CCACATATT-----TTTAATTTGTCTTGCTTTGTTTATTTT---
GGTTATGCAA 2738

Qy      2073
AATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGGCTCAAAT 2132
                      |  ||||  |              |||  |||       ||  ||      ||  |||||
Db      2737  GTCCTTTCTCT------------TCATGAA-------ACAAGT----
GTAAGGCTC---- 2705

Qy      2133
GGAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAATGGAAAC 2192
                      |||  |||  ||       ||  |||    ||
Db      2704  --------------------TAAGGCTAAAA------
TAATAGTTATTT----------- 2682

Qy      2193
ATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAGTGGATCATTT 2252
                      ||||||  |   |           |||  |||       |  |        ||||||
```

```
                |||| 
Db      2681 ----TTGTGGGCCCC-----AAATAGC----TAC----TTTTGA------------
ATTT 2651

Qy      2253 TTGTCCTACAT---
TAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCCTGGCCCTA 2309
                      |  || |    |    |  || ||||| ||  |     |||| |   | | | ||
                ||||
Db      2650 CTTTCTTTAGTATATCTCAAATCTGGGGAAC------ATGGAACTTGAAGACT---
CCTA 2600

Qy      2310 ACTTCAGATGGTCATGTTG----TGGTTGCAGACTCTGGAAATCACTGTTTCAAAG-
TCT 2364
                      ||            |||| |    ||| |   | |  | ||||| ||||| ||
                |
Db      2599 AC----------CATGAAGCATTTGGAAAAATAC-ATATCATTCACT-
TTTCACAGAACC 2552

Qy      2365 ATCGATACTTACAGTAATGGTGGGCAGGTGGATA-CCCGCTTC-
CATGGTCTTGCACTAT 2422
                      ||   | ||||| |  |||    ||||     ||| |  | | ||| |||| | || |
                ||
Db      2551 AT--TTTCTTAAA--AATAAGAGGCA-----ATATCCAGATTCACATG--CATGTTC-
AT 2504

Qy      2423
AAACTGGAATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCAGAAG 2482
                      ||   |  | ||| ||||||  || |    ||| | |      || || || ||| |  |||
Db      2503 AATAAAGCTTTGTTTT---AAAACAAATCCA------CACCAGCATTATTTT--
CAGCTT 2455

Qy      2483
GAATCATTGGTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACT 2542
                      |   |||| |   |  ||||| | ||| |  | ||||| ||                    |
                |
Db      2454 AATATTTTGGC-CCCAACCCAAG---AATTCAG-GTATAACATTT------------
AAT 2412

Qy      2543 TATCCAATTTCTGTATTTCACCTTTAGG--
GTTAAAAAAAACTCTTCTACTGAATCTATA 2600
                      | ||    ||||| | || |    | || |  |||| |  | | | | | ||
                |
Db      2411 TTTC----
ATCTGTAATGCATATATTGGAAGGACAAAATATATATGCAAATAACACTGGA 2356

Qy      2601 AAAACTGCAGTTT--TACATCTGTGAAC----
TATGGCTTAAGGGACAGGATTTATGTAG 2654
                      |||  ||  ||||  |    |  | ||| |       ||| | || |
                |||
Db      2355 AAA--
TGTTGTTTCCTATACAAGTGATCAAGAAAAAAACAAAGAAAAAGAAAACCCATAG 2298

Qy      2655 CTAAACTAATTTTGC--
AAATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTAT 2712
                      |   ||||| ||||| | | ||      | |        | | ||| | ||
                ||
Db      2297 C---ACTAAGTTTGCTGTAGTGAAAATATGGTTAACGGTGCCGTGCAAAATTAG----
AT 2245

Qy      2713 TCGTTAATCCTGTGAATGGTAG--
```

```
CTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACA 2770
  | ||         |||| |||| || || ||   ||||||||||   | ||
||
Db      2244 TTGT--------TGAAAAGTAGTTCTATTACAGGGAG----CAAAAGCAA---
AGAAGCA 2200


Qy      2771
AAATCTATTGTAGTTATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTA 2830
             |    ||||  |       | |         || |||   |||| ||| |
|
Db      2199 AG----TTTGTGG------GCAAC------------TCGGAAG----
AGGGGATCATAT- 2167


Qy      2831 ACCTCACTTTTACAGTAGGTATTACTCTTGTGACATTTTTTTGGTTATCA-
ACAACTAAA 2889
                     || | ||||      ||| |||| |    |||  | |||| | |
||
Db      2166 ---TCTCATTTCC--------TTA--ATTGTAA-----
TTTAAATAATCATTCTCCATAA 2125


Qy      2890
TATAAATTACTTTGGAAAAAGTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCA 2949
             || |  || ||           || ||| |||||          || || |
Db      2124 TTTCTCTTTC-----------TAGAGCTTTCTT---------------
CTTTGTAT---- 2095


Qy      2950 GCCCTCTGGAGTTCAGAACTTAAGTATCAGTGCAAATTTCTCAACCTTTCTG---
GGTTA 3006
             || ||       || ||||   ||| | |||||  |||||           ||
|
Db      2094 GCTATC-----------ACGTAAGGT--AGTAC-TATTTC---
ACCTTAAAAAATGGAAA 2052


Qy      3007
GACAAAGATCCTTTTTTGTGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCA 3066
             ||||||| ||  |   | ||| |||  |         |||||       | |
|
Db      2051 GACAAATTTCAGCCTAAGAATGATGTATTCTGAG-----TTGGC------
AATTACTTAA 2003


Qy      3067 AACAAAGTACTTCTTCAGGGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTAC-
AA 3125
             |||||          || ||                    | ||| ||| ||
|
Db      2002 AACAATG---------AGAGAG--------------------
TAAAACACATCAAACTTA 1972


Qy      3126 AAGTAATGCTACCTTTTGGGAAACAAACTGCC---
CCGTTAACTCCAGATCATTGCACTG 3182
             ||||  |  ||| |||||    | ||| |     | | ||| | |||| | |
Db      1971 AAGTGTT--
TACTTTTTGAACATTAAAATAAATGTCAGGTAAATACAGAAAAAT------ 1920


Qy      3183 GAATGTAATCAAGAAAGTTAGTCATGTTTTATGTACCATGTTTTCACAC-----
GTGTCT 3237
               || ||||||        |  ||| |  || |||| || ||| |       ||
|||
Db      1919 --ATATAATCA-----------CTAGTTCTCAG---
CATTTTATCAATCCCTTTGTTTCT 1876
```

```
Qy       3238 CTTCTCTTCGAC-TTCCTGAAAGCGAAAGCTTTACCTCC-
TGCAAATGTCAGCACATGTA 3295
              ||||| | ||    | ||   |||   |  | |  ||||   |||| || | | ||
||
Db       1875 CTTCTTCTAGAAGATTCTATGAGCATTA--TGTTGCTCCGATCAAAAGTAACCTCAC-
TA 1819

Qy       3296 GTAGGACACCAGTATCCTAG-
GACAGAGAGCCATAAGTAGCCCTTTGGAGGACTGATGGT 3354
              |  | | ||| |||  ||| ||   | ||| ||                      |  ||
|
Db       1818 CTCAAATACC---ATCATAGCTTCAATGTGCATTA------------------
TAGTGAT 1780

Qy       3355
GTCAACCAAAGGCATGTGATTGATTAATGATTCCCCCTTAGAAAGCAAGTGTTACCAAAG 3414
                |||            ||          |||||| | ||      ||| | ||   ||
Db       1779 TTCA-----------GT----------AGATTCACACT-------
CAAATCTTTTCA--- 1751

Qy       3415
TTGTGTTATCTTGAAAGCATTACAGGTAAGGGCATGTTATGGTTATTTATCATTGTTTAA 3474
                   |||| ||     |||    | | ||   ||||  || | | 
|
Db       1750 --GTGTCAT-------ACATTT---ATTAAGCCA---TAAAGTTATGAAACC----
CTCA 1710

Qy       3475
TGAATAGTAGAGGTGTCAAGGGACTATGTATACATGATTAGGGTAAGATAGAATGTATTA 3534
                 | || |||    ||  || |  || |||||| ||        |||| || |
|
Db       1709 GCTCTTGTGGAGAGATCTGGGCAGAATTTATACAAGA------------AGAA-
GTTTAA 1663

Qy       3535
TATATATATATATATATACACACACACATATATATAGCTGAATCTTTGGTGTATTGAAAT 3594
              | ||||              ||| || | ||    ||||
Db       1662 TTTAT------------------CACTTAAAAAT-----
CATCT-------------- 1642

Qy       3595
AGGCAGCACTCTGAAAGACAGAAGCTTCGTCCAGCCACTCTTCAGCACATTCCTTTACTA 3654
                || | | | | ||||| | | | ||     ||| ||              |||||
|
Db       1641 ---CATAATTGTGGTA-ACAGA---TTTTTAAAGTAAC-------------
CCTTTGGAA 1602

Qy       3655
AGCAGTTTAAAGCCGTCCTAGTGGAGCAAGCCCTAAAGCAGATTTAATTTTTGCCATTTT 3714
                |  | |||||   ||| || |          ||| ||| |
|
Db       1601 AAAATTTTA----CGTGATA----------CCCAAAGGCA--------------
CTAGTT 1570

Qy       3715
CCAAGAATGACGGTGGTGGCTTTTAGTCAGAAAATGGCCTTCTGTGCTTTCAAAAAAAAA 3774
                |  | || | ||| |||||||     ||||| |        |||||
|||
Db       1569 CACATAAGG--GGT-GTGGCT--------GAAAAAG--------------
CAAAACAAAG 1535
```

```
Qy        3775
ACAAAAAAAAAAACCACACACACACATAAAAAACCCAACAGGTCAAAATAAAAGTTGAACT 3834
            ||      ||  |  |||||| ||||        ||| | | |||||| |
||
Db        1534 CCATTGTGTAAGTAAAGAGCACACAAAAAA--------AGG--
ATATTAAAAGGAAACCT 1485


Qy        3835 TGAGTTA--
CATTTAATTTAAATATAAATGCATTTTGAGAAATGTTAAGAACAATTTAGT 3892
                ||||  | || ||| |||           || | |||||        || |||
|
Db        1484 ---GTTAAGCTTTAAAGTTA-------------TTCTAAAAATG------
GCACTTT--T 1449


Qy        3893 CAATCGTTCATCTGTCAT--TGGTACTGTAAAATAAGCTGT---
GGTCTATTTCCACTGT 3947
                || |||| | |  ||     || || ||| || | | |    || | ||| |
Db        1448 CA--
CGTTGGTATAAAATGAAAGTGCTTTAAGATGAAATTTTTATGTATTTTTTTAAAGC 1391


Qy        3948
TTAATTTTCTACTCAGTTCTACCAAATAGGATGTCATGTTTGACATTTTTGATAGTGACT 4007
              | | |||| | | ||    || |||||| ||  | | |||         ||
Db        1390 TGATTTTTAACCCC----CTG-AAAATAGGGGGT----TATAACA--------
AG----- 1353


Qy        4008
TTGGGGTCTTCTTCACTGAAAGCACCTTAGAACTGTACTATAAGAAAACATTTCCCCTAT 4067
                          ||||||| || || |||        ||| | |
||
Db        1352 -----------AACACTGATAGACTCT---AACT--------------
CATAGCGGCAAT 1321


Qy        4068
GTATAATTATATGAATGTGATGTTTATTGCTTATTAATTTATAATTCAGTCATTCTCTAT 4127
                           | || ||  | | |||        || ||||
|
Db        1320 --------------AAGTAGTGGATGTCACTAA-----------------
AATGCTCTGT 1292


Qy        4128
ATAGGACTTCTTAAAATTTAGAAGGGAAATCTAGCTACTTCAAATTGTCTGTTAAATTTA 4187
                | | ||| |||  ||| |            || |  ||| || ||| |
||
Db        1291 GTGTGTCT--TTATTTTTTAGTA---------------TTTTTAATGT-
TAGATAGACTTG 1250


Qy        4188 TTATGCCCAAATCAACCTCTGAAAAAAGGTTTTCC--
AGGAAGATTTACATTTAGGTTT 4245
                | |    ||| | || ||        || | ||    || ||||||| | |||
Db        1249 CTTT------ATCTATCT----------
GTGTATCATTAGTGAGATTTGCTTTTC----- 1211


Qy        4246 AATATTTTTTTAGTTAGGTAGAGTT--
TTAAAAAAATACTTGAGCCTGTCCGTGATAAAGC 4303
                 ||| ||| ||| |||| | ||||   || |    | | |
|||||
Db        1210 AATTCTTTACTAGAAAGTTACAGCTCATTTAAAATAGCTGGTAAAT-ACAG----
```

```
AAAGC 1156

Qy        4304 TATAAAATTCAATAACTTTTTAGAATGTTAAATGAAGACACTGTT--
TCCTAACATCAGT 4361
                  || || || ||| |||                 |  ||||||| |  | ||||
Db        1155 ATAAATATACAGTAAGTTT----------------
AAACACTGATTGTACTAA------- 1119

Qy        4362
GAGATACATCTTTGAATTTAAACATTCATATTTACTGAGTACCTACTAGGTACCA----A 4417
                  || || |    ||| ||| | || ||    | ||  |    |||| ||
|
Db        1118 ---ATGCAAC----AATACAAAGAAGCAAAT------
GGAACACAAATGGTAACACAATA 1072

Qy        4418 GTACTCTTTTAGGCACTGGAAATACAGTGATGGACAAAACA-
GGTAAAAAATCGCTGCCC 4476
                  ||| ||| | ||| ||  | || |  | |||| |||   || | ||| |
Db        1071 AAACTGTATTA--CATTTGTGCTTCAAATAT-
TACAATACATTATATACAATAG------ 1021

Qy        4477
CCTCAGAGCTGACATTCTGGGGTGGGAATTTCATTTTGCCACGTACTAACGTTCTGCACA 4536
                    ||  |  | |  ||               |||   |||||| |   | ||         ||
|
Db        1020 --TCCAAAATAAACATC-------------TCA---TGCCAAG---TGAC-----
ACAAA 987

Qy        4537
AAAGACAGGCTAGACTCTTGTCTAGATTGTTTAAAAGAAACTTTTCAAATTGGTTACATT 4596
                  || ||    || ||                 |||| || |  || ||
||||||
Db        986 AACGAATAGCAAGC------------------AAAAAAATCCAGCCATAT---
GTACATT 948

Qy        4597
AATTTTAGTTTATTTTCACAAGTAAAAATGGCTTTTTATTTAGATTCTTTCTGTCCCAGG 4656
                  | ||        |||||             |||| | | |  |||
Db        947 ACTT--------TTTTC------------------
TTTAATAATAAACATTC--------- 922

Qy        4657
CTGTTGATCTTAAAACTAGTTGATTTAAAGAGTTTTTTTGCACAACATTTCAATTATATT 4716
                    | ||   |||| |          |   ||||    ||| || | ||
Db        921 ------AACTCTGAACTGG---------GGCAATTT----CACTACA-
TACAG------- 889

Qy        4717
TGTGAACTTAGAAATTAACTTACAATCTAACCAGCCATCATATCATATCCTATCAGGCTA 4776
                  || |   |    || |  | | | |||||| | |  | |       ||||||
|||
Db        888 -ATGCAGTCCGCCTTTTA--TTCCATATAACCATCCTGCCT------TCCTATAT--
CTA 840

Qy        4777 -
GATATCTCAATAGTAGACTGAATACAAAGCTAATTTTTTTTTACATGTCAATATTGGCAC 4835
                  | ||| ||| |||   ||| |      | | | |  | |||||||         |||
Db        839 CGCTAT-TCAGTAGGTTCCTGTGT------CAATTCTTATGTACATG-------
TGGAGC 794
```

```
Qy      4836
AAACTGGAATGAAAGAATAGTTTGATTCAGACCTGCTCCACTATGTGTTGCTAAAACACA 4895
          |||   | || |||||||           |    ||||||     ||| || || |
Db      793 AAAAAAG-ATAAAAGAAT-----------GTAGTGCTC-----TGTATT-
CTTA------ 758

Qy      4896
TGCTATGAGCACTCGAGGAAACACTATATTTTTTCCAAAAAATATGTGATTATATATGTT 4955
                  ||| |                                      |||
|||||
Db      757 ----ATGGG---------------------------------GTG-------
ATGTT 745

Qy      4956
AAAGTATAGATAACATTTCACACTTGGATACATATGTGCATTTACTGTATTTCTTGGTAA 5015
                    ||||||  |    |  || |||    ||||||  || | |||| |
|||
Db      744 G----ATAGATCA----GCGAACCTGGG-------GTGCATAACCT-TCTTTCAT--
TAA 703

Qy      5016
GCATATTTTTGGGGGAAAGTGCTGCTGATATGATACAAGTAGACAAAATTTAAATGAAAT 5075
               |   ||  |  |  |   || |||  |  |   || ||       |   || |
|||
Db      702 AC--CTTCCTCGTAGTCCGT-CTG--GCAAAGGATCATGT----
TATTCTTTAGGAAAAA 652

Qy      5076 TTTGTCACATTCTATGGAAAATGGTTTCTGGT----
AAACTGAGAAGGATATTAAAATAA 5131
                |||||| | |   | | |  | |||| |    || |||| | | | |  |
|
Db      651 TTTGTCTCCAAC------
ACAAAATCTCTGATTACAAAGCTGACATGCAAAGCAGTCCAG 598

Qy      5132 GTGG----
CTTTTTTCTGGGCTACCATTATTGTTTGATTTCTCTTTGTCAAGTGTATAGA 5187
                ||||   | | | ||| | ||| | |    ||| |    ||||  | || |   |
||
Db      597 GTGGTAAACATTGTCCTTGGCACGCATCA-------CCATCTCAAAGGCAGGGAT---
GA 548

Qy      5188
ACCTGTCATACATTCATGATAAGTAGCACTGAAAAATTACTCATTCAAATTTCCCCTG-- 5245
               |  |  |||| || | ||| |  |       | | |    ||||  | ||||   ||| | |
Db      547 GCT--TACTACAGGCA-GCGCAGTTTCCC------GTTACAC--
CAAAGAGCCTCAGAT 500

Qy      5246 -GGCACGTAAGGCAAAATATTGCCGGTTGGGATTTCAAGGTCAGTGACGA-
CGCATTTCC 5303
               | | | | |||| | |   | | |||   |  | || | || | || ||
|||
Db      499 AGTCTC-TGCGACAAAGGAT---
AAGATTAGCTTTAGTGTACAGGGTGGAGCCCACCTCC 444

Qy      5304 TCCCAGT-
ACAGACCCCCCAGCCCCCCTTGCTGGACATGGGGAGGCAGAGAGTCACTTGA 5362
               || || |||| | ||| | ||| | | |||         |     |||||||       |||
Db      443 CCCAAGCGACAGTCACAGCAGGCACACTT------C------AGGCAG------
TCTT-- 404
```

```
Qy        5363
CCATCCAGAAATACATGACTACAAGTCCTTTATGACTGTTTGCCATTTTTTTTAATGGTA 5422
          |    ||||| |  | || |  ||||||  |     | ||
|||
Db        403 CATGCCAGTATT---TGTC--CAGTGCCTTTAGAA---GATACC------------
GGTC 364


Qy        5423 CTTAGTATTTTGATCAAACTTTAGTCTCCAGAACTAAACAAGTC-
CCTAAGTTTCCTTAT 5481
          |      ||||||  |  | |  |||| ||  |||   ||  ||  || || |
Db        363 C--------TTGATCTTTCGGTTGCAGCCAGCAC--
AACCTTTCGGCTTGGTGTC----- 319


Qy        5482
TTTAATTTACTGTGACTAGATTTGAAGCAAATAAATACTCCAGATCCATGCAGCTAGAAC 5541
                        || || || |  |||| |  ||| ||| ||| |  |
|
Db        318 ------------TGGCTGGACTGAGAGCATTTGTATA--
CCAAAACTTT----------- 284


Qy        5542
ACACTTGCTTCCACTACTAAATATACAGGGTATGTCCTAACATGGAGTTAACTGGAATAG 5601
                          || ||  | ||  |  |||  |  ||| |  |  | |
|
Db        283 ------------TCTCCTTTTTCTGCATGAGTTGACTTA----GGCG-TGTCT-
GAGTTG 242


Qy        5602
CAGTACACTAGCAAGTATCTGTGAATCCTTAGCACTGACGGGTTAACAGAAATGCTTTGG 5661
              ||| |   | |||      ||| |  | | |  | |   |  ||||  |
||
Db        241 CAGCAGCTTCGCAT-------TGAGCACCAAACCCAAAGGTAGAAGTAGAAGGG----
GG 193


Qy        5662
TAATACCTACTTAGTTAATTGGAGGAAGTAGTAAATAAACATTAGGTAATCTGCAGATTA 5721
               |   || || | ||||  | |   | | |  ||  | | | |     ||||
||
Db        192 T-----CTCCTTGAT---TTCGCTTAAGT-----GTGGACCT--GGTGC---
GCAGCCTA 151


Qy        5722
CTTCAAATGGGAAAAATCTTTTTGTAGACTCTATAGTACCCTCTCTATTCACTAGCTTCT 5781
              | |     |||  | || || | |  |     |  |  |  ||   |  | | ||
|
Db        150 CACCGCCGAGGACCGACTATTGTGAAGCCACTTTGGGAGCGGGTCGG---
AGTTGGCGGCA 94


Qy        5782
GAAAAGGGAGGAGTATTTTTAGTTTGACAATTTAATAATTTAAAAACAAGACATCTCCAG 5841
              |   | || |||  |  | ||  | |     |  || || |  | |||||||
Db        93 GGGGGTGGGGGAAGGGATGAGGACGGCC----------------
AGACAAGAC-------- 57


Qy        5842
GTAGGAAAAAATGAAAGCTATTTCATGCAAACATTATCTAATTTAGCTTAAAAGTGAAAG 5901
                 |||         ||    || |  |||| |  |  || ||  ||   ||| |||
|
Db        56 --AGG-----------GCGCACACACGGAGCCC--CTCGCAGTGTGC---
AAAATGATGG 15
```

```
Qy       5902 TGGTAATACTGTTGG 5916
              |  ||| | || ||
Db         14 CG--AATCCAGTAGG 2


RESULT 3
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match           20.8%;  Score 7966.5;  DB 1;  Length 3210;
  Best Local Similarity  38.3%;  Pred. No. 0;
  Matches 2028;  Conservative   0;  Mismatches 1136;  Indels 2131;
Gaps  280;

Qy        1 CCCAGTTGTCTGCGGGCTGCGGGGAGCTAAGTCCCCAGATTGGAGGAGGCTG--
GCTCTG 58
             | | |||| |      || | ||       ||| | | |  | || | ||||
Db        2 CACTGTTGGC------CTACTGG---------
CCCAGGCCTTGCACACGCAGGTGCTC-- 44

Qy       59
GTCTTCGATGCACAGGAGTGGCCGTTATGGAACGCAGCAGCAGCGTGCAGGGTCAAAGAC 118
              |||| | ||| |     |||| |    |||| | |        || ||    ||| ||
Db       45 -TCTTAG-TGCTC---CCTGGCAAGGATGGGAAG--------
GCATGTTCAGTCCTAGG- 90

Qy      119
AGCCGGCCCCCCATGTCAGTGGTCTAGGATGGCCAGTGAAGGCACCAACATCCCAAGTCC 178
             || | ||       | ||| ||| |        ||| ||| || |||
Db       91 AGTAGG----AAGGGGCAGAGGTGT-----------
TGATGGCCCCTACA---------- 125

Qy      179 TGTGGTGC-GCCAGATTGACAAGCAGTTTCTGAT--
TTGCAGTATATGCCTGGAACGGTA 235
                | || ||||   |||||| || | ||| |   ||| |   |||| |
|
Db      126 ----GAGCGGCCAAG--GACAAGGAGCTGCTGTTCGAAACAGCCTT--
CCTGCTCCCCAA 177
```

```
Qy         236 CAAGAATCCCAAGGTTCTCCCCTG--TCTGCACACTTTCTGC----
GAGAGGTGCCTGCA 289
               | |  |||||     | |  | |  |||| |   ||| |     ||||| |
|
Db         178 CCTGCCTCCCA-----
CCCAACAGGTTTTGCATATACTCTACTGGGAAGAGGGACACACC 232


Qy         290
GAACTACATTCCTGCCCACAGTTTAACCCTCTCCTGCCCAGTGTGCCGCCAGACCTCCA- 348
                  ||| ||| |||||| |   |    | ||| |||||||| |      |||| |
||||
Db         233 CGACTGCATCACTGCCCTCCAAGT--CTCTC-CCTGCCCTGT------CCAG-
CATCCAG 282


Qy         349 -
TCCTGCCCGAGAAAGGGGTGGCCGCGCTCCAGAACAATTTCTTCATCACAAACCTGATG 407
                 |  ||| ||  |||| ||   ||         |||| | | ||
Db         283 GAGCACCCCTAG-TTGGGGAAGC----------------TTCTGTGACTC---
CC----- 317


Qy         408 GACGTGCTGCAGCGAACTCCAGGCAGCAACGCTGAGGAGTCTTCCATC-----
CTGGAGA 462
                 | | |||     | ||| | |      || || |  | |       | |
||
Db         318 --CCTACAACAGC-----CTAGGATGGA-----
GTGGGGTTTGTGAACAAATGCAGAAGG 365


Qy         463
CAGTCACTGCTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCACGATGGGAATGT-G 521
               ||||           || |||| |  | ||  |||||         ||  |||
|
Db         366 CAGT-----------CTTAGGGAGGTCAGCTGACATGCCCCT---------
GGCCTGTGG 405


Qy         522
ATGGAATTTTACTGCCAGTCCTGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAG 581
               ||| | | | | ||| |   || || |   ||| ||| |||| |
Db         406 CTGGGAAGTAGCAG--AGG-
CTAAGGTTCTTCCCCGCTCTGGGGTTGCCAGGAGTAG--- 459


Qy         582
CACGCAGAGCACCCCACAGTTCCACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTC 641
                         ||| |  || ||       |||| | ||| |      ||||
|||
Db         460 --------------CACTGGATCAGTCA-------GGTGACAGGGCTCT---
CCTCTCTC 495


Qy         642 ----
CAGGTCCAGCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCA 697
                  |||||||| | |||  ||    || | | | |
|
Db         496 TGAGCAGGTCCGG-TGGCAGCCTTC----AAGGTCGCCACG-----------------
CC 533


Qy         698
GTTCATCTCTGAAATCATTCATCAGTTAACCAACCAAAAGGCCAGCATCGTGGATGACAT 757
                | |  ||| |||    | |||        || | ||||| | |  |  | |||
Db         534 G-TATTCCCTG------TATGTCTGT-------CCCGAGGGGCAG-
AACGT--------- 569
```

```
Qy         758
TCATTCCACCTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTAT 817
                |||| ||      |  || |||| ||  ||          || ||   | |
|
Db         570 ------CACCCT-------CACCTGCAGGCTCT--------------TGGGC--
CCTGT 599


Qy         818
GGAATTGGAGGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGATACTCT 877
               |||   |  | || |||| ||           ||  |||  ||     ||| |
|
Db         600 GGACAAAGGGCACGA-TGTGACCT----------TCTACAAGACG----
TGGTACCGCA 643


Qy         878
GCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCCTCAACCA 937
               |||| |||||| |  |  ||    ||| ||||      ||| ||||| |||| ||
||
Db         644 GCTCGAGGGGC-GAGGTGC----AGACCTGC-------TCAGAGCGCCGGCC--
CATCC- 688


Qy         938
TGGCACGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAGCT 997
               |||   ||| |||    ||                                 |||
Db         689 --GCA-----ACC----TC--------------------------------
ACGT--- 700


Qy         998
GGCCGACCAGGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCATCGTGGA 1057
               ||||||| | | | |||||                                |
||||
Db         701 -----TCCAGGACCTTCACCTGCAC---------------------------
CATGGA 726


Qy         1058
AACCGAGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCTTAACCACCAACGCCGT 1117
               || | |||||       ||| | |||    |                   |||
Db         727 GGCCACCAGGCTG-------CCAACACCAGCCACG--------------
ACC-------- 757


Qy         1118
TGCCTCAGAGACAGTGGCCACGGGCGAGGGGCTGCGGGCAGACCATCATCGGGCAGCCCAT 1177
               || | |||||     ||||||||| | | || || |  |||||| |||| |
Db         758 TGGCTCAGC-------GCCACGGGCTGGAGTCGGCCTCCGACCACCAT--
GGCAACT--- 805


Qy         1178
GTCCGTCACCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAACGCCTA 1237
               || ||||||||| |                    |||  |||| |
|
Db         806 -----TCTCCATCACCA------------------------
TGCGCAACCTG--------A 829


Qy         1238
CCTCACCGCCGAACTGAGCACCCCCGACGGGGAGCGTGGCAGACGGGGAGATCCTGGACAA 1297
               || |  | || | |    ||| |||| | || |  ||| |    |  |||||||
Db         830 CC---CTGCTGGAT--AGCGGCCTCTACTGCTGCCTGGTGGT---
GGAGATC-------- 873


Qy         1298 CAAGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTT--
```

```
TACCCTG 1355
                      | | | | | |              | | | |   | | |    | | | |  | |   |  | | |
                                                                                         | |
Db      874 ------AGGCACC------------ACCACT---
CGGAGCACAGGGTCCATGGTGCCATG 912


Qy      1356
TCTCTGAGACTCTATGACCAGCACATCCGAGGCAGCCCGTTTAAGCTGAAAGTGATCCGA 1415
                      | | |                      |  |  | | | |  |  |   | | | | |  |   | |
Db      913 GAGCTG--------------------CAGGTGCAGACAGGCAAAGATGCA------
CCAT 946


Qy      1416 TCCGC--
TGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGGA 1473
                      |  |   | |  | | | |   | |  | | |  | |                    | | | |  | |
                                                                                         | |
Db      947 CCAACTGTGTGGTGTACCCATCCTCC------------------------
TCCCAGGAGA 982


Qy      1474
GCGGCCACGTCAAGCAGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAAC 1533
              |                | | | | |    | |   | | | |    |                 |  | |   |
Db      983 G--------------TGAAAGT----AAGGGACCAAC------------
CTCTTG----- 1007


Qy      1534
GAAAAGAGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAAATA 1593
                              | | |                          | | | |     | | | | |  |
Db      1008 -----------CCC------------------CTTT----
TGGGTTCTC------------ 1023


Qy      1594
AAGGAGAGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGATATTAATTG 1653
                      | | | |      | | | | |  |       |    | | | |
                                                                                         | |
Db      1024 ------TGTTT-----TCTTCTG------TCCTCATC--------------------
CTG 1046


Qy      1654
CAGACAGTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTCGTT 1713
                    | |   | | |      | | |   | | | |  |           | | | | |                 | |
                                                                                         |
Db      1047 CACCCAG-----ACC-CTGTTTGGAACT-----------CTGGCC----------
TCAT- 1078


Qy      1714
TTGGCATACGGGGACGGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTACATC 1773
                      |  |  | |                  | | | |  | | |                         |
                                                                                         |
Db      1079 -----------------CACCCC-------------AAGCCCTCAG------------
AAC 1097


Qy      1774
CCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCTCCG 1833
                    | |                          | |                  | | | |
| | | | | | |
Db      1098 CCC--------------------CC------------------GGTC--------
CTCCTCC- 1113


Qy      1834
```

```
ATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTTCTG 1893

||||||
Db      1114 ----------------------------------------------------
TTTTCTG 1120

Qy      1894
TGGACCGCAATGGGCACATTATTGTTGTGGACAACAAGGCGTGCTGCGTGTTTATCTTCC 1953
             | ||     ||||||                |  | | |||
||||
Db      1121 ----CTGCT----GCACAT---------------C----CCTTCTG---------
CTTC- 1143

Qy      1954
AGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGTTTG 2013
                       | ||     ||||
||
Db      1144 -------------------CTCC----TTGG-------------------------
TG 1153

Qy      2014
CAGGTCCCCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATTTCCATA 2073
             || ||||||    | |||                               |||
Db      1154 CA-ATCCCCA----GAAGC------------------------------------
CCACT 1172

Qy      2074
ATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGGCTCAAATG 2133
             || |||  ||       |  | |||        ||           |  ||||
|
Db      1173 CTCCTTCCATC--------TGCTCTGGAG-------TC----------
TCTGCTCCTCTT 1207

Qy      2134
GAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAATGGAAACA 2193
             ||                    |||  | ||| || |||| |    ||| |
Db      1208 GA---------------------CTC--TCTGGAGTGGCTGTGCCT-----
TGGCAGTG 1238

Qy      2194 TCATTGTGGCCGACTGGGGAAACAGCAGGAT-
CCAGGTTTTTGATGGGAGTGGATCATTT 2252
             | || |||||     ||| ||  ||   || ||||    |  ||||
Db      1239 ACCTT-TGGCC----AGGGCAAGTGCCTCATGACAGG----
TACTGGG----------- 1277

Qy      2253 TTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCC-
AAGGCCTGGCCCTAAC 2311
                 || || ||     |     |  ||| | ||   | |     |||||| | ||| |||
|
Db      1278 -TGCCC--CAGGCAGCTAAGTGCCGCCCTGCCCACCAGCCCCCTATGGCTTGG----
GAA 1330

Qy      2312
TTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTATCGATA 2371
               | |  |||| ||      || || |   | ||| ||  |  || |||   |
|
Db      1331 GGCTGGGGGTCCTCTTG-----GCCAACAGGGTGAAACCCCATCTCTA---
CTAAAAACA 1382

Qy      2372 CTTACAGTAATGGTGGGCA-
```

```
GGTGGATACCCGCTTCCATGGTCTTGCACTATAAACTGGA 2430
     |  |  |  ||  |    |||| |||| |||||  |  |||  |   |  |   |||
        |
Db     1383 CAAAAATTA--GCCAGGCATGGTGG-TGCGCGC--CTGTAGTC-----
CCAGCTACTCAA 1432


Qy     2431
ATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCAGAAGGAATCATT 2490
                ||  |           |  | |||  ||  ||  ||            ||  |  ||| |||
Db     1433 GAGGCT----------GAGGCAAGAGAATCGCTTGA--------ACCCG--
GGAGTCAGA 1472


Qy     2491
GGTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACTTATCCAAT 2550
                ||               ||    | | ||  |   |           |    |||
Db     1473 GG-----------------TTGCAG--TGAGCCGAGATC----------GC---
GCCA-- 1498


Qy     2551
TTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAAAACTGC-- 2608
                |||  | | | ||  |      | |   ||  | ||||  |  ||     || | ||||||  |
Db     1499 --CTGCACTCCAGCCTGCTGATAGAGCAAGACTC--CATC----
TCAAAAAAAACAACCC 1550


Qy     2609 -
AGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATTTT 2667
                |  | |||  |           ||||  |  | ||||  | ||     |||  |  |
Db     1551 AAAATTTGC-----------CTGGCAT-GGTGGCAGGC-ATCTG----
TAATCCCA---- 1589


Qy     2668 GCAAATC---
AAACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTG 2724
                || | ||  |   | ||||  |   | |             || |
|||||
Db     1590 GCTACTCGGGAGGCTGAGACAT--GAGAGCT-GC-----------------
TTGAACCTG 1629


Qy     2725
TGAATGGTAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAAATCTATTGTAGT 2784
                ||   ||  ||     |||||  ||          ||  ||  |||||  ||
Db     1630 GGA--GGCAGAAGTTGCAGTGAG---
CCGAGATCACACCA-------------------- 1664


Qy     2785
TATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCTCACTTTTACA 2844
                |  |||  |     | ||| |||      ||| |  ||  || ||  |  ||
Db     1665 -CTGCACTCC----AGCCTGGGT-----GACAGAGCGAGAC-
TCTGTCC----------- 1702


Qy     2845
GTAGGTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATATAAATTACTTTGG 2904
                                    ||| || || | |||| |||||
|
Db     1703 ------------------------------------CAAAAAATCAA-
AAAAATCACTTTTG 1727


Qy     2905
AAAAAGTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCCCTCTGGAGTTCA 2964
                | ||            ||||        ||  | ||| ||  |      |||  | ||
|
```

```
Db      1728 GTAGAG----------ATGCA-----CTCTC-GCTATGTT-----GCC--CAGG----
CT 1760

Qy      2965
GAACTTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGATCCTTTTTTG 3024
             |  ||| |                   | | |     ||||| |  |||
Db      1761 GGTCTTGA---------------ACTC-------CTGGGCT---
CAAT------------ 1783

Qy      3025
TGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCTTCAG 3084
               || ||||              | |||||||     |    |||||| ||
                                                                      |
Db      1784 --TGATCTT----------------CCCACCTTG-----
ACCTCCAAAGTGCT------G 1814

Qy      3085
GGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTTGG 3144
             ||                            |||||| ||| || |||
Db      1815 GG-------------------------------ATTACAGGTGTGA-
GCCACC------ 1835

Qy      3145
GAAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGTTAGT 3204
                  ||||   || |  |||   ||| ||   | | |  | |  |||
|||
Db      1836 --------ATGCC----TAGCCTCAGGGAATT---CTTATAAGAACTCTATGAAG-
TAGG 1879

Qy      3205 CATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTTCCT-
GAAAGCGAA 3263
               |||        ||||            ||||||||  |   | | | |||||
              ||
Db      1880 CAT--------CACCA----------------TCTTCTCT--
GTATCCATGGAAAGAGAG 1913

Qy      3264 AGCTTTACCTCCTGCAAATGTCAGC--
ACATGTAGTAGGACACCAGTATCCTAGGACAGA 3321
               |||  |  |||| | || ||              || ||  ||
                                                              |
Db      1914 G---------CCTAGAGATGTATGCTAACTTG----------------
CCCAAGCTCACA 1948

Qy      3322
GAGCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGTGATTGATTAA 3381
               ||||   |||||      |   ||| | ||| | | ||||  | |      |
              ||
Db      1949 TAGCCCAGGGTAGC-------ATAGCTGG-
GATGTTGAGCTGAGGCCGGAGGAGAAGTAG 2000

Qy      3382 TGATTCCCCCTTAGAAAGCAAGTGTTAC-
CAAAGTTGTGTTATCTTGAAAGCATTACAGG 3440
               | ||| |     ||| || |    | | |  | | ||||  | ||  || ||
              |||
Db      2001 C-AGTCGCTGGCAGAGCACACAGGCTGCTCTGGG--GGATGAGCTGG--
TGCGTTTAAGG 2055

Qy      3441
TAAGGGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGACTA 3500
             |  ||| |   | |||     || ||    |   ||| | |||| || | |||
```

```
|
Db      2056 AACAGGCCAGCACTGG--
CATTCGCAAGCAGTGGGGAAGGGGAGAGATGCCGAGGTGGTC 2113

Qy      3501
TGTATACATGATTAGGGTAAGATAGAATGTATTATATATATATATATATACACACACA 3560
              |||| | ||| |   | || |    ||  || ||||| | |||| |

|
Db      2114 AGTAT--CCTGACTT---TCAG--
AGGCCTTTTTTTGTTTGTTTTAATTTTTGCT-----A 2162

Qy      3561
CATATATATAGCTGAATCTTTGGTGTATTGAAATAGGCAGCACTCTGAAAGACAGAAGCT 3620
             || | |||| | | ||   |||      || | |||| ||| || |
Db      2163 GATTGATATTAAAAACTC----ATGT--------GGAGGAACTC--
AAGGAATGTTTAG 2207

Qy      3621
TCGTCCAGCCACTCTTCAGCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGTGGAG 3680
             |  |||                                 |||| | || | ||
Db      2208 AAGACCA------------------------------------AAAGTC--
CCCAATG--A 2228

Qy      3681
CAAGCCCTAAAGCAGATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCTTTTAG 3740
             || | |||||  |      |||||||  | || ||    || | |||
Db      2229 CAGGAACAAAAGCAAC--
CAATTTTTAACTTTCTCTTCTCATTCCTGT------------ 2274

Qy      3741
TCAGAAAATGGCCTTCTGTGCTTTCAAAAAAAAAACAAAAAAAAAAACCACACACACACAT 3800
               ||| || |||| |                          |||||  |  |
|
Db      2275 ------------TTTCATTGATTTC----------------------
CCACATGTAGTCCT 2301

Qy      3801
AAAAAACCCAACAGGTCAAAATAAAAGTTGAACTTGAGTTACATTTAATTTAAATATAAA 3860
             | || | |||    |              |   || ||| ||   | ||| ||
Db      2302 --TTTGCTCAGGAAGTC------
TTTGGGGAAATTAAGGATCTTTGAA------------ 2341

Qy      3861
TGCATTTTGAGAAATGTTAAGAACAATTTAGTCAATCGTTCATCTGTCATTGGTACTGTA 3920
             ||  | ||| || ||  |  | ||| |     | |||||     | |  ||||||
|||||
Db      2342 -GC--TCTGAAATAGGT---GATCAGGTTAGT-----GGT-GTCTGTCA-----
GCTGTC 2384

Qy      3921
AAATAAGCTGTGGTCTATTTCCACTGTTTAATTTTCTACTCAGTTCTACCAAATAGGATG 3980
             ||      | |||      ||    |||     |||||||          ||
|
Db      2385 TAA------GAGGT----------TGGAAAATGAACTACTCA------------
AGATAG 2416

Qy      3981
TCATGTTTGACATTTTTGATAGTGACTTTGGGGTCTTCTTCACTGAAAGCACCTTAGAAC 4040
             |||    || | ||| || |  ||||    || | |||
Db      2417 TCA----CGAAAATACTGAAAG----TTTG----
```

```
ATTTTTC------------------ 2445


Qy      4041
TGTACTATAAGAAAACATTTCCCCTATGTATAATTATATGAATGTGATGTTTATTGCTTA 4100
                         |||||              ||| |||
|
Db      2446 -----------------TTTCC----------
ATATTTGA------------------A 2459


Qy      4101
TTAATTTATAATTCAGTCATTCTCTATATAGGACTTCTTAAAATTTAGAAGGGAAATCTA 4160
            ||||||| |                 ||| | |||            | ||||||
Db      2460 TTAATTTTT------------TCTGTTT--GAC-----------
TGGAAGGG------- 2486


Qy      4161
GCTACTTCAAATTGTCTGTTAAATTTATTATGCCCAAATCAACCTCTGAAAAAAGGTTTT 4220
                           ||    ||| ||| | |  ||  | ||  ||||||| |    | |
Db      2487 -----------------GT----TTTTGTATAACTAA---
AACCTCAGCGCATA------ 2516


Qy      4221 TCCAGGAAGATTTACATTTAGGTTTA-
ATATTTTTTTAGTTAGGTAGAGTTTTAAAAAAT 4279
                | | |||||||| |    |||   | ||   |||   | | | ||       |
Db      2517 ---AAGGAGATTTAAA---AGGAGCACATGATTTAGTGGGTGGGCCATG---------
AA 2561


Qy      4280 ACTTGAGCCTGTCCGTGATAAAGCTATAAAAT--
TCAATAACTTTTTAGAATGTTAAATG 4337
                ||| |||         | ||||    |   | ||| |  |||||| ||      | || ||||
Db      2562 ACTAGAG-----ATGGGATTTGGGGGTGAATTTGTCAATATCT-----
GGATTTTAA--- 2608


Qy      4338
AAGACACTGTTTCCTAACATCAGTGAGATACATCTTTGAATTTAAACATTCATATTTACT 4397
                           ||| |||| ||     ||        ||| | |   |||
|
Db      2609 -----------TCCAGACATCTCTG--------CT---------AACGAGC--
CTTTGGT 2638


Qy      4398
GAGTACCTACTAGGTACCAAGTACTCTTTTAGGCACTGGAAATACAGTGATGGACAAAC 4457
                ||| ||  || |  ||||       | ||| |||       |||  ||| | |||  |
Db      2639 AAGTCACTTC-AGATACTTT-TCCTCCTTTTTAC-----AAAGAGAGGGCTGG-
CTTA-- 2688


Qy      4458 AGGTAAAAAATCGCTGCCCCCT-
CAGAGCTGACATTCTGGGGTGGGAATTTCATTTTGCC 4516
                   || |      |  ||||| | ||| ||||  | |      || || || |    ||
Db      2689 --GTTATTTGCCAAAGCCCCTTCCAGGCCTGAATTCCACAAGTACGATTTAC----
TGTA 2742


Qy      4517
ACGTACTAACGTTCTGCACAAAAGACAGGCTAGACTCTTGTCTAGATTGTTTAAAAGAAA 4576
                   ||   || |   |||       || |||| ||  ||  |   |
|
Db      2743 GTGTCTTATCACTCT--------------------TTCATGTCACAATAGCGT----
GGAG 2779
```

```
Qy        4577
CTTTTCAAATTGGTTACATTAATTTTAGTTTATTTTCACAAGTAAAAATGGCTTTTTATT 4636
              | ||  | |    |    |    | ||||||| |   |  | ||| |||| | ||
Db        2780 CATTAGAGAAAAG--CCTAGACTTTTAGTTGA---
TAGCCAGTTGAAATATCATT----- 2829


Qy        4637
TAGATTCTTTCTGTCCCAGGCTGTTGATCTTAAAACTAGTTGATTTAAAGAGTTTTTTTG 4696
                 |||            || | |TT |||| |  |  | ||| ||    | ||| |
|
Db        2830 --GAT------------AGAATTTTAGTTTTAGGAAAAATTGGTTT-----
GATTTCTAG 2870


Qy        4697
CACAACATTTCAATTATATTTGTGAACTTAGAAATTAACTTACAATCTAACCAGCCATCA 4756
                 |   ||| |  ||||  |  ||||| ||  |        || ||
|
Db        2871 --CTTTATTACTATTAGGTATGTGAGCTTGG----------------------
GCAA--A 2904


Qy        4757
TATCATATCCTATCAGGCTAGATATCTCAATAGTAGACTGAATACAAAGCTAATTTTTTT 4816
                 |  | ||  ||  || |||| | |||| |  ||  |  | ||||| |
|||
Db        2905 TCGCTTAATCTTTGAGTCTAGTTTTCTCTCAAAATGA--
GAACATTAGGCTAAATGATTT 2962


Qy        4817
TACATGTCAATATTGGCACAAACTGGAATGAAAGAATAGTTTGATTCAGACCTGCTCCAC 4876
                              | |            ||||||         || || |||
Db        2963 ----------------------CCG------------AGTTT--------
CCAGCT---- 2976


Qy        4877
TATGTGTTGCTAAAACACATGCTATGAGCACTCGAGGAAACACTATATTTTTTCCAAAAA 4936
                               || || |||    |||||||| | |  |
Db        2977 --------------------------AGTCCTAGAG----
TTCTATATTTCTACATA--- 3003


Qy        4937
ATATGTGATTATATATGTTAAAGTATAGATAACATTTCACACTTGGATACATATGTGCAT 4996
                            ||| || |||     ||| |||                   |||
Db        3004 ----------------GTTGAATTAT--------TTTATCA--------------
TGCTG 3025


Qy        4997
TTACTGTATTTCTTGGTAAGCATATTTTTGGGGGAAAGTGCTGCTGATATGATACAAGTA 5056
                || || |||     || |  |  |||     ||| ||| ||| | || | ||
Db        3026 TTGCTGGGGAATATGACTAACCCTTTT------GAA---
GCTACTAATTTTAT------- 3069


Qy        5057
GACAAAATTTAAATGAAATTTTGTCACATTCTATGGAAAATGGTTTCTGGTAAACTGAGA 5116
                 | | |  ||||||       ||| |||        || | ||||         | ||
|
Db        3070 GTCGAGCTTTAAA---------GTC-CAT-------AATTGTTATCT-----
TCAGAAA 3106


Qy        5117
AGGATATTAAAATAAGTGGCTTTTTTCTGGGCTACCATTATTGTTTGATTTCTCTTTGTC 5176
```

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                 |                    |  ||  |  ||  ||||      || ||      ||
  ||
Db      3107 A------------------TATTATTTGACCTAC------AGTATG-----
TCCAAATC 3136

Qy      5177
AAGTGTATAGAACCTGTCATACATTCATGATAAGTAGCACTGAAAAATTACTCATTCAAA 5236
             ||  |  ||| ||  |    |  |     ||  || ||   |   |   |||||  |     |
  |||
Db      3137 AATTTAATAAAATC--
GCTTTATAACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3194

Qy      5237 TTTCCCCTGGGCACG 5251
             |  |  ||  ||  ||
Db      3195 GGCCACATGTGCTCG 3209


RESULT 4
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match            19.0%;  Score 7277;  DB 1;  Length 3210;
  Best Local Similarity   35.5%;  Pred. No. 0;
  Matches 1963;  Conservative    0;  Mismatches 1130;  Indels 2434;
Gaps  307;

Qy       13 CGGGCTGCGGGGAGC------------------------
TAAGTCCCCAGATTGGAGGA 47
             ||  ||  |  |  ||                        |   |  ||  |  |      |
  |
Db      3209 CGAGC-
ACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTGTTATAAAGC 3151

Qy       48 GGCTGGCT---CTGGTCTTCGATGCACAGGAGTGGCCGTTATGGAACGCAGCAGC-
AGCG 103
             |   |   |    |  |  ||  ||   ||  |  ||  ||    ||       |  | ||  |
  |
Db      3150 GATTTTATTAAATTGATTTGGACATACTGTAG-
GTCAAATAATATTTTCTGAAGATAACA 3092
```

```
Qy        104 TGCAGGGTCAAAGACAGCCGGCCCCCCATGTCAGTGGT--CT--
AGGATGGCCAGTGAAG 159
                | || |      |      || |  |||    | | || || |  | || |||
Db       3091 ATTATGGACTTTAA-----
AGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGT---- 3041


Qy        160 GCACCAACATCCCAAGTCCTGTGGTGCGCCAGATTGACAAGCAGTTTCTGATTTGCAG-- 217
                   ||   |||| |        || |||  ||| ||     ||| | || ||
Db       3040 ----CATATTCCCCA----------
GCAACAGCATGATAAAATAATTCAACTATGTAGAA 2995


Qy        218 -TATATGCCT---GGAACGGTACAAGAATCCCAAGGTTC---
TCCCCTGTCTGCACACTT 270
                   ||||    ||   |||    |  | ||| |      ||   | |||   || | |
|
Db       2994 ATATAGAACTCTAGGACTAG--CTGGAAACTCGGAAATCATTTAGCCT-
AATGTTCTCAT 2938


Qy        271 TCTGCGAGAGGTGCCTGCAGAACTACATTCCTGCCCACAGTTTAACCCTCTCCTGCCCAG 330
                | || |||        | |||||| |      | || || |||| |      |
||||||
Db       2937 TTTGAGAG----------AAAACTAGA------CTCAAAGATTAAGCGATT--
TGCCCA- 2897


Qy        331 TGTGCCGCCAGACCTCCATCCTGCCCGAGAAAGGGGTGGCCGCGCTCCAGAACAATTTCT 390
                            || || | |||  |||| | ||  |   | |      || | ||||||
|
Db       2896 ---------AGCTCACATACCTAATAGTAATAAAGCTAG----
AAATCAAACCAATTT-T 2851


Qy        391 TCATCACAAACCTGATGGACGTGCTG-
CAGCGAACTCCAGGCAGCAACGCTGAGGAGTCT 449
                || |  ||| ||    |   | ||  ||  ||  |          ||||         |
||
Db       2850 TCCT---AAAACT----AAAATTCTATCAATGATAT------TTCAAC-------
TGGCT 2811


Qy        450 TCCATCCTGGAGACAGTCACTGCTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCAC 509
                || |      || | |  | |||| | ||         ||||| |||| | | |
|
Db       2810 ATCAAC----TAAAAGTCTAGGCTTT---------------TCTCTAATGCTCCA--
CGC 2772


Qy        510 GATGGGAATGTGATGGAATTTTACTGCCAGTCCTGTGAGACTGCCATGTG----
TCGGGA 565
                || | |   ||| || || || | || ||| || | |   | | |||||     || ||
Db       2771 TATTGTGACATGAAAGAGTGATA-
AGACACTACAGTAAATCGTACTTGTGGAATTCAG-- 2715


Qy        566 GTGCACGGAGGGGGAGCACGCAGAGCACCCCACAGTTCCACTCAAGG--
ATGTGGTGGAA 623
                || ||| ||||        ||| |  ||       |  | ||| |  |  | |     ||
||||
Db       2714 --
GCCTGGAAGGGGCTTTGGCAAATAACTAAGCCAGCCCTCTCTTTGTAAAAAGGAGGAA 2657
```

```
Qy         624 CAG---CACAAG-GCCTCGCTCCAGGTCC---
AGCTGGATGCTGTCAACAAAAGGCTCCC 676
                   ||    |  ||| ||  |  ||| |   ||| |   |  |||| |  |   |
||
Db        2656 AAGTATCTGAAGTGACTTACCAAAGGCTCGTTAGCAG--AGATGTCTGGATTAAAAT-
CC 2600


Qy         677 AGAAATAG----
ATTCTGCTCTTCAGTTCATCTCTGAAATCATTCATCAGTTAACCAACC 732
                   ||| ||  |  |||| |  |  ||||||  ||| |        | |  |||
|||
Db        2599 AGATATTGACAAATTCACCCCCAAATCCCATCTCTAGTTTCA---------
TGGCCCACC 2549


Qy         733
AAAAGGCCAGCATCGTGGATGACATTCATTCCACCTTTGATGAGCTCCAGAAGACTTTAA 792
                   |     |   ||| ||  |  | | |  | ||||| ||| |||      ||
||||
Db        2548 CA-----CTAAATCATGTGCTCCTTTTAAATCTCCTTT-ATGCGCT----
GAGGTTTTAG 2499


Qy         793 ATGTGCGCAAG------
AGTGTGCTGCTTATGGAATTGGAGGTCAACTATGGCCTCAAAC 846
                   | |  ||     ||      | |  |||| |  |||| |||||
|||
Db        2498 TTATACAAAAACCCCTTCCAGTCAAACAGAAAAAATT--
AATTCAAATATGGAAAGAAAA 2441


Qy         847 A-
CAAAGTCCTCCAGTCGCAGCTGGATACTCTGCTCCAGGGGCAGGAGAGCATTAAGAGC 905
                   | |||| | |||  |  |  ||| | || | |  |  ||||
AGTAGTTCATTT----- 2397
Db        2440 ATCAAA--CTTTCAGTATTTTC--GTGACT---ATCTTG----


Qy         906 TGCAGCAACTTC-ACAGC--GCAGGC-
CCTCAACCATGGCACGGAGACCGAGGTCCTACT 961
                   | |  ||  ||| ||||| |||  | || | ||    | ||   ||||
|
Db        2396 TCCAACCTCTTAGACAGCTGACAGACACCACTAAC------------
CTGATCACCTATT 2349


Qy         962
GGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAGCTGGCCGACCAGGACTTCCCCTTGCA 1021
                   |||         |||| | | |       ||  | ||||||
|
Db        2348 ---------TCAG----------AGCTTCA-AAGAT------
CCTTAATTTCCCCAAAGA 2315


Qy        1022 C--CC---GCGGGAGAACGACCAGCTGGATTTCATCGTGGAAACCG--
AGGGGCTGAAGA 1074
                   |  ||   ||  || || | |     || |||| |  | |  ||
|
Db        2314 CTTCCTGAGCAAAAGGACTACATGTGGGAAATCA--
ATGAAAACAGGAATGAGAAGAGAA 2257


Qy        1075
AGTCCATCCACAACCTCGGGACGATCTTAACCACCAACGCCGTTGCCTCAGAGACAGTGG 1134
                   |||         | ||  | ||  |                 ||| |||    | ||
||
Db        2256 AGT-----TAAAAATT--GGTTGCTTTT-------------GTT-CCT----
```

```
GTCATTG- 2223

Qy        1135 CCACGGGCGAGGGGCTGCGGCAGACCATCATC-
GGGCAGCCCATGTCCGTCACCATCACC 1193
                        ||| ||    |        || ||     || || ||          |
||
Db        2222 ----------GGGACTTTTG------GTCTTCTAAACATTCCTTG---------
AGTTCC 2188

Qy        1194 ACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAACGCCTACCT---
CACCGCCGAA 1250
                        ||    |||       |||| | | | | | | | | |    | |     || |
||
Db        2187 TCC----ACA-------TGAGTTTTTAATATCAATCTA-
GCAAAAATTAAAACAAACAAA 2140

Qy        1251 CTGAGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCCTGGACAACAAGAACGGCACC 1310
                          ||   || |          || || |    ||| ||| ||  || |        |||||
|
Db        2139 AAAAG-GCCTC-----------TGAAAGTCAG---GATACTGACCACC----
TCGGCATC 2099

Qy        1311 TATGAGTTTTTGTACACTGTCCAGAAGGAAGGG---GACTTTAC---
CCTGTCTCTGAGA 1364
                          |           | | || ||    |   | |   | | | | |   ||||| || |
|
Db        2098 TC----------
TCCCCTTCCCCACTGCTTGCGAATGCCAGTGCTGGCCTGTTCCTTAAA 2049

Qy        1365 CTCTATGACCAGCACAT---
CCGAGGCAGCCCGTTTAAGCTGAAAGTGATCCGATCCGCT 1421
                          | |     |||||| |||   | |   ||| | |       ||| |
|||
Db        2048 CGC----ACCAGCTCATCCCCCAGAGCAGCCTGTGTGCTCTGCCAG-----CGA-
CTGCT 1999

Qy        1422 GATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGGAGCGGCCAC 1481
                          |    |||| || ||                     ||   | |||| |     ||  ||
Db        1998 ACTTCTCCTCCGGCCTCA----------------
GCTCAACATCCCAGCTATGCTACCCT 1955

Qy        1482 GTCAAGC--
AGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAACGAAAAG 1539
                          |    || |   |||| ||    | |   |  ||||   |||| | || |
Db        1954 G---GGCTATGTGAGCT-TG----GGCAAGTTAGCA--
TACATCTCTAGG---------- 1915

Qy        1540 AGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAAATAAAGGAG 1599
                          | ||       |||||| | ||| |||        ||| | | ||
|
Db        1914 -------CCTC--------------TCTTTCCA-TGGATAC-------
AGAGAAGATGGTG 1883

Qy        1600 AGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGATATTAATTGCAGACA 1659
                          |   | | |||| | || |         |||              ||| ||||
Db        1882 A---TGCCTA-CTTCATAGAGT-------TCTT-----------
```

```
                                  ATAAGAATT------- 1852

Qy       1660
GTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTCGTTTTGGCA 1719
                   ||          | ||                  |||                      |
Db       1851 -------CC--------CTGA--------------GGC----------------
TAGGCA 1837

Qy       1720
TACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTACATCCCAGTG 1779
     |                       ||   |||         |  |||        |||||  |||||||
Db       1836 T----------------GGTGGCT-------CACAC--------CTGTA-
ATCCCAG-- 1812

Qy       1780
GGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCTCCGATGGGA 1839
                   ||    | |||           ||         |||||             |
Db       1811 ----CA-----CTTTG--------GA---------GGTCA-------------
AGGTGGGA 1790

Qy       1840
AATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTTCTGTGGACC 1899
     |                          |||||         || |  |||  |||||  |||
Db       1789 A----------------GATCA---------ATTGAGCCC--AGGAG-TTC--
AAGACC 1761

Qy       1900 GCAATGGGCACATTATTGTTGTGGACAACAAGGCGTGC-
TGCGTGTTTATCTTCCAGCCA 1958
                   ||               ||| ||||| ||| | |||     |||| |
Db       1760 ------AGCC-----------TGGGCAACATAGCGAGAGTGC------ATCT--
CTACCA 1726

Qy       1959 AACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGT-TTGC-
AG 2016
                   || | ||   |        |||| |         | ||||||  ||| ||
Db       1725 AAAGTGATTTT----------TTTGAT--------TTTTTGGGACAG--
AGTCTCGCTCT 1686

Qy       2017 GTC-CCCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATTTC--
CATA 2073
                   ||| ||||     |||| |  ||| | || |       || | | | |  ||
Db       1685 GTCACCCA------GGCTG--GAGTGCAGTGGTGTG------
ATCTCGGCTCACTGCAAC 1640

Qy       2074
ATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGGCTCAAATG 2133
                   ||   || | ||||     || |  ||| || ||||||                |||
Db       1639 TTCTGCCT-CCCAGGT------TC---AAGCAGCTCTCATGT----------
CTCA---- 1604

Qy       2134
GAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAATGGAAACA 2193
                                ||              ||||     | ||||| | |  | || |||
Db       1603 -------------GC---------CTCCC----
GAGTAGCTGGGATTACAGATGCCTGCC 1570
```

```
Qy        2194
TCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAGTGGATCATTTT 2253
          |  ||        |  | |||    ||  |  ||||  || || ||||
Db        1569 ACCATG-------CCAGGCAAATTTTGGGTT----GTTTTTTTTGAGA-
TGGA------- 1529


Qy        2254 TGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCC-
TGGCCCTAACT 2312
              ||| | |   ||| |     | |||         |||   |  || |||| | |
|
Db        1528 -GTCTTGCTCT-----ATCAGCAGGC--------TGG-----
AGTGCAGTGGCGCGATC- 1489


Qy        2313
TCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTATCGATAC 2372
              || |   |||       |||| ||||| | |  |  | |
|
Db        1488 TCGGC---TCA--------CTGCAACCTCTG--ACTCCCGGGTTCAAG------
CGATTC 1448


Qy        2373
TTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCACTATAAACTGGAAT 2432
              |            | |   || |   ||||| | |  ||||
|
Db        1447 T--------------CTTG-------CCTCAGCC----TCTTG----
AGTAGCTGGGA- 1419


Qy        2433 GGATTTCTCAATGCG-
GGACCAGATTATGACTAGAGTTTTTATGCCAGAAGGAATCATTG 2491
              || | |||| ||||                        |||
Db        1418 ------CTACAGGCGCGCGCACCA----------------------
CCA------------- 1400


Qy        2492
GTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACTTATCCAATT 2551
              | | | |||| |  |  |     ||| | ||| ||| |||
Db        1399 -------TGCCTGGCTAATTTTTG--TGT-----
TTTTAGTAGAGATG----------- 1366


Qy        2552
TCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAAAACTGCAGT 2611
              |  ||||||| ||  || || |   ||||||                    | ||
Db        1365 ---GGGTTTCACCCTGTTGGCCAAGAGGACCCC--------------------
CAGC--- 1332


Qy        2612
TTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATTTTGCAA 2671
              | |     | | |   | |   |  |   | | ||       || |
|||
Db        1331 ----CTTC------CCAAGCCATAGGGGGCTG-------GTGG-------------
GCAG 1302


Qy        2672
ATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGTGAATGG 2731
              |     | |||||     | ||    || |  || | |  || ||||| |
Db        1301 GGC-----GGCACTT-----AGCT-GCCT-----GGGGCACCCAGTA--
CCTGTCAT--G 1262
```

```
Qy       2732 TAGCTTTTGCACAGAACTTCCAAAAG-
CAAAACAAAAACAAAATCTATTGTAGTTATATA 2790
                   || |||| |  ||     ||||| | ||   | ||  || |  |
|
Db       1261 AGGCACTTGCCCTGG----
CCAAAGGTCACTGCCAAGGCACAGCC--------------A 1220


Qy       2791
CTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCTCACTTTTACAGTAGGT 2850
              || || |   |    |||| || | ||| || || |  |                  |||
||
Db       1219 CTCCAGAGA------GTCAAGAGGAGCAGAGACTC--CAGA----------
GCAGATGGA 1178


Qy       2851
ATTACTCTTGTGACATTTTTTGGTTATCAACAACTAAATATAAATTACTTTGGAAAAAG 2910
               |   |   ||| || | ||| | |   ||| |                    ||||
||
Db       1177 AGGA---GAGTGG-GCTTCTGGGGATTGCACCAAGGA----------------
GGAAGCAG 1137


Qy       2911 TAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCCCTCTGGAGTTC--
AGAAC 2968
                 | || |||  ||| |       ||| |   || ||  |   || |||| ||
|
Db       1136 AAGGGATGTGCAGCAG--------CAGAAAAGG--
AGGAGGACCGGGGGGGTTCTGAGGGC 1087


Qy       2969 TTAAG--TATCAGTGCAAATTTCTCAACCT--
TTCTGGGTTAGACAAAGATCCTTTTTTG 3024
               || |  || | ||  ||  | ||| |||  |   ||||||||     ||
Db       1086 TTGGGGTGATGAGGCCAGAGTTC-CAAACAGGGTCTGGGT---
GCAGG-----------A 1042


Qy       3025
TGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCTTCAG 3084
               || | |                            |   | ||  ||||| || ||
Db       1041 TGAGGAC----------------------------
AGAAGAAAACAGAGAAC-------- 1018


Qy       3085
GGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTTGG 3144
                                           ||  |  |||     || |||   || | ||||
Db       1017 ----------------------CCAAAAGGGGCA------AGAGGT--
TGGTCCCTT---- 991


Qy       3145
GAAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGTTAGT 3204
                                   |||   || |||  ||  |   ||||         || | | |
|
Db        990 -------ACT------TTCACTC----TC------CTGG---------
GAGGAGGATGG- 964


Qy       3205
CATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTTCCTGAAAGCGAAA 3264
                               |||||        ||||| ||             ||  | |
|
Db        963 ----------GTACAC------CACAC-AGT------------------
TGGATGGTGCA 939
```

```
Qy      3265 GCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCA-
GTATCCTAGGACAGAGA 3323
             |||| ||        |||| |||| || ||     | ||| |   || ||||
|
Db       938 TCTTTGCC---------TGTCTGCACCTGCAG-----
CTCCATGGCACCATGGACCCTGT 893


Qy      3324
GCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGTGATTGATTAATG 3383
             ||          ||    || || ||||| ||          ||        ||||
Db       892 GC---------TCC-------GAGTGGTGGTG----CC-------------
TGAT----- 871


Qy      3384
ATTCCCCCTTAGAAAGCAAGTGTTACCAAAGTTGTGTTATCTTGAAAGCATTACAGGTAA 3443
             ||| ||           ||||              |  ||||
|||
Db       870 -CTCCACC----------------ACCA---------------GGCAGCA------
GTAG 849


Qy      3444
GGGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGACTATGT 3503
             |||                                   | || ||
Db       848 AGGC----------------------------------------
CGCTATCCAG--------- 835


Qy      3504
ATACATGATTAGGGTAAGATAGAATGTATTATATATATATATATATACACACACACAT 3563
             ||||| || ||                                               |
||
Db       834 ---------CAGGGTCAGGTTG---------------------------------
CGCA- 818


Qy      3564 ATATATAGCTGAATCTTTGGTG-
TATTGAAATAGGCAGCACTCTGAAAGACAGAAGCTTC 3622
                              ||||| | |||| | | ||      ||   | | || ||
Db       817 -----------------TGGTGATGGAGAAGTTGCCA------
TGGTGGTCGGAGGCCGA 781


Qy      3623 GTCCAGCCACTCTTCAGCAC-
ATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGTGGAGC 3681
               |||||||   | || ||     ||    |   || |    || | ||| |||
| |
Db       780 CTCCAGCC---CGT-GGCGCTGAGCCAGGTCGTGGCTGGTGTTGGCAG-CCTGGTG--
GC 728


Qy      3682
AAGCCCTAAAGCAGATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCTTTTAGT 3741
             || | |||| |                     |  || ||| | |  | ||| || |
|
Db       727 CT-CCATGGTGCAGGTGAAG-----------GTCCTGGAACGT--
GAGGTTGCGGATGGG 682


Qy      3742
CAGAAAATGGCCTTCTGTGCTTTCAAAAAAAAAACAAAAAAAAAACCACACACACACATA 3801
             |        ||| |||| ||               | | ||| | |
Db       681 CC------GGCGCTCTGAGC---------------------AGGTCTGCAC-
CTCGC--- 653


Qy      3802
```

```
        AAAAACCCAACAGGTCAAAATAAAAGTTGAACTTGAGTTACATTTAATTTAAATATAAAT 3861
                   |||                    | || ||   || ||
        Db     652 ----CCC-----------------               
        TCGAGCTGCGGTACCA------------------ 634


Qy      3862
        GCATTTTGAGAAATGTTAAGAACAATTTAGTCAATCGTTCATCTGTCATTGGTACTGTAA 3921
               | | |||         |||||        |||||          ||||
        Db     633 -CGTCTTG---------TAGAA------GGTCA------
        CATC----------------- 613


Qy      3922
        AATAAGCTGTGGTCTATTTCCACTGTTTAATTTTCTACTCAGTTCTACCAAATAGGATGT 3981
                        ||| || | ||||| |                ||  || || ||
        ||
        Db     612 -------GTGCCCTTTGTCCACAG--------------------
        GGCCCAAGAGCCTG- 582


Qy      3982
        CATGTTTGACATTTTTGATAGTGACTTTGGGGTCTTCTTCACTGAAAGCACCTTAGAACT 4041
                     || |           ||| |||||  ||
        ||
        Db     581 CAGG-----------TGAGGGTGACGTT-----------------------------
        CT 563


Qy      4042
        GTACTATAAGAAAACATTTCCCCTATGTATAATTATATGAATGTGATGTTTATTGCTTAT 4101
                  |           | |||||   | |
        Db     562 G------------------
        CCCCTCGGGA------------------------------ 552


Qy      4102
        TAATTTATAATTCAGTCATTCTCTATATAGGACTTCTTAAAATTTAGAAGGGAAATCTAG 4161
                         ||| ||| |               ||||||  |
        Db     551 ------------CAGACATAC-------------------------
        AGGGAATACGG- 532


Qy      4162
        CTACTTCAAATTGTCTGTTAAATTTATTATGCCCAAATCAACCTCTGAAAAAAGGTTTTT 4221
                             |     | |||| ||||       |
        Db     531 ---------------------------------CGTGGCGACCT-
        TGAAGGCTG------ 512


Qy      4222
        CCAGGAAGATTTACATTTAGGTTTAATATTTTTTTAGTTAGGTAGAGTTTTAAAAAATAC 4281
                        |||
        Db     511 
        CCA--------------------------------------------------------- 509


Qy      4282
        TTGAGCCTGTCCGTGATAAAGCTATAAAATTCAATAACTTTTTAGAATGTTAAATGAAGA 4341
                         || | ||         ||         |||           |  | | ||
        Db     508 -----CCGGACC-------TGC--------TCA----------------
        GAGAGAGGAGAG 484


Qy      4342
        CACTGTTTCCTAACATCAGTGAGATACATCTTTGAATTTAAACATTCATATTTACTGAGT 4401
                 | |||| ||| ||        ||| ||
        Db     483 CCCTGTCACCTGAC-------
        TGATCCA------------------------------ 463
```

```
Qy       4402
ACCTACTAGGTACCAAGTACTCTTTTAGGCACTGGAAATACAGTGATGGACAAAACAGGT 4461
                        ||| | ||||||           |||
Db       462 ---------GTGC----TACTC---------
CTG------------------------- 451


Qy       4462
AAAAAATCGCTGCCCCCTCAGAGCTGACATTCTGGGGTGGGAATTTCATTTTGCCACGTA 4521
                        ||  || ||||||        |||| |    || ||| |
                                                                        |
Db       450 -----------GCAACCCCAGAGC---------GGGGAAGAA-----CCTTAGCCTC-
TG 417


Qy       4522
CTAACGTTCTGCACAAAAGACAGGCTAGACTCTTGTCTAGATTGTTTAAAAGAAACTTTT 4581
                   |||    || ||  ||||| ||   | |||| |    || |
Db       416 CTA-----CTTCCCAGCC-ACAGGCCAGGGGCATGTC-AGCT-----------
GACCTCC 375


Qy       4582
CAAATTGGTTACATTAATTTTAGTTTATTTTCACAAGTAAAAATGGCTTTTTATTTAGAT 4641
                   | ||  | | || |          |  | ||||||||
Db       374 CTAA--GACTGCCTTC-----
TGCATTTGTTCACAAACCC------------------ 342


Qy       4642
TCTTTCTGTCCCAGGCTGTTGATCTTAAAACTAGTTGATTTAAAGAGTTTTTTTGCACAA 4701
                 |  ||  ||| |||||||||       ||| |      ||||
                |||||
Db       341 -CACTCCATCCTAGGCTGTTG----------TAGGGG-------GAGT-------
CACAG 307


Qy       4702
CATTTCAATTATATTTGTGAACTTAGAAATTAACTTACAATCTAACCAGCCATCATATCA 4761
                                       | |||| |             ||| |
Db       306 ----------------------------AAGCTTCC-----------
CCAAC------ 294


Qy       4762
TATCCTATCAGGCTAGATATCTCAATAGTAGACTGAATACAAAGCTAATTTTTTTTTACAT 4821
                   |  || |    |||       ||| |           |
                |||
Db       293 -------TAGGGGTG-----CTC---------CTGGATGC-------------
TGGACAG 268


Qy       4822
GTCAATATTGGCACAAACTGGAATGAAAGAATAGTTTGATTCAGACCTGCTCCACTATGT 4881
                   | ||    || | ||||| ||  |       |||| ||| |   |
                |||
Db       267 GGCA-----GGGAGAGACTTGGAGGGCAG-------TGATGCAGTCGGG--------
TGT 228


Qy       4882
GTTGCTAAAACACATGCTATGAGCACTCGAGGAAACACTATATTTTTCCAAAAAATATG 4941
                   ||                      | |||            ||||
Db       227 GT-----------------------CCCTC-------------------
TTCC---------- 217


Qy       4942
```

```
TGATTATATATGTTAAAGTATAGATAACATTTCACACTTGGATACATATGTGCATTTACT 5001
                         ||||  ||                          ||| ||||
||
Db      216 --------------CAGTAGAG-----------------------
TATATGCAAAACCT 195


Qy     5002
GTATTTCTTGGTAAGCATATTTTTGGGGGAAAGTGCTGCTGATATGATACAAGTAGACAA 5061
           |                      ||||| |  ||     || |
Db      194 G--------------------TTGGGTGGGAG----
GCAGGT----------------- 177


Qy     5062
AATTTAAATGAAATTTTGTCACATTCTATGGAAAATGGTTTCTGGTAAACTGAGAAGGAT 5121
                                           ||| | | |||||
|
Db      176 ------------------------------------------TGGGGAGCAG-
GAAGGCT 160


Qy     5122
ATTAAAATAAGTGGCTTTTTTCTGGGCTACCATTATTGTTTGATTTCTCTTTGTCAAGTG 5181
             ||   |   ||  |||          ||           || ||  ||| |
|
Db      159 GTTTCGAACAGCAGCT-------------CC--------------
TTGTCCTTGGCCGCTC 126


Qy     5182
TATAGAACCTGTCATACATTCATGATAAGTAGCACTGAAAAATTACTCATTCAAATTTCC 5241
          | ||| | ||               | |||      |||        |
||
Db      125 TGTAGGGGCCATC-----------------AACAC----------CTC--------
TGCC 101


Qy     5242
CCTGGGCACGTAAGGCAAAATATTGCCGGTTGGGATTTCAAGGTCAGTGACGACGCATTT 5301
             ||                    | ||
|
Db      100 CC---------------------
TTCC------------------------------T 94


Qy     5302 CCTCCCAGTACAGACCCC-CCAGCCCC-
CCTTGCTGGACATGGGGAGGCAGAGAGTCACT 5359
             |||| || || || |   || ||  ||||||          ||| |||
||||
Db       93 ACTCCTAGGACTGAACATGCCTTCCCATCCTTGC-------------CAGGGAG-
CACT 49


Qy     5360 ---
TGACCATCCAGAAATACATGACTACAAGTCCTTTATGACTGTTTGCCATTTTTTTA 5416
                || || |     | || | |||| ||  | | || |||
|
Db       48 AAGAGAGCA-CCTG-----CGTG--TGCAAGGCC--
TGGGCCAGTAGGCC---------A 8


Qy     5417 ATGGTAC 5423
            |  ||| |
Db        7 ACAGTGC 1


RESULT 5
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US-10-478-914-61
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

  Query Match           15.9%;  Score 6088.5;  DB 1;  Length 2437;
  Best Local Similarity   39.6%;  Pred. No. 0;
  Matches 1528;  Conservative   0;  Mismatches  860;  Indels 1471;
Gaps  211;

Qy        5 GTTG--TCTGC-----
GGGCTGCGGGGAGCTAAGTCCCCAGATTGGAGGAGGCTGGCTCT 57
             |||  |||||        |||||||     || |||
Db        1 GTTACTTCTGCTCTAAAAGCTGCGG------
AATTCC---------------------- 31

Qy       58
GGTCTTCGATGCACAGGAGTGGCCGTTATGGAACGCAGCAGCAGCGTGCAGGGTCAAAGA 117
                 |||| |||| |  ||||| |     || |  | | |   |
||||||||
Db       32 -----TCGA-GCACTG--TTGGCCTACTGGGTGTACTGTGGAGAC------
TGTCAAAGT 77

Qy      118
CAGCCGGCCCCCCATGTCAGTGGTCTAGGATGGCCAGTGAAGGCACCAACATCCCAAGTC 177
             |  ||||  ||| || || ||           ||| |  | |||
|||
Db       78 CTCCCGGAGCCCAATTTC--------CGGAAG--CGGTG-----------------
AGTT 110

Qy      178
CTGTGGTGCGCCAGATTGACAAGCAGTTTCTGATTTGCAGTATATGCCTGGAACGGTACA 237
             |||                |||| ||||                    |||| | ||
Db      111 CTG---------------AAAGAAGTT------------------
CCTGCACCG----T 132

Qy      238
AGAATCCCAAGGTTCTCCCCTGTCTGCACACTTTCTGCGAGAGGTGCCTGCAGAACTACA 297
             ||| |||||||                    ||||||
|
Db      133 AGTTTCCCAAG----------------------
TCTGCG--------------------A 150
```

```
Qy        298
TTCCTGCCCACAGTTTAACCCTCTCCTGCCCAGTGTGCCGCCAGACCTCCATCCTGCCCG 357
          |||  || || |  |||       | ||  | | ||| | || ||
Db        151 ATCC--CCAACCATGAGCGCCTC-----------
GGGCGTACTGTCCTTTACCCAGC--- 194


Qy        358
AGAAAGGGGTGGCCGCGCTCCAGAACAATTTCTTCATCACAAACCTGATGGACGTGCTGC 417
          | || ||| || || |      || |||      | || ||| |||
||||
Db        195 ----AAGGATGG----------GAGCAGGTGCTG----GCCAAAGTGA--
AACGGGCTGT 234


Qy        418
AGCGAACTCCAGGCAGCAACGCTGAGGAGTCTTCCATCCTGGAGACAGTCACTGCTGTGG 477
          |  |  ||| || ||| | ||  |              || ||| | ||   |||
||
Db        235 GGTTTA--CCTGGACGGCCGC-CTGCG-----------CCGAGAGCCTG-CA--- 
CTGGGG 276


Qy        478 CTGCGGGAAAGCCTCTC-
TCTTGCCCAAACCACGATGGGAATGTGATGGAATTTTACTGC 536
          ||||||  | || |||| ||       ||  | ||||          ||
Db        277 CTGCGG---ATCCACCCGTCT---CCTGGAGGCGGTGGG--------
GG----------- 311


Qy        537
CAGTCCTGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAGCACGCAGAGCACCCC 596
          | |||  ||||| || ||  || || |||| |          |||| |
|
Db        312 --GCCCT----GACTGTCACCTG-CGAGAGTTC------------------
GAGCCCGAC 346


Qy        597
ACAGTTCCACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTCCAGGTCCAGCTGGAT 656
          || ||  |||||||||  | |||       |          ||||
Db        347 GCAATT-----------GGTGGTGGAGC----CAAG--------------- 
CAGC----- 371


Qy        657
GCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCAGTTCATCTCTGAAATCATT 716
          || ||  |  | || |||| |   | |
Db        372 -----------------
CCAAGGCAGTGTTTGTGCTGAGCTG-------------------- 396


Qy        717
CATCAGTTAACCAACCAAAAGGCCAGCATCGTGGATGACATTCATTCCACCTTTGATGAG 776
          ||  |   |   |||||||| | |||||||  | | || | |
Db        397 ----------CCTGCTGAAAGGCCGG-
ACCGTGGAGATCCTACGGGACATCAT------- 438


Qy        777 CTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTATGGAATTGGAGGT--
CAACT 834
          || | | ||| |          || | |||             ||| |||
||||
Db        439 CTGCCGCAGTCACTTC-------CAGTATTGTG-------------- 
TGGTGGTCACAACC 478


Qy        835 ATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGATACTC-
```

```
TGCTCCAGGGGCAGGAG 893
   ||  |     |||   ||||  ||   ||  ||||     || || ||   |||| |||
Db      479 GTGAGC-----CACGCTGTCCACC--TCACAGC----
TAATCATGTCCCAGCGGC----- 522


Qy        894
AGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCCTCAACCATGGCACGGAGACCGAG 953
                          ||  || || |   | |   | |   ||  |  ||      ||| |
                  ||||
Db      523 ---------GGCAGCGGC--CGAGATGGAG--GGGCAGCAGC-------
CGGTGTTCGAG 562


Qy        954
GTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAGCTGGCCGACCAGGACTTC 1013
                  |  ||||| | |||||||   || |       |||| |  ||| | | ||   | |||
               |
Db      563 ---CAGCTGGAGGAGAAGC---TGTG--------TGAATG-
GATGGGCAACATGAACTAC 607


Qy        1014
CCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCATCGTGGAAACCGAGGGGCTGAAG 1073
                  |                                       ||   ||||||| |
Db      608 AC----------------------------------------GG---
CCGAGGTG------ 619


Qy        1074
AAGTCCATCCACAACCTCGGGACGATCTTAACCACCAACGCCGTTGCCTCAGAGACAGTG 1133
                      ||||  ||    || | ||    ||    | ||||| |
Db      620 ------TTCCATGTCC------CGTTATTGCTTGCCC---
CTGTTGCTCC---------- 654


Qy        1134
GCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCAGCCCATGTCCGTCACCATCACC 1193
                    ||||          || | |   ||| |   ||| |||| | ||| |||
Db      655 -CCAC------TTTGCCTTGAC--TCCAGCTTT-TGCATCCCTTTTCC--
CACTGCTAC- 701


Qy        1194
ACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAACGCCTACCTCACCGCCGAACTG 1253
                  || |||||                        ||| | |  |
Db      702 -CCCAGGA--------------TGTGCA------------
CCTCCTTAATAG-------- 726


Qy        1254
AGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCCTGGACAACAAGAACGGCACCTAT 1313
                  |  ||||||              | ||| |  || ||||      |||
Db      727 ----CGCCCGAC----------CGGACAAGAGGAAGCTGGG----
AAG----------- 756


Qy        1314
GAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTACCCTGTCTCTGAGACTCTATGAC 1373
                              || |   || | |||| | | |        || |||
               ||
Db      757 -----------------CCTGGGTGATGTGGAC--TCCACT---------ACGCTA--
AC 786


Qy        1374
CAGCACATCCGAGGCAGCCCGTTTAAGCTGAAAGTGATCCGATCCGCTGATGTGTCTCCC 1433
                      |          ||   || ||    ||||         | |||| | ||
```

```
Db        787 C-------CCAGAGCTGC-------TGCTG--------
CAGATCAGATG----------- 813

Qy        1434
ACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGGAGCGGCCACGTCAAGCAGAAA 1493
                                               ||  |  |  ||||      |||
Db        814 --------------------------------CCTAGTGTCAGGCCT-------
CAGTTC 834

Qy        1494
GCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAACGAAAAGAGAATCCCATCGAA 1553
                |||||  ||        |||  ||      |||  |||  | |||
Db        835 TCTGTGTGAA----------CATTTA-------
GGAGTACGGGAGGAGT----------- 866

Qy        1554
GACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAAATAAAGGAGAGTTTACAAATCTT 1613
                   |  |||| |       ||  ||| ||  | |                  ||  ||
                                                                          |
Db        867 ---GTTTTGCT-------GTAGGTTCCTTAAG--------------------
TCAGGTCAT 897

Qy        1614 CAGGGGGTAGCTGC--
ATCTACAAATGGAAAGATATTAATTGCAGACAGTAACAACCAAT 1671
                 |        |||||  |||      |||  |  ||      |||   |  | ||   | ||
Db        898 C--------GCTGCGGATC------TGGCCAATTA-----TGCC-
CCTGCAAAGAACA-- 935

Qy        1672
GTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTCGTTTTGGCATACGGGGACGCT 1731
                |  | |||  |  ||  |   | ||  ||| ||  || |||| ||||     |  ||||
Db        936 GGAAGAAGA------CTGCTGCAGG-CAGGGCATCAGTGGTTTT------
TGTGGACAGA 982

Qy        1732
CTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTACATCCCAGTGGGGACATAATCA 1791
                       ||  ||          |          | ||||||| | ||  |  ||| | ||   |
                                                                          |
Db        983 ACCCTGGAT-----------CTCACAGGAGCAGTTGGACATC---ATGGAGAC---
AACT 1025

Qy        1792 TTGCCGATTATGATAATAAATGGGTCAGCATTTTCTC--
CTCCGATGGGAAATTTAAGAC 1849
                   |  |  |       ||  || |  ||||||| || |  |||| |  ||  |
                ||
Db        1026 TAGTAGA----GAAGATCATT---TCAGCACTTCCCCAGCTCCCA--GGCCAC-----
AC 1071

Qy        1850 AAAAATTG-GATCAGGAAAGC-TGATGGGACCCAAAGGAGT---
TTCTGTGGACCGGCAAT 1904
                |||   || |||  ||  || | | ||  |  | |     ||| |||
Db        1072 AAATGATGTGAT--
GGTTAACATGATAGCGCTCACTGCACTCCATACTGAGGA------- 1122

Qy        1905 GGGCACATTAT--
TGTTGTGGACAACAAGGCGTGCTGCGTGTTTATCTTCCAGCCAAACG 1962
                  ||| |  |||||  ||| ||   || ||||           | |||| ||| | |
                |
Db        1123 -GGAAAATTATAATGTGGTTG--CACCAGGC-----------TGTCTTTCA-
CAATTCA 1166
```

```
Qy        1963
GGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGTTTGCAGGTCCCC 2022
          |     |  |||||        ||| |  |  |  |  | ||   ||| |   |
|
Db        1167 G------TGACACCA-------CAGCCAAAGCCCTATGGG-AAGC--
TTTACTGAACACT 1210


Qy        2023
ATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATTTCCATAATCATTCTG 2082
          |       |||  ||    ||| |||  |                ||  |  |   |||
|
Db        1211 A------AGCACAAAGAGGCAGTGATG--------------
GAAGTTCGGAGACATCTAG 1250


Qy        2083
TCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGGCTCAAATGGAGAAGGAA 2142
         |   | |||       ||  |   | ||||| | |   |           | |||  ||| |
Db        1251 TGGAAGCG-----GCAAGCA-GAGAAAACCTG-------------
CCAATCAAGATGAGT 1291


Qy        2143
ATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAATGGAAACATCATTGTGG 2202
         |||||| ||            ||  || ||   |||          |||   |      |   |||
|
Db        1292 ATGGGGAGAG------TCACACCGGGACAGC-------TCATGT----
CCTATATTCAGC 1334


Qy        2203 CCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAGTGGATCATTTTTG-----
TC 2257
              |  |  | |||| |    || | | | |       | || ||||||| | |
||
Db        1335 TCTTCAAG---AACAAC---CTCAAAGCTCT-------
AATGAATCATTGTGGCCTCCTC 1381


Qy        2258 CTACATTAAC--
ACATCTGCTGACCCACTCTATGGCCCCCAAGGCCTGGCCCTAACTTCA 2315
              |  | ||  || |      |||| | | |    |  ||||  | ||| | ||
|
Db        1382 CAGCTTGGACTGGCCACAGCT--CAAACGTTGAAACACCCACAGACTG--CC------
AA 1431


Qy        2316
GATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTATCGATACTTA 2375
         |  || || ||           |||||    || || | |  || |||| | ||  |   |
Db        1432 GTGGGACAACTT------------TCTGG------CT-TTTGAAAGGC--
TCCTTCTTCA 1470


Qy        2376 CAGTAATGGTGGG-
CAGGTGGATACCCGCTTCCATGGTCTTGCACTATAAACTGGAATGG 2434
              || | ||| | || | |||        |    ||| ||| | ||     || | |||
Db        1471 GAGCATTGGGGAGTCAG--------CAATGTCCGTTGTGTT---
AAATCAGCTG------ 1513


Qy        2435 ATTTCTCAATGCGGGACCA-
GATTATGACTAGAGTTTTTATGCCAGAAGGAATCATTGGT 2493
              ||          | |||     |  |||        ||  ||||| ||| || |
Db        1514 ----CT--------GCCCATGATTAAGCCTG-------TAACCCAGA--
GAACCAACGAG 1552
```

```
Qy        2494 GA--ACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCT--
TAAAAATGACTTATCCAA 2549
               ||  ||   ||  |   | | ||||          ||||  | |    | |||| |
Db        1553 GACTACAGCCCTGAGGAACTGCTGA-----------
TCCTTCTCATATATATTTATTCTG 1601

Qy        2550
TTTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAAAACTGCA 2609
               | ||| |  | |      |  |   ||| |   || |        ||| |     || | |
|
Db        1602 TCACTGGAGAGCTC----ACGGTAGACAAAGAC-------CTGTGT-----
GAAGCAGAA 1645

Qy        2610
GTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATTTTGC 2669
               |  |    |   |    | |     |||||     |||| ||||   || ||     ||
Db        1646 GAAAAAGTCAAGAAAGCATTGGCT-------
CAGGTCTTCTGTGAGGAATCTGGATT--- 1695

Qy        2670
AAATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGTGAAT 2729
                  | |||      | || |     | ||  |||  || || ||        ||| ||
|
Db        1696 ----------GTCACCT--------TTGC---TGCAAAAAATTACG----
GACTGGGACT 1730

Qy        2730
GGTAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAAATCTATTGTAGTTATAT 2789
                  |  |   ||   || |   || |   ||     ||||| ||||||| |   || | |
|
Db        1731 CTT--CAATTAATCTGACATTTC---------ACAAATCCAAAAT-
TGCCGTGGATGAAC 1778

Qy        2790 ACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCT-
AACCTCACTTTTACAGTAG 2848
                   ||| | || ||          |||| | || | ||  |
Db        1779 TCTTTACTTCACTT--------------
CGGGATATTGCTGGAGCTC------------G 1812

Qy        2849
GTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATATAAATTACTTTGGAAAA 2908
               | |  | |||  ||   ||  || |||          || | |||| || |
||||||
Db        1813 GAGT--CTCCTGAAACAGTTT-------------AAGTCTGTATATGTTCC--
TGGAAA- 1854

Qy        2909 AGTAAGGCTGTCTTGCAAAATGATCCCAGC-
TCTGATTAGCAGCCCTCTGGAGTTCAGAA 2967
                             | | | |  || || |||| || |      || ||     |
Db        1855 ----------TCATACCCA-----CCAGGCATCTTATAAG----CCATTG----
TTGAAG 1891

Qy        2968 CTTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGATCC-
TTTTTTGTG 3026
               | |||||    | | |||| | ||| | | |   | | ||||| |   ||| || |
||
Db        1892 C--AAGTTGTGGAGGAAATATTTCATCC---C---
```

```
GAGAGGCCAGATTCCGTTGATATTG 1943

Qy       3027 TGTTCTTTTCACCA--
CCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCTTCAG 3084
              | | || || || | ||| || |||| | | |   |   |  ||| |
|
Db       1944 AACACATGTCTTCAGGCCTCACT-GATCTCCTTAAAACTGGATTTAGCATG-
TTCATGAA 2001

Qy       3085
GGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTTGG 3144
              || | | |              |||||                  |  |||
||
Db       2002 GGTGAGCCG-----------GCCT-------------------------
CATCCTAGTG- 2024

Qy       3145
GAAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGTTAGT 3204
                    ||| ||||   |||| ||||   | |
Db       2025 -------ACTACCCC-----CTCCTGATC----
CTC------------------------ 2044

Qy       3205
CATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTTCCTGAAAGCGAAA 3264
                   ||| ||   ||  |||||  ||||||     || |   | |
|||
Db       2045 -----TTTGTGGTAGGTGGGGTCACA---GTCTCT-------
GAAGTGAAAATGGTCAAA 2089

Qy       3265
GCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCAGTATCCTAGGACAGAGAG 3324
                  | |            |  || ||  || |   |||| || |||   | |
|
Db       2090 GAT----------CTTGTGGCATC----GTTGAAG----
CCAGGAACCCAGGTAATCGTG 2131

Qy       3325
CCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGTGATTGATTAATGA 3384
                 |                    | |||| ||                   |
||
Db       2132 C--------------------------TGTCCAC--------------------
ACGA 2143

Qy       3385
TTCCCCCTTAGAAAGCAAGTGTTACCAAAGTTGTGTTATCTTGAAAGCATTACAGGTAAG 3444
                   |||              || | |||           ||| | |||| |
|
Db       2144 CTCC---------------TGAAGCCA------------CTT---AACATTCC-----
TG 2168

Qy       3445
GGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGACTATGTA 3504
                  | |    |||||||| | |     ||     |  |  |  | ||| ||
Db       2169 AGCT-------GTTATTTGCAACTG---ACCGACT-------GCATCCA--
GACCTTGGC 2209

Qy       3505
TACATGATTAGGGTAAGATAGAATGTATTATATATATATATATATATACACACACACATA 3564
                  | |   | | | | | ||| |             ||| | ||  || ||
Db       2210 TTC----TGAGCATCCGCTAAGAAG----------------ATA-
```

```
AGACCTACTCA---- 2244


Qy      3565
TATATAGCTGAATCTTTGGTGTATTGAAATAGGCAGCACTCTGAAAGACAGAAGCTTCGT 3624
                |||||                               |||| | || ||
|
Db      2245 -----AGCTG------------------------------
GAAATGCCGATGCAATTT 2267


Qy      3625
CCAGCCACTCTTCAGCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGTGGAGCAAG 3684
             | |||||  ||   | | |||| || || |||       ||||| ||
Db      2268 TCTGCCACCACTCCAAATACTCCTCCAC-AACCAG--------
CGTCCCTGT-------- 2310


Qy      3685 CCCTAA-AGC-AGATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCTT-
TTAGT 3741
             | |||| || ||| | |    ||  ||| | | ||| |    || |  || |
|||
Db      2311 CACTAATTGCGAGAATGA-----
TGGAATTCTGCCTGAAGGGTCTTGATACCTACTCAGT 2365


Qy      3742 CAGAAA------
ATGGCCTTCTGTGCTTTCAAAAAAAAAAACAAAAAAAAAAACCACACACA 3795
                || |     ||| | ||||| ||  ||||||||| ||||||||  |||||
Db      2366
GAGGTACTTTGCTTGGATTGCTGTGATTCTTAAAAAAAAAAAAAAAAAAAAAGGCCACATGTG 2425


Qy      3796 CACATAAAAAACCCAACAG 3814
             | |            | |||
Db      2426 CTCGAG-------CTGCAG 2437


RESULT 6
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2437
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-61

   Query Match           15.3%;  Score 5858;  DB 1;  Length 2437;
   Best Local Similarity  37.3%;  Pred. No. 0;
   Matches 1528;  Conservative   0;  Mismatches  844;  Indels 1722;
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Gaps   230;


Qy          17
CTGCGGGGAGCTAAGTCCCCAGATTGGAGGAGGCTGGCTCTGGTCTTCGATGCACAGGAG 76
              ||||     ||||    | |        | | |||   || |  | ||    |
Db        2437 CTGC----AGCTCGAGCAC--------ATGTGGC--- 
CTTTTTTTTTTTTTTTTT------ 2399


Qy          77
TGGCCGTTATGGAACGCAGCAGCAGCGTGCAGGGTCAAAGACAGCCGGCCCCCCATGTCA 136
              ||| | | |||| ||||||    |  ||| |||      ||      | | |    ||
Db        2398 ------TTAAGAATCACAGCAATC-CAAGCAAAGT-----AC------ 
CTCACTGAGTAG 2357


Qy         137 GTGGTCTAGGATGGCCAGTGAAGGCA-----CCAACATCC---CAAGTCCTG-- 
TGGTGC 186
                || || | | | || | |||||     ||| ||| | ||| |  || | 
|
Db        2356 GT-ATC----AAGACCC- 
TTCAGGCAGAATTCCATCATTCTCGCAATTAGTGACAGGGAC 2303


Qy         187 GCCAGATTGACAAGCAGTTTCTGAT----TTGCAGTATATGCCTGGAACGG--- 
TACAAG 239
               | | ||| || ||| | ||    | |||| | || ||  |||    | |
||
Db        2302 G-CTGGTTGTGGAGGAGTATTTGGAGTGGTGGCAGAAAAT--- 
TGCATCGGCATTTCCAG 2247


Qy         240 AATCCCAAGGTTCTCCCCTGTCTGCACACTTTCTGCGAGAGGTGC- 
CTGCAGAACTACAT 298
               |    ||||        | | ||| |    |   ||| | | ||
Db        2246 CTTGAGTAGGT-----CTTATCTTC------TTAGCG--- 
GATGCTCAGAAG-------- 2209


Qy         299 TCCTGCCCACAGTTTAACCCTCTCCTGCCCAGTGTGCCGCCAGAC----- 
CTCCCATCCTG 353
                    ||| |||             | | ||| | | |     |        |
|
Db        2208 ------CCAAGGT---------------- 
CTGGATGCAGTCGGTCAGTTGCAAATAACAG 2171


Qy         354 CCCGAGAAAG--GGGTGGCCGCGCTCCAGAACAATTTCTTCATCACAA-- 
ACCTGATGGA 409
               | | ||| |  ||||| || || || | | || ||| | |||||
               ||
Db        2170 CTCAGGAATGTTAAGTGGC----TTCAGGAGTCGTGTGGACAGCACGATTACCTG-- 
GGT 2117


Qy         410 CGTGCTGCAGCGAACTCCAGGCAGCAACGCTG----AGGAGTCTT--- 
CCATCCTGGAGA 462
                        ||| ||| ||||| || | || | | ||| | |    ||||
Db        2116 ---------------TCCTGGCTTCAACGATGCCACAAGA- 
TCTTTGACCAT-------- 2081


Qy         463
CAGTCACTGCTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCACGATGGGAATGTGA 522
              ||||| | | ||             || | ||    |||||
Db        2080 -TTTCACTTCAGAGACTG-----------------TGACC--- 
CCAC------------- 2055
```

```
Qy         523
TGGAATTTTACTGCCAGTCCTGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAGC 582
                         || ||| || | ||| |              || | |||||||||
Db      2054 ----------CTACCA---CAAAGAGGAT----------------CA-
GGAGGGGGT-- 2028


Qy         583
ACGCAGAGCACCCCACAGTTCCACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTCC 642
                              ||| | | |||||| ||    | || || |||
||
Db      2027 ----------------AGT----CACTAGGATGAGG----CCGGCTCA---CCT---
TCA 1998


Qy         643
AGGTCCAGCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCAGTTCA 702
              | | ||| || | | || |      | ||                    |||||
Db      1997 TGAACATGCTAAATCCAGTTTTAAGGAG-----------------------
ATCAGTGAG 1961


Qy         703 TCTCTGAAATCAT-TCATCAGTTAACCAACCAAA--
AGGCCAGCATCGTGGATGACATTC 759
              | ||||| ||| | ||| | | |||| ||   ||||     ||| |||||| |
                                                                      |
Db      1960 GC-CTGAAGACATGTGTTCAAT--ATCAACGGAATCTGGCCT--CTCG-GGATGA-
AATA 1908


Qy         760 ATTCCACCTTTGATGAGCTCCA--
GAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTAT 817
              |||| ||    | |||| | ||| || |||               ||
                                                                      |
Db      1907 TTTCCTCCACAACT-TGCTTCAACAATGGCTTATAAGATGC--------------
CTGGT 1863


Qy         818
GGAATTGGAGGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGATACTCT 877
                        || | ||      || | ||  |||| |  | ||| |         ||
Db      1862 GGGTATG----------ATTTCCAGGAACATA------TACAGAC--------
TTAAACT 1827


Qy         878 GCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCAC--AGCGCAG----
GCCCT 931
              | | |||| |          | | ||||| ||||| || | || || ||     |
                                                                      |
Db      1826 GTTTCAGGAG---------
ACTCCGAGCTCCAGCAATATCCCGAAGTGAAGTAAAGAGTT 1776


Qy         932
CAACCATGGCACGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAA 991
              || ||| |||| |      |   || | |  | | ||||| |||||            |
|||||
Db      1775 CATCCACGGCA-----ATTTTGG----ATTTGTGAAATGTCAGAT-------
TAATTGAA 1732


Qy         992
CGAGCTGGCCGACCAGGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCAT 1051
              ||| | | ||| | | ||| | |    ||||| |  | || ||    |||| |||
                                                                      |
Db      1731 -GAG-TCCCAGTCCGTAATTT---TTTGCA-GCAAAGGTGACAATCCAG-----
ATTCCT 1683
```

```
Qy        1052
CGTGGAAACCGAGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCTTAACCACCAA 1111
          |    || | |  ||            ||| |     |||| ||
Db        1682 C------ACAGAAGACCTGAG---------CCAATGCTT--------
TCTTGACTT---- 1650

Qy        1112
CGCCGTTGCCTCAGAGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCA 1171
          || | || |  ||      ||            ||  |            || |
Db        1649 -----TTTCTTCTGCTTCA-----CACAGG--------------------
TCTT-----T 1625

Qy        1172 GCCCATGTCCGTCACCATCACCACCAAGGACAAAGACGGTG-
AGCTGTGCAAAACCGGCA 1230
              |  |  |  |||| |     | |||  |||| |     |   | || |  | | |
|||
Db        1624 GTCTA---CCGTGAGCT----
CTCCAGTGACAGAATAAATATATATGAGAAGGATCAGCA 1572

Qy        1231
ACGCCTACCTCACCGCCGAACTGAGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCC 1290
                   | ||||| || | |        || ||  ||     ||| || ||
|
Db        1571 G----TTCCTCAGGGCTGTAGT------
CCTCGTTGGTTCTCTGGGTTACAGG------C 1528

Qy        1291
TGGACAACAAGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTA 1350
                 |    | | | | ||| | |  | ||| ||||         |  ||||
Db        1527 T--TAATCATGGGCAGCAGCT----GATTT--AACAC------------
AACGGACATTG 1488

Qy        1351
CCCTGTCTCTGAGACTCTATGACCAGCACATCCGAGGCAGCCCGTTTAAGCTGAAAGTGA 1410
               ||| |||    | ||| |     |   |||  ||| | |  | || | ||||
Db        1487 --CTGACTC-----CCCAATGCTCTGAA-----GAAGGAGCC--TTTCA----
AAAG--- 1449

Qy        1411
TCCGATCCGCTGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGG 1470
               ||   |  | ||     ||||||   ||         |||            ||||
|
Db        1448 --CCAGAAAGTTG-------TCCCAC-----TTGGC----------------
AGTCTGT-G 1419

Qy        1471
GGAGCGGCCACGTCAAGCAGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAA 1530
               || |   | ||||        |||||||  || |   ||||| |
|||
Db        1418 GGTGTTTCAACGTT------TGAGCTGTGGCCAGTC---CAAGCTGG--------
AGGAG 1376

Qy        1531
AACGAAAAGAGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAA 1590
               |  || |||        ||       ||| || ||||
Db        1375 GCCCACAATGA-------TTC-------
ATTAGAGCTTT----------------------- 1352
```

```
Qy      1591
ATAAAGGAGAGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGATATTAA 1650
                |||  ||      |||| |  |    ||||| || |       |  || ||
|
Db      1351 --------GAGGTT---GTTCTTGAAG----AGCTGAATAT---------
AGGACATGA- 1317


Qy      1651
TTGCAGACAGTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTC 1710
               | | |        ||  ||||      | | |||      ||| | |
||
Db      1316 --GCTGTC--------CCGGTGTG-------ACTCTCC--------CCA-TAC-----
TC 1288


Qy      1711
GTTTTGGCATACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTAC 1770
               | |||     | ||     |||| |          ||| ||  ||  ||  ||  | |
||
Db      1287 ATCTTGATTGGCAGGTTTTCTCTGC-------
TTGCCGCTTCCACTAGATGTCTCCGAAC 1235


Qy      1771
ATCCCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCT 1830
               |||             |||| ||||              ||      ||| |
||
Db      1234 TTCC-------------ATCACTGCC--------------------TC-----
TTTGTGCT 1212


Qy      1831
CCGATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTT 1890
               |          |  |||| |||||       |||| |  ||||| ||||
|||
Db      1211 TAGT----------------------GTTCAGTAAAGCT------
TCCCATAGGGCTTT 1181


Qy      1891 --CTGTGGACCGCAATGGGCACATTATTGTTGTGGACAACAAGGCG-
TGCTGCGTGTTTA 1947
               ||||||        | |||   |||||     |||| |  || |    |  |  |   |
|
Db      1180 GGCTGTGGT--------
GTCACTGAATTGTGAAAGACAGCCTGGTGCAACCACATTATAA 1129


Qy      1948
TCTTCCAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGC 2007
               |  ||||           |||       ||  |||          |||| |
||
Db      1128 TTTTCC------------------TCCTCAG----------------TATGGAGT---
GC 1106


Qy      2008
AGTTTGCAGGTCCCCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATT 2067
               |||  ||      |||  ||          |||             || | ||    |
|
Db      1105 AGTGAGC-------------------------GCTATCAT---------------
GTTA 1087


Qy      2068 TCCAT--
AATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGG 2125
               ||||   ||||||        ||| |   | || ||        ||  |||||
|
```

```
Db       1086 ACCATCACATCATT---------TGTGTGGCCTGGGAG--------
CTGGGGAAGT---G 1047

Qy       2126
CTCAAATGGAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAA 2185
             ||        ||||||  |       |  |||| |        ||| |  ||
Db       1046 CT------------GAAATGATC-------TTCTCTACTA--------
AGTTGTCTC--- 1017

Qy       2186
TGGAAACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAGTGG 2245
                         |||  || || |||   |   |   ||||||||
Db       1016 ---------CATGATGTCCAACT---GCTCCTGTGAGATCCAG---------------
GG 984

Qy       2246
ATCATTTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCCTGGC 2305
              ||       ||||| ||| || ||  ||| |
Db        983 TTC-----TGTCC-ACA--AAAACCACTGAT--------------------------
GC 959

Qy       2306
CCTAACTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTA 2365
              |||  || | ||             |||| ||
Db        958 CCTGCCTGCA------------------
GCAGTCTT----------------------- 941

Qy       2366
TCGATACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCACTATAAA 2425
                                                  ||||| || ||||
Db        940 ----------------------------------------CTTCC-
TGTTCTT---------- 929

Qy       2426
CTGGAATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCAGAAGGAA 2485
                                 ||| || ||                | | ||||||
Db        928 -------------------TGCAGGGGCA----------------
TAATTGGCCAGA----- 907

Qy       2486
TCATTGGTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACTTAT 2545
                             |||                | | || | |||||||
Db        906 ---------------TCC----------------GCAGCGATGACC-------
TGACTTA- 885

Qy       2546
CCAATTTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAAAAC 2605
                             | |     |||| ||        ||||| ||| | |
Db        884 --------AGGA----ACCTACAG-------CAAAACACTCCTCCCGTA-CT------
CC 851

Qy       2606
TGCAGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATT 2665
                             | |  || ||| | | |||||  |||
Db        850 TAAATGTTCACA-
CAGAGAACTGAGGC-------------------------------- 825
```

```
Qy        2666
TTGCAAATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGT 2725
                            |  ||||||            |||| ||           |||
Db         824 ------------CTGACACT---------AGGCATCTG---------------
ATCT--- 804

Qy        2726
GAATGGTAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAAATCTATTGTAGTT 2785
                      |  |||   || | |     ||  |        |||
|||||
Db         803 -----GCAGCAGCAGCTCTGGGGTT-----AGC--------------------
GTAGTG 775

Qy        2786 ATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCT--
CACTTTTAC 2843
                                  || |||| |||||||    |||| || |  ||| |
|
Db         774 G----------------AGTCCACATCACCCAGG----
CTTCCCAGCTTCCTCTTGTCC 736

Qy        2844
AGTAGGTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATATAAATTACTTTG 2903
                  || ||   | ||     |||      ||| ||  |  |      |  |
||
Db         735 GGTCGG----GCGCT------ATTAAGGAGGTGCACATC--CTG-----
GGGTAGCAGTG 693

Qy        2904
GAAAAAGTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCCCTCTGGAGTTC 2963
                 | ||||| ||  |      ||||||        |||| ||| |   ||   ||| |
Db         692 GGAAAAG---GG-----ATGCAAA--------AGCT-
GGAGTCAAGGCAAAGTGGGG--- 653

Qy        2964 AGAACTTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGA--
TCCTTTT 3021
                         || ||| |     ||| |  | ||  |||| ||  |||
Db         652 --------AGCAACAGGG--------GCAAGCAATAACGG---
GACATGGAACACCTCGG 612

Qy        3022 TTGTGT-
GTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCT 3080
                         |||| |||| | | ||  ||| ||        |||         | ||
||
Db         611 CCGTGTAGTTCATGTTGCCCATCCAT----TCAC------ACAGC--------
TTCTCCT 570

Qy        3081
TCAGGGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTT 3140
                    |||      ||| || || ||  ||               |||| ||
Db         569 CCAG------CTGC----TCGAACACC------GGC---------------
TGCTGCCCC 541

Qy        3141
TTGGGAAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGT 3200
                  |       | | ||  ||| | | |            | |||| |       || ||
|
Db         540 T-------CCATCTCGGCCGCTGCCGC----------CGCTGGGA------
CATGA---T 507
```

```
Qy      3201 TAGTCATGTTTTATGTACCATGTTTTCACACG--
TGTCTCTTCTCTTCGACTTCCTGAAA 3258
               |||   |||    || ||   | |  | |||| |||  | | |  |     | |||
||
Db       506 TAG--CTGTGAGGTGGACAGCG-TGGCTCACGGTTGTGAC--
CACCACACAATACTGGAA 452

Qy      3259
GCGAAAGCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCAGTATCCTAGGAC 3318
               | |        || | ||| ||| |  |   | ||||||   | ||| ||
|
Db       451 GTGA---------CTGCGGCAGATGATGTCCC-----GTAGGA------
TCTCCACGGTC 412

Qy      3319
AGAGAGCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGTGATTGAT 3378
                |            ||| ||  | |||   ||| || | ||| |  ||
|
Db       411 CG-------------GCCTTTCAGCAGGCAGCTCAGCACAAACACTGCCTTG-
GGCTGCT 366

Qy      3379
TAATGATTCCCCCTTAGAAAGCAAGTGTTACCAAAGTTGTGTTATCTTGAAAGCATTACA 3438
                || ||| ||          ||||| ||| ||
Db       365 ---TGGCTCCACC----------------ACCAA--
TTGCGT------------------ 345

Qy      3439
GGTAAGGGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGAC 3498
                 ||||  |         |  | ||               ||||| ||    |
|
Db       344 ----CGGGCTCG--------AACTCTCGC-----------------AGGTGACA---
GTC 317

Qy      3499
TATGTATACATGATTAGGGTAAGATAGAATGTATTATATATATATATATATACACACA 3558
                                |||
|
Db       316 ---------------AGGG----------------------------------------
CCC 310

Qy      3559
CACATATATATAGCTGAATCTTTGGTGTATTGAAATAGGCAGCACTCTGAAAGACAGAAG 3618
                | ||                               | || |||    |||| |
|
Db       309 CCCA----------------------------------CCGC-
CTCCAGGAGACGGGTG 286

Qy      3619 CTTCGTC-CAGCCACTCTTCA-
GCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGT 3676
                || | ||||| | | || || |         |   |||| |       | |||||
||
Db       285 GATC--CGCAGCCCCAGTGCAGGCTC--------TCGGCGCAG----
GCGGCGTCCAGGT 240

Qy      3677 GGAGCA-
AGCCCTAAAGCAGATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCT 3735
                | || |||||       ||| | ||| |||| |
||
Db       239 AAACCACAGCCC--------GTTTCACTTTGGCCA----------------------
```

GCA 210

```
Qy        3736
TTTAGTCAGAAAATGGCCTTCTGTGCTTTCAAAAAAAAAACAAAAAAAAAAACCACACACA 3795
                   |  ||          || ||  ||||        |||  ||     |  |  || |
|
Db       209 CCTGCTC---------CCATCCTTGCT---GGGTAAAGGAC----
AGTACGCCCGAGGCG 166

Qy        3796 CACATAAAAAACCCAACAGGTC--
AAAATAAAAGTTGAACTTGAGTTACATTTAATTTAA 3853
                   |  ||||         ||| |  |     ||    ||||| |  ||
Db       165 CTCAT------------GGTTGGGGATTCGCAG----
ACTTGGGAAAC----------- 134

Qy        3854
ATATAAATGCATTTTGAGAAATGTTAAGAACAATTTAGTCAATCGTTCATCTGTCATTGG 3913
                         |||            | ||||          || ||||    |||
|
Db       133 --TACGGTGC--------------AGGAAC----------
TTCTTTCAGAACTCACCGC 101

Qy        3914
TACTGTAAAATAAGCTGTGGTCTATTTCCACTGTTTAATTTTCTACTCAGTTCTACCAAA 3973
                   |  |  |||  |  |||  ||   |  ||  || |      ||| | |||| | |||
|
Db       100 TTCCGGAAATTGGGCTCCGGGAGACTTTGACAG--------TCTCCACAGTAC-
ACCCAG 50

Qy        3974
TAGGATGTCATGTTTGACATTTTTGATAGTGACTTTGGGGTCTTCTTCACTGAAAGCACC 4033
                   ||||      |                  ||||  | | ||  ||| | |    |||
Db        49 TAGGCCAAC------------------AGTGC--TCGAGGAATTC--CGC----
AGCT-T 17

Qy        4034 TTAGAACTGTACTA 4047
                   ||||| | | | ||
Db        16 TTAGAGCAGAAGTA 3
```

RESULT 7
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495

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  Query Match            15.2%;  Score 5811;  DB 1;  Length 2495;
  Best Local Similarity  38.0%;  Pred. No. 0;
  Matches 1597;  Conservative   0;  Mismatches  842;  Indels 1766;
Gaps  217;
```

```
Qy        326
CCCAGTGTGCCGCCAGACCTCCATCCTGCCCGAGAAAGGGGTGGCCGCGCTCCAGAACAA 385
             | | || ||| | | | ||| | |       |||||
Db         1 CACTGTTGGCCTACTGGCTACTATCAGGATC---------
GTGGC--------------- 36
```

```
Qy        386 TTTCTTCATCACAAACCTGATGGACGTGCTGCAGCGAACTCCA----
GGCAGCAACGCTG 441
              | | ||                   || | |||    || | |||    || |||| |
|||
Db         37 TATTTT----------------GAAGAGCT-----
GATCACCATGTTGGAAGCAGCACTG 75
```

```
Qy        442 AG----
GAGTCTTCCATCCTGGAGACAGTCACTGCTGTGGCTGCGGGAAAGCCTCTCTCT 497
               |       ||| | ||| | |||    | ||||  |||  | |||     | | ||||
|
Db         76 GGACTTGAGCGAGCTCACATGGGAATGTTTACTGAATTAGCTATTCTATA--
CTCTAAAT 133
```

```
Qy        498
TGCCCAAACCACGATGGGAATGTGATGGAATTTTACTGCCAGTCCTGTGAGACTGCCATG 557
              |    || || |   ||| ||| |||        ||   |||| ||| |||
||
Db        134 T---TAAGCCTC----AGAAAATGAGGGA--------GC---ACCTG-GAG-
CTGTTCTG 173
```

```
Qy        558
TGTCGGGAGTGCACGGAGGGGGAGCACGCAGAGCACCCCACAGTTCCACTCAAGGATGTG 617
              ||| ||||| |                   |||| ||   || |  | ||
Db        174 -GTCTAGAGTGAAT-------------------ATTCCCAAGGT---
GCTAAGAGCTG-- 208
```

```
Qy        618 GTGGAACAGCACAAGGCCTCG-
CTCCAGGTCCAGCTGGATGCTGTCAACAAAAGGCTCCC 676
              ||| ||||| ||| ||  ||    | ||||  | | |  | | |
Db        209 ------CAGAACAAG--
CTCATCTTTGGGCAGAACTGGTGTTTTTGTATGACAAGTATGA 260
```

```
Qy        677
AGAAATAGATTCTGCTCTTCAGTTCATCTCTGAAATCATTCATCAGTTAACCAACCAAAA 736
              ||||  |||  || |||| ||  || |||||||| || || | |  |        |
||
Db        261 AGAAATATGATAATGC-CATAATTACCATGATG-
AATCATCCAACTGATGCCTGGAAAGAA 318
```

```
Qy        737 GGCCAGCATCGTGGATGACATTCATTCCACCTTTGATGAGCTCCA--GAAG-
ACTTTAAA 793
              || || |  ||  ||| ||||      |||  | ||   ||| |  | ||| ||
Db        319 GGGCA-ATTCAAAGATATCATT------ACCAAGGTTG----
CCAATGTGGAACTATACT 367
```

```
Qy        794
TGTGCGCAAGAGTGTGCTGCTTATGGAATTGGAGGTCAACTATGGCCTCAAACACAAAGT 853
          | |||| |  || |||| ||||       |||| |    ||||||          ||
|
Db        368 ACAGAGCAATACAGTTCTACTTA--GAAT------TCAA-----
GCCTCTGTTGTTAAAT 414


Qy        854
CCTCCAGTCGCAGCTGGATACTCTGCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAA 913
            |    | || ||| ||| || |||||| ||         |  ||
Db        415 GAT----TTGCTGATGG-TGCTGT-CTCCACGG------------
TTGGA---------- 446


Qy        914 CTTCACAGCGCAGGCCCTCAACCAT---
GGCACGGAGACCGAGGTCCTACTGGTGAAGAA 970
            ||||| | |  || |||| ||    ||| ||  |   || | ||||||||
Db        447 --TCACA-
CTCGTGCAGTCAATTATTTCAGCAAGGTTAAACAGCTACCACTGGTGAAACC 503


Qy        971
GCAGATGAGCGAGAAGCTGAACGAGCTGGCCGACCAGGACTTCCCCTTGCACCCGCGGGA 1030
            | |  ||                       || ||| |||    | |||
|
Db        504 GTATTTG-----------------------CGTTCAG---TTC----
AGAACC------A 527


Qy        1031
GAACGACCAGCTGGATTTCATCGTGGGAAACCGAGGGGCTGAAGAAGTCCATCCACAACCT 1090
            ||| || |         ||| ||  |        |||| | || |   | ||||
||
Db        528 TAACAACAA----------ATC-TG-------------
TGAATGAATCATTGAACAATCT 563


Qy        1091
CGGGACGATCTTAACCACCAACGCCGTTGCCTCAGAGACAGTGGCCACGGGCGAGGGGCT 1150
                         | |||
|
Db        564 --------
TTTTAT--------------------------------------------T 570


Qy        1151
GCGGCAGACCATCATCGGGCAGCCCATGTCCGTCACCATCACCACCAAGGACAAAGACGG 1210
            | | ||| || ||| |||        || |  | |||||            | |||
|
Db        571 ACAGAAGAAGATTATCAGGC--------TCTGCGAACATCA-----------
ATAGATGC 611


Qy        1211 TGAGCTGTG-
CAAAACCGGCAACGCCTACCTCACCGCCGAACTGAGCACCCCCGACGGGA 1269
            |    | || |||| |||||||||||                 || |
|
Db        612 T----TATGACAACTTTGACAA----TATCTCGCT---------
TGCTC----------A 644


Qy        1270 GCGTGGCAGACGGGGAGATCCTGG-
ACAACAAGAACGGCACCTATGAGTTTTTGTACACT 1328
            ||||                ||| | |||| ||||      |  ||||||
Db        645 GCGT----------------TTGGAAAAACATGAAC----
TCATTGAGTT---------- 674
```

```
Qy        1329 GTCCAGAAGGAAGGGGACTTTAC--
CCTGTCTCTGAGACTCTATGACCAGCACATCCGAG 1386
                 ||| || |     || |  | |||||                    ||
  ||
Db         675 ---CAGGAGAA-------TTGCTGCTTATCTCT--------------------
TCAAAG 703


Qy        1387
GCAGCCCGTTTAAGCTGAAAGTGATCCGATCCGCTGATGTGTCTCCCACCACAGAAGGCG 1446
              ||| |                        |  |||||              |||||
|
Db         704 GCAAC----------------------AATCGCTG-----------
GAAACAGA----G 725


Qy        1447
TGAAGAGGCGCGTTAAGTCCCCGGGGAGCGGCCACGTCAAGCAGAAAGCTGTGAAAAGAC 1506
               || |||         || |        | |||  || || | || ||
Db         726 TGTAGAG-------CTGTGCAAGAAAGACAGCCTTTACA---
AGGATGCAATG------- 768


Qy        1507
CCGCAAGCATGTACAGCACTGGAAAAACGAAAAGAGAATCCCATCGAAGACGATTTGATCT 1566
                | | || | |  | |    || |  ||| |         |  || ||
  ||
Db         769 CAGTATGCTTCTGAATCTAAAGATACTGAATTG-----------GCTGAAGA---
ACTCC 814


Qy        1567
TTCGAGTGGGTACCAAAGGAAGAAATAAAGGAGAGTTTACAAATCTTCAGGGGGTAGCTG 1626
               | | |||||| |   |||||||| ||  |          ||| | |   |
  |||
Db         815 TGC-AGTGGTTTTTGCAGGAAGAAAAAAGAGAGTG---------
CTTTGGAGCTTGTCTG 864


Qy        1627
CATCTACAAATGGAAAGATATTAATTGCAGACAGTAACAACCAATGTGTGCAGATATTTT 1686
                 | |||                        |  | ||
  |||
Db         865 --TTTAC----------------------CTGTTAC--------------
GATCTTTT 884


Qy        1687 CCAATGATGGCCAGTTCAAAAGTCGTTTTGGCA--TACGGGGACGCTCTC---
CGGGGCA 1741
                 | |||||| |    ||||| | | | | |  ||| || |      | ||
Db         885 ------AAGGCCAGAT-----
GTCGTCCTAGAAACTGCATGGAGGCACAATATCATGGAT 933


Qy        1742
GCTGCAGCGGCCCACAGGAGTGGCTGTACATCCCAGTGGGGACATAATCATTGCCGATTA 1801
               |||  |||| | ||||||  || |    || | | ||| | |
Db         934 TTTGCCAT-GCCCTAT----------
TTCATCCAGGTCATGAAGGAGTACTTGACAAAGG 982


Qy        1802 TG---
ATAATAAATGGGTCAGCATTTTCTCCTCCGATGGGAAATTTAAGACAAAAATTGG 1858
               ||    | | ||| |||  |||| ||      | |           | ||| || ||
  |
Db         983 TGGATAAATTAGATGCTTCAGAAT------CAC------------
TGAGAAAAGAAGAAG 1024
```

```
Qy        1859
ATCAGGAAAGCTGATGGGACCCAAAGGAGTTTCTGTGGACCGCAATGGGCACATTATTGT 1918
              | |   ||||| | ||| ||  |  |  | | | ||| | ||      | ||
|||
Db        1025 AAC----AAGCTACAGAGACACAACCCATTGTTTATGGTCAGC------CCCA--
GTTGA 1072


Qy        1919 TGTGGACAACAAGGC---
GTGCTGCGTGTTTATCTTCCAGCCAAACGGGAAAATAGTCAC 1975
              || ||||| || | | |||  ||| |||         | ||| ||  | ||
|||
Db        1073 TGCTGACAGCAGGACCCAGTGTTGC--------CGTCCCTCC--CCAGG--------
CAC 1114


Qy        1976
CAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGTTTGCAGGTCCCCATTTTGCAGCTGT 2035
         |  ||||||  ||||    |||||        | | | || |  | ||
Db        1115 CT--TTTGGT---------TATGG---------
TTATACCGCACCACCGTATG------- 1147


Qy        2036
AAATAGCAATAATGAGATTATTATTACAGATTTCCATAATCATTCTGTCAAGGTGTTTAA 2095
                                 ||||   |||    ||  ||| |   | ||
Db        1148 ------------------------GACAG---CCA----
CAGCCTGGCTTTGGGT---- 1171


Qy        2096
TCAGGAAGGAGAATTCATGTTGAAGTTTGGCTCAAATGGAGAAGGAAATGGGCAGTTTAA 2155
              |||        ||||||               |||| |   | | ||
Db        1172 ACAG----------CATGT------------------GAGATG---
AAGCGC------- 1192


Qy        2156 TGCTCCAACAGGTGTAG-CA-
GTGGATTCAAATGGAAACATCATTGTGGCCGACTGGGGA 2213
              || |||     ||||| |   ||| |  ||||||||| |  |  || |||
Db        1193 TGATCC------
TGTAGTCACCTATTTTCGTACTGAAACATCGTCTTTACCCACT----- 1241


Qy        2214
AACAGCAGGATCCAGGTTTTTGATGGGAGTGGATCATTTTTGTCCTACATTAACACATCT 2273
                      ||  ||||  | ||||| |              || |||
Db        1242 ----------TCTCAGTTTATAATGGGGG----------------------
AAAACA--- 1266


Qy        2274 GCTGACCCACTCTATGGCCCCCAAGGCCTG--GCCCTAACTTCA-
GATGGTCATGTTGTG 2330
                         |||  |      | ||   || | |||| || || | ||
|
Db        1267 ------ ---------------
GGCAACGTGTTCTTGTAACCTTTATTTCATGAAGGACTTCTTTT- 1310


Qy        2331
GTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTATCGATACTTACAGTAATGGTGGGCA 2390
                          ||||||| || |||| | |||
Db        1311 --------------------TGTTTCTAA--CTAT--
AAACT----------------- 1328


Qy        2391
GGTGGATACCCGCTTCCATGGTCTTGCACTATAAACTGGAATGGATTTCTCAATGCGGGA 2450
```

```
                   |||||  ||   |         ||         ||  || ||          |||||  || |
Db        1329 --TGGATCACCTAT------GT-------TAAAACCT------
TATTTCACATT------ 1361


Qy        2451
CCAGATTATGACTAGAGTTTTTATGCCAGAAGGAATCATTGGTGAACTTTCCAAGGTTAT 2510
                   ||| || ||    |||| ||| | | |  |||||        ||   | |||| |  | ||
Db        1362 CCACATCAT-TTTAGAATTTATTTTC--GAAGG-------
GGAATAGTTTCAATGTTTTA 1411


Qy        2511
TTCTGAATGTAACAATTTCCTTAAAAATGACTTATCCAATTTCTGTATTTCACCTTTAGG 2570
                   |||              |||        |  | |||  |    ||||         ||| ||
Db        1412 TTC--------------ACTTG-----GGCTTTT----TTTC-----
TTCCCC------ 1436


Qy        2571 GTTAAAAAAAACTCTTCTACTGAATCTATAAA-AACTG--
CAGTTTTACATCTGTGAACT 2627
                         |||||       ||| |||| |||||  || | ||  ||||||
Db        1437 -----------CTCTT--------
TCTTTAAAGAACTGCTCAATATTCAATCTGT----- 1472


Qy        2628
ATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATTTTGCAAATCAAACAGACACTTA 2687
                     ||   | | | || |||||     ||   ||| ||    |   | ||| ||
Db        1473 -TG---TGAAGAACCTGATTT-----GC---ACTC----
TGTAGTGTTTAAAGAAAC--A 1514


Qy        2688
AAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGTGAATGGTAGCTTTTGCACAGAA 2747
                     ||| |||||  ||||        |    || | |||   ||| |||         |  ||||
Db        1515 AAGAAACTCTAATAT----TGAATCTCTTAAATTTAGTGTATG--------
TAAACAG-- 1560


Qy        2748
CTTCCAAAAGCAAAACAAAAACAAAATCTATTGTAGTTATATACTTCATTTAACCTAGGT 2807
                     ||| |||| |          |||||||   || ||     ||||||
Db        1561 CTTACAAATACG----------------TATTGTC--TAAATG---
CATTTA-------- 1591


Qy        2808
CACAAGACCCAGGGAATCTTCTAACCTCACTTTTACAGTAGGTATTACTCTTGTGACATT 2867
                              |||||  |        || || ||| | |    ||   |
Db        1592 --------------AATCTGTT--------TTATTCA--
AAGAAAAGCTAAAG------- 1620


Qy        2868
TTTTTGGTTATCAACAACTAAATATAAATTACTTTGGAAAAAGTAAGGCTGTCTTGCAAA 2927
                            ||| |||         | | |  | | ||| |||||
|
Db        1621 -----------CAAAAAC--------
ACTGGCATATGACCATGCAAGACTGTC------A 1655


Qy        2928
ATGATCCCAGCTCTGATTAGCAGCCCTCTGGAGTTCAGAACTTAAGTATCAGTGCAAATT 2987
                       ||   ||| | ||  | ||||        ||       |||| ||      ||| ||| ||
Db        1656 GTG---CCAACAAAGA----CAACACT-----AATCAGCAC------ATC-
GTACA---- 1692
```

```
Qy        2988
TCTCAACCTTTCTGGGTTAGACAAAGATCCTTTTTTGTGTGTTCTTTTCACCACCCCTTT 3047
                      |||| ||   ||  | | |                       |||
||
Db        1693 -----------CTGGATT--GCAGTGCTTC--------------------
CCAGATTATT 1719


Qy        3048
GGCTCACCTTGTATCAGCAAACAAAGTACTTCTTCAGGGAAACCTGAAATTTCTAATGCC 3107
       |    |   ||| |||        || |||       ||||| |||  ||||
Db        1720 G---AAAAATGTTACAG----------ACAACTT-------GCCTGATTTTT-
AAATG-- 1756


Qy        3108
TTGAAAAGCATATTACAAAAGTAATGCTACCTTTTGGGAAACAAACTGCCCCGTTAACTC 3167
                ||| |    |||||   |||| | | ||     ||   | |||| |||
Db        1757 ------AGCGT-----AAAAGGCCCTCTAACCTATG-----
CAGGTTTCCCCATTA---- 1796


Qy        3168 CAGATCATTGCACTGGAATGTAATCAAGAAAGTTAGTCATGTTTTATGTAC--
CATGTTT 3225
                  ||||        || | || | |||| |||||||    ||  |||
|
Db        1797 --------TGCA---------TATAGAAATGCTAGT-ATGTTTTGCTCACTTCAT-
ATG 1837


Qy        3226 TCACACGTGTCTCTTCTCTTCGACT---
TCCTGAAAGCGAAAGCTTTACCTCCTGCAAAT 3282
            | |||| ||| | ||| | ||    ||    |||||        ||||| ||
Db        1838 TAACAGGTG-CCCTTATGTTGTGCTGTATCCTG--------
TGCTTTTTCT--------- 1879


Qy        3283
GTCAGCACATGTAGTAGGACACCAGTATCCTAGGACAGAGAGCCATAAGTAGCCCTTTGG 3342
                     || ||||     || | |  || | |||||
Db        1880 --------------
GTGGGACCATTCCATTCAGGAGCAAAGAGC----------------- 1909


Qy        3343
AGGACTGATGGTGTCAACCAAAGGCATGTGATTGATTAATGATTCCCCCTTAGAAAGCAA 3402
                          |||           ||||||||     || |
Db        1910 ----------------ACC-------------------ATGATTCC--------
AATCTT 1926


Qy        3403 GTGTTACCAAAGTTGTGTTATCTTGAAAGCATTAC---
AGGTAAGGGCATGTTATGGTTA 3459
           |||        |||||| ||   || |||   ||||  | | |||| |
||
Db        1927 GTG----------TGTGTTTACT---AACCCTTCCCTGAGGTTTGTGTATGT--
TGGATA 1971


Qy        3460 TTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGG--
ACTATGTATACATGATTAGGG 3517
            ||                     | |||||    |    ||| || ||||
Db        1972 TT----------------------
GTGGTGTTTTAGATCACTGAGTGTACA--------- 2000


Qy        3518
TAAGATAGAATGTATTATATATATATATATATATACACACACACATATATATAGCTGAAT 3577
              |||| ||||                       || || |||     | |||| ||||
```

```
Db       2001 GAAGAGAGAA---------------------ATTCAAACA-----
AAATATTGCTGT-- 2031

Qy       3578
CTTTGGTGTATTGAAATAGGCAGCACTCTGAAAGACAGAAGCTTCGTCCAGCCACTCTTC 3637

             |||||
Db       2032 ---------------------------------------------------------
TCTTC 2036

Qy       3638
AGCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGTGGAGCAAGCCCTAAAGCAGAT 3697
              ||         |||        ||||              |||||     |    |    |   ||
                                                                              ||
Db       2037 AG--------TTT-------TGTTT------------
GTGGAATTTGAAATTACTCAAAT 2069

Qy       3698
TTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCTTTTAGTCAGAAAATGGCCTTCT 3757
              ||||  |     ||||  |   |  |   ||  |     ||||   |||  |  || |  ||| |
Db       2070 TTAAAAT-----AAATTACTGGACT-------GTGGAAATAA--
CATAGAATTG------ 2109

Qy       3758
GTGCTTTCAAAAAAAAAACAAAAAAAAAACCCACACACACACATAAAAAACCCAACAGGTC 3817
              |  |||              ||  |||  |||||| ||  ||
Db       2110 AAGTTTT-------------
AATTAAATACCACTCAAACG-------------------- 2136

Qy       3818 AAAATAAAAGTTGAACTTGAGTTACATTTAATTTAAATATAAATGCATTT-
TGAGAAATG 3876
              ||||  ||  |||  |      |||     ||  ||||   ||   |||     |  |||||     |||
                                                                                  |||
Db       2137 AAAAGAACAGTAGTTTTTG---
TAGTTTTATATTGGATACTGAGGCATTAGGGAGGCATG 2193

Qy       3877
TTAAGAACAATTTAGTCAATCGTTCATCTGTCATTGGTACTGTAAAATAAGCTGTGGTCT 3936
              |  |||                                  |    |||  ||
Db       2194 AAAGGAA-----------------------------------
GAGGAATGAG--------- 2210

Qy       3937 ATTTCCACTGTTTAATTTTCTACTCAGTTCTACCAAATAGGATGTCATGT-
TTGACATTT 3995
              |  ||  |                                  |  |||||
                                                                      ||||||
Db       2211 ---------GATTGA----------------------------
GACATGTGAAGACATTG 2233

Qy       3996
TTGATAGTGACTTTGGGGTCTTCTTCACTGAAAGCACCTTAGAACTGTACTATAAGAAAA 4055
              |  ||   |   |   || |       | |  |||   ||  |  | |||   |  ||||
Db       2234 TGCATTATATCAATGTG-----CATTCCTG-
TAGTTCATTAACAAGGTAC---------- 2277

Qy       4056
CATTTCCCCTATGTATAATTATATGAATGTGATGTTTATTGCTTATTAATTTATAATTC- 4114
                                                            |||  | || ||  |
              |
Db       2278 --------------------------------------ATGC--
```

```
AATAGTCTAAAGAACC 2297


Qy      4115 --
AGTCATTCTCTATATAGGACTTCTTAAAATTTAGAAGGGAAATCTAGCTACTTCAAAT 4172
              ||||| | ||||| ||  ||||| ||||      ||||| || |
Db      2298 AGAGTCACT-ACTATAGTGG----CTTAACATTT-------- 
AATCTGTCTCC------- 2337


Qy      4173
TGTCTGTTAAATTTATTATGCCCAAATCAACCTCTGAAAAAAGGTTTTTCCAGGAAGATT 4232
                    |||| | |||| | || | ||| | ||||||| ||||
|
Db      2338 -----------AATATTTTAACCAAGT-GACACCGG------GGTTTTTATC-
GAAGCAT 2378


Qy      4233
TACATTTAGGTTTAATATTTTTTTAGTTAGGTAGAGTTTTAAAAAATACTTGAGCCTGTC 4292
              | ||| |                                   || ||| |
||
Db      2379 TTCACT----------------------------------------
TAAATGAACAAATC 2398


Qy      4293
CGTGATAAAGCTATAAAATTCAATAACTTTTTAGAATGTTAAATGAAGACACTGTTTCCT 4352
                  |  ||| | | ||   |||||
Db      2399 ------ATGGCTGTTATAT---- 
TAACT------------------------------ 2416


Qy      4353
AACATCAGTGAGATACATCTTTGAATTTAAACATTCATATTTACTGAGTACCTACTAGGT 4412
                  ||| ||| |   | ||||||   ||| | | | | |   |
|||
Db      2417 --------TGAAATAAA---ATATATTTAAA----
CATGTAAAAAAAAAAAAAAAAAGGC 2461


Qy      4413
ACCAAGTACTCTTTTAGGCACTGGAAATACAGTGATGGACAAAACAGGTAAAAAATCGCT 4472
                  || || |||       |  |||                      ||||
||||
Db      2462 CACATGTGCTC------GAGCTG--------------------CAGG-------
TCGCG 2487


Qy      4473 GCCCC 4477
              ||| |
Db      2488 GCCGC 2492


RESULT 8
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
```

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  Query Match        14.9%;  Score 5722;  DB 1;  Length 2495;
  Best Local Similarity   36.9%;  Pred. No. 0;
  Matches 1615;  Conservative   0;  Mismatches  844;  Indels 1920;
Gaps  220;

Qy      1949 CTTCCAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGC-
CGAGGAAATGGGGACAGGC 2007
             || | |||  ||           |||       | ||| |||| | ||| ||
Db      2495 CTAGCGGCC--GCG-----------ACCT------
GCAGCTCGAGCACATGTGG------ 2461


Qy      2008
AGTTTGCAGGTCCCCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATT 2067
                             || ||||   |||||| |          | |   || || |||||
||
Db      2460 -------------CCTTTTT------------------TTTT----
TTTTTTTACATGTT 2435


Qy      2068
TCCATAATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGGCT 2127
             |  |||    || | ||||| |  |  | |||        |||     | || |
Db      2434 TAAATATATTTTATTTCAAGTTAATATAACAG----------CCAT------
GATTGTT 2391


Qy      2128 CAAATGGAGAAG-
GAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAAT 2186
             || |   ||| |||||| | ||||||| | |    ||||           |||
|
Db      2390 CATTT----AAGTGAAATGCTTCGATAAAAACCCC----GGTG-----------
TCACTT 2350


Qy      2187
GGAAACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAGTGGA 2246
             || | | |||               ||| ||||
Db      2349 GGTTAAAATATT-----------
GGAGACAG--------------------------- 2330


Qy      2247
TCATTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCCTGGCC 2306
                          |||||       || | | ||||| ||
Db      2329 ---------------ATTAA-----
ATGTTAAGCCACTATA------------------- 2309


Qy      2307
CTAACTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTAT 2366
                             || ||    ||||||||                     |||
|
Db      2308 ----------------------GTAGT----GACTCTGGT----------------
```

```
TCTTT 2290


Qy        2367
CGATACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCACTATAAAC 2426
                 ||    || ||                    ||          | || ||  |  || |||
||
Db        2289 AGACTATTGCA---------------TG---------TACCTTGTTAATGAACT----
AC 2258


Qy        2427
TGGAATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCAGAAGGAAT 2486
              ||||||    |  || |                            | | | ||||
Db        2257 AGGAATG-----CACATT----------------------
GATATAATGC---------- 2235


Qy        2487 CATTGGTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACT-
TAT 2545
                                 ||||| ||   |   | ||| ||
||
Db        2234 ------------------------------------ACAATGTC--
TTCACATGTCTCAAT 2212


Qy        2546
CCAATTTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAAAAC 2605
              |    |||                            ||||||        || | |
|
Db        2211 CCTCATTC---------------------------CTCTTC--------
CTTTCATGCC 2188


Qy        2606
TGCAGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATT 2665
                     | |                 ||| || |    ||| ||                |
Db        2187 TCC----------------CTAATGCCT------CAGTAT-------------
CCAAT- 2165


Qy        2666
TTGCAAATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGT 2725
                   || ||||        || |||||    ||| |   | |||||||
|
Db        2164 ------ATAAAAC-------TACAAAAACTA----CTGTTC---
TTTTCGTT-------T 2132


Qy        2726
GAATGGTAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAAATCTATTGTAGTT 2785
                       || |||||    |||     | ||||||               || |||||
|||
Db        2131 GAGTGGTA---TTTAATTAAAACTTC-------------------AATTCTAT----
GTT 2098


Qy        2786
ATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCTCACTTTTACAG 2845
                       || |             || |    ||| |
|||
Db        2097 ATTT-----------CCACAGTC-------------------------------
CAG 2083


Qy        2846
TAGGTTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATATAAATTACTTTGGA 2905
                       ||               |||| |||                         | | ||||
```

```
Db      2082 TA----------------ATTTATTT----------------------
TAAATTTG-- 2065

Qy      2906 AAAAGTAAGGCTGTCTTGCAAAATGATC--
CCAGCTCTGATTAGCAGCCCTCTGGAGTTC 2963
                        |||||      || |||| |    |   ||   |||| | |||| | |
|||
Db      2064 ---AGTAA-------
TTTCAAATTCCACAAACAAAACTGAAGAACAGCAATATTTTGTT- 2016

Qy      2964
AGAACTTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGATCCTTTTTT 3023
                          ||  |||||||||      |||||  || ||      ||
Db      2015 ----------------TG--AATTTCTCTC---TTCTG---TACAC-----
TC------- 1992

Qy      3024
GTGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCTTCA 3083
                  ||| ||  |  | |||| |  | |          || || ||| |
|||
Db      1991 -AGTGATC--TAAAACACCACAATATC-----------CAACATACACAAACC----
TCA 1950

Qy      3084
GGGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTTG 3143
                   |||||
|
Db      1949
GGGAA-------------------------------------------------G 1944

Qy      3144
GGAAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGTTAG 3203
                   || |    || ||| |            ||| || || ||||| |
Db      1943 GGTTA-----------GTAAACAC---------
ACACAAGATTGGAATCATG-------- 1912

Qy      3204
TCATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTTCCTGAAAGCGAA 3263
                              ||| |||| ||| |     |  ||||||| |
|||
Db      1911 ----------------------------GTG-CTCTTTGC-------TCCTGAATG-
GAA 1889

Qy      3264
AGCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCAGTATCCTAGGACAGAGA 3323
                   | |   ||  | ||  |||    ||||||       |||| ||
Db      1888 TGGT---CCCACAGAAAA----AGCAC-------
AGGATAC------------------ 1862

Qy      3324
GCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGTGATTGATTAATG 3383
                         |||                 |||| ||||
Db      1861 ---------AGC--------------------
ACAACATAAGG----------------- 1848

Qy      3384
ATTCCCCCTTAGAAAGCAAGTGTTACCAAAGTTGTGTTATCTTGAAAGCATTACAGGTAA 3443
                   ||| |||||| | | |||         |||| |||
||
Db      1847 ----------------GCACCTGTTACATATGAAGTG----------AGCAAAACA--
```

```
TAC 1815


Qy        3444
GGGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGACTATGT 3503
                ||||          ||| |    ||  |||||                |||
Db        1814 TAGCAT----------TTTCTATATGCATAATG------------------
GGG------- 1789


Qy        3504
ATACATGATTAGGGTAAGATAGAATGTATTATATATATATATATATACACACACACAT 3563
               | || ||  |||     | |||| |  || |              || |
|||
Db        1788 AAACCTGCATAG-----GTTAGAGGGCCTTTT--------------------
ACGCTCAT 1754


Qy        3564
ATATATAGCTGAATCTTTGGTGTATTGAAATAGGCAGCACTCTGAAAGACAGAAGCTTCG 3623
               || | | |        || || |   | |    || | ||||       |||||
|
Db        1753 TTAAAAATCAGGCAAGTT-GTCTGTAACATTTTTCAATAATCTG------GGAAGC-
ACT 1702


Qy        3624
TCCAGCCACTCTTCAGCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGTGGAGCAA 3683
               | | ||| | |         |  | || |||| |   ||| | || |
Db        1701 GCAATCCAGTGTAC-------------
GATGTGCTGATTAGTGTTGTCTTTGTTG----- 1660


Qy        3684
GCCCTAAAGCAGATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCTTTTAGTCA 3743
               || | ||  |||        | ||| ||| ||   ||| | |||       ||||
Db        1659 GCACTGA--CAG-------TCTTG-CATGGTC---ATATGCCAGTG-----
TTTTT---- 1622


Qy        3744 GAAAATGGCCTT--
CTGTGCTTTCAAAAAAAAAAACAAAAAAAAAAACCACACACACACATA 3801
                         || ||  || | |||   | || |     |   |||
|||
Db        1621 -------GCTTTAGCTTTTCTTT---GAATAAAACAGATTTAAAT----------
GCATT 1582


Qy        3802
AAAAACCCAACAGGTCAAAATAAAAGTTGAACTTGAGTTACATTTAATTTAAATATAAAT 3861
               | |   ||| ||| | ||| |  | ||| ||    || |  |||| | |||||||    |
||
Db        1581 TAGA---CAATACGT--ATTTGTAAGCTG---TTTACATACACTAAATTTAAG---
AGAT 1533


Qy        3862
GCATTTTGAGAAATGTTAAGAACAATTTAGTCAATCGTTCATCTGTCATTGGTACTGTAA 3921
               | | | |||            |||         || ||| | ||
|||
Db        1532 TCAATATTAGA-------------------------GTT------
TCTTTGTTTCTTTAA 1504


Qy        3922
AATAAGCTGTGGTCTATTTCCACTGTTTAATTTTCTACTCAGTTCTACCAAATAGGATGT 3981
               |    | | | || |   | |      |||| |    | || || | ||
|
Db        1503 ACACTACAGAGTGCAAAT----CAG------GTTCTTCAC------
```

```
AACAGATTGAATAT 1460


Qy      3982
CATGTTTGACATTTTTGATAGTGACTTTGGGGTCTTCTTCACTGAAAGCACCTTAGAACT 4041
                |   |  || || || |    |||| |         |    ||||| |    |||
Db      1459 TGAGCAGTTCTTTAAAGAAAGAG-----GGGGAAG-----
AAAAAAAGCCCAAGTGAATA 1410


Qy      4042
GTACTATAAGAAAACATTTCCCCTATGTATAATTATATGAATGTGATGTTTATTGCTTAT 4101
                  ||  |     |||| |||||||| | |  ||    ||   || |||||| | ||
|
Db      1409 AAACATT---
GAAACTATTCCCCTTCGAAAATAAATTCTAAAATGATGTGGAATGTGAAA 1353


Qy      4102
TAATTTATAATTCAGTCATTCTCTATATAGGACTTCTTAAAATTTAGAAGGGAAATCTAG 4161
                  ||                     ||| | |||| |  ||||      || | |||
Db      1352 TA-------------------------AGG---TTTTAACAT------
AGGTGATC--- 1331


Qy      4162
CTACTTCAAATTGTCTGTTAAATTTATTATGCCCAAATCAACCTCTGAAAAAAGGTTTTT 4221
                      ||| ||     |||| |              |||      |||| | ||
||
Db      1330 ------CAAGTTTATAGTTAGA----------------AAC----
AAAAAGAAGTCCTT 1298


Qy      4222
CCAGGAAGATTTACATTAGGTTTAATATTTTTTTAGTTAGGTAGAGTTTTAAAAAATAC 4281
                   |  | ||                                 || || || || ||
||
Db      1297 CATGAAA-----------------------------------
TAAAGGTTACAAGAACAC 1273


Qy      4282
TTGAGCCTGTCCGTGATAAAGCTATAAAATTCAATAACTTTTTAGAATGTTAAATG---- 4337
                | |||||||              |||         | || || || || || ||
Db      1272 GT-TGCCTGT------------------TTTCC--
CCCATTATAAACTGAGAAGTGGGTA 1234


Qy      4338
AAGACACTGTTTCCTAACATCAGTGAGATACATCTTTGAATTTAAACATTCATATTTACT 4397
                |||||  ||||||   || |  ||  |  | | ||     | ||||| |
|
Db      1233 AAGACGATGTTTCAGTACGAAAATAGGTGACTAC--AGGATCAGCGC-
TTCATCTCACAT 1177


Qy      4398 G-
AGTACCTACTAGGTACCAAGTACTCTTTTAGGCACTGGAAATACAGTGATGGACAAAA 4456
                | ||||| || |   || || |||    | ||| |||| ||| ||
Db      1176 GCTGTACC--CAAAG--CCAGG----CTGT--GG--
CTGTCCATACGGTGGTG------- 1136


Qy      4457
CAGGTAAAAAATCGCTGCCCCCTCAGAGCTGACATTCTGGGGTGGGAATTTCATTTTGCC 4516
                   |||| ||   | |  ||      | ||   |||||| ||||      |
Db      1135 -CGGTATAA---CCATAACCAAAAGGTGC-------CTGGGGAGGGA----CG----
GCA 1095
```

```
Qy       4517
ACGTACTAACGTTCTGCACAAAAGACAGGCTAGACTCTTGTCTAGATTGTTTAAAAGAAA 4576
         ||  |||   || |||   | |||  |  |||                      |
Db       1094 AC--ACTGG-GTCCTGC-----TGTCAGCATCAACT--------------------
GGGG 1063

Qy       4577
CTTTTCAAATTGGTTACATTAATTTTAGTTTATTTTCACAAGTAAAAATGGCTTTTTATT 4636
         ||    | |    ||| |  | |    |   | | |      | |||| ||
||
Db       1062 CTGACCATA-----AACAATGGGTTGTGTCTCT--------------
GTAGCTTGTTCTT 1022

Qy       4637
TAGATTCTTTCTGTCCCAGGCTGTTGATCTTAAAACTAGTTGATTTAAAGAGTTTTTTTG 4696
              ||||||   || |||    |||| |||| |         || |||      |||
|
Db       1021 ---CTTCTTT---TCTCAG-----TGATTCTGAAGC------ATCTAA------
TTTATC 985

Qy       4697
CACAACATTTCAATTATATTTGTGAACTTAGAAATTAACTTACAATCTAACCAGCCATCA 4756
              |||                    ||| |  |   |||              ||
|||
Db       984 CAC-----------------------CTTTGTCAAGTACT--------------
CCTTCA 962

Qy       4757 TATCAT--ATCCTATCAGGC-
TAGATATCTCAATAGTAGACTGAATACAAAGCTAATTTT 4813
              | | |  || |  ||||  ||  || | ||   ||   | | |  | | |
Db       961 TGACCTGGATGAAATAGGGCATGGCCAAAATCCATGATATTGTGCCT-
CCATGCAG----- 908

Qy       4814 TTTTACATGTCAATAT-TGGCACAAACTGGAATGAAAG-
AATAGTTTGATTCAGACCTGC 4871
               |||  | | | ||| |||        || | || |  | || | || |  |  |||||
||
Db       907 -TTTCTAGGACGACATCTGGC-----CTTAAAAGATCGTAACAGGT--
AAACAGACAAGC 856

Qy       4872 TCCA-------
CTATGTGTTGCTAAAACACATGCTATGAGCACTCGAGGAAACACTATAT 4924
              ||||        || | | || ||       | ||| |  | |||| ||||
Db       855 TCCAAAGCACTCTCT-TTTTTCT-----
TCCTGCAAAAACCACTGCAGGAG--------- 811

Qy       4925
TTTTTCCAAAAAATATGTGATTATATATGTTAAAGTATAGATAACATTTCACACTTGGAT 4984
              || |||    || |    || |  | |    ||| ||  | |||| || |  ||||
|
Db       810 TTCTTCAGCCAATTCAGTATCTTTAGATTCAGAAGCAT--
ACTGCATTGCATCCTTGTAA 753

Qy       4985
ACATATGTGCATTTACTGTATTTCTTGGTAAGCATATTTTTGGGGGAAAGTGCTGCTGAT 5044
                 |            |||| |||||||   |||                   || |
|
Db       752 A------------GGCTGTCTTTCTTGCACAGCT------------------CTAC-
ACT 724
```

```
Qy      5045
ATGATACAAGTAGACAAAATTTAAATGAAATTTTGTCACATTCTATGGAAAATGGTTTCT 5104
          || | |  ||  |  |               |||| |
Db        723 CTGTTTCCAG----CGA---------------
TTGTTGC-------------------- 704


Qy      5105
GGTAAACTGAGAAGGATATTAAAATAAGTGGCTTTTTCTGGGCTACCATTATTGTTTGA 5164
             ||  ||||    |  ||||| ||
|
Db        703 ------CTTTGAAG-------
AGATAAGCAGC----------------------A 684


Qy      5165 TTTCTCTTTGTCAAGTGTATAGAACCTGTC-
ATACATTCATGATAAGTAGCACTGAAAAA 5223
             ||||| |          |||| || ||   |||||| |
Db        683 ATTCTCCT------------GAAC---
TCAATGAGTTCATGTT--------------- 656


Qy      5224
TTACTCATTCAAATTTCCCCTGGGCACGTAAGGCAAAATATTGCCGGTTGGGATTTCAAG 5283
             || |   |||| | |||| | | || |  | |||||
||||
Db        655 TTTC-----CAAA----CGCTGAGC-----AAGCGAGATATTG------------
TCAAA 622


Qy      5284
GTCAGTGACGACGCATTTCCTCCCAGTACAGACCCCCCAGCCCCCCTTGCTGGACATGGG 5343
             ||          | | | |             |||  |  ||| || |
Db        621 GT------------TGTCAT----------------
AAGCATCTATTGATGTTC----- 596


Qy      5344
GAGGCAGAGAGTCACTTGACCATCCAGAAATACATGACTACAAGTCCTTTATGACTGTTT 5403
              ||||||              || || | | |         |||       ||
Db        595 ---GCAGAG--------------CCTGATAATCTT-----------CTT-----
CT---- 573


Qy      5404
GCCATTTTTTTAATGGTACTTAGTATTTTGATCAAACTTTAGTCTCCAGAACTAAACAA 5463
                            ||| | |  ||| |||| || |
Db        572 ----------------
GTAATAAAAGATTGTTCAATGATTCAT--------------- 545


Qy      5464 GTCCCTAAGTTTCCTTATTTTAATTTACTGTGACTAGATTTGAAGCAAATA--
AATACTC 5521
             || |  || ||  || || |  ||        ||  | |  | ||||||    | |
|
Db        544 -TCAC--AGATTTGTTGTTATGGTT--------
CTGAACTGAACGCAAATACGGTTTCAC 496


Qy      5522 CAGATCCATGCAGCTAGAACACACTTGCTTCCACTACTAAATATACAGGGTATG-
TCCTA 5580
             |||     | |||           |||||| || || ||| ||| ||| ||
|
Db        495 CAG----TGGTAGCTGTTTAAC-CTTGCTGAAATAATTGACTGCAC-
GAGTGTGATCCAA 442


Qy      5581 ACATGGAGTTAACTGGAATAGCAGTACA-CTAGCA--
```

```
AGTATCTGTGAATCCTTAGCACT 5637
   | ||||| || |  |  | |||| || || || ||  || ||||| || || |
Db       441 CCGTGGAGACAGCACCATCAGCAAATCATTTAACAACAGAGGCT-
TGAATTCTAAGTA-- 385


Qy      5638
GACGGGTTAACAGAAATGCTTTGGTAATACCTACTTAGTTAATTGGAGGAAGTAGTAAAT 5697
                   ||| | | |||| ||              ||||          ||||
|
Db       384 -------GAACTGTATTGCTCTG------------TAGT------------
ATAGT---T 359


Qy      5698
AAACATTAGGTAATCTGCAGATTACTTCAAATGGGAAAAATCTTTTTGTAGACTCTATAG 5757
               ||||| || ||  |          ||| ||  || | ||||
|
Db       358 CCACATT-GGCAACCT--------------TGGTAATGATATCTTTG---------
AAT 324


Qy      5758 TACCCTCTCTATTCACTAGCTTCTGAAAAGGGAGGAGTATTTTTAG----
TTTGACAATT 5813
             | |||| ||| ||| | || || |      ||| || |  | |    | || ||
|
Db       323 TGCCCT-TCT-TTC-CAGGCATCAGTT---
GGATGATTCATCATGGTAATTATGGCATTA 270


Qy      5814
TAATAATTTAAAAACAAGACATCTCCAGGTAGGAAAAAATGAAAGCTATTTCATGCAAAC 5873
             | ||| | |  | || |                             ||||
||||
Db       269 TCATATTCTTCATACTTG------------------------------
TCATACAAAA 242


Qy      5874
ATTATCTAATTTAGCTTAAAAGTGAAAGTGGTAATACTGTTGGTTTCTGTAAATGTTGCA 5933
             |   | || || ||| ||| ||| |  ||                ||| 
||||
Db       241 A--CACCAGTTCTGCCCAAAGATGAGCTTG--------------TTC---------
TGCA 207


Qy      5934
GGGTTTTAAACTTTATAATTACTTTAATATTTTTGATAACTAGAAATCTAGTATTGCCAT 5993
             |   || || |       ||| ||| | | |||||  | || | || || 
Db       206 GCTCTTAGCAC----------CTTGGGAATATTCACT--CTAGA---
CCAGAACAGC--- 165


Qy      5994 AAAGGAAACTAAGTGC-
CCATCAAAGATTTGTTTGGTATAAATAAAGAATTATTTGTTTT 6052
              | | |||| || ||| | ||| | ||||| ||| |  | |
|
Db       164 -------TCCAGGTGCTCCCTCA---TTTTCTGAGGCTTAAATTTAGAGT--
ATAGAATA 117


Qy      6053
GTTTTCAATGACAGTAAGCTACAAATCATGATGCTTAAAAACTTTCTAAAGATGAATTGT 6112
             |    |  |   |||||| |    | ||        | |    | || || ||
Db       116 G----CTAATTCAGTAAAC----ATTCC-----
CATGTGAGCTCGCTCAA---------- 80


Qy      6113
```

```
GTGGCAGTGATTGGTCTGTTTGTGGAGAATGTATGAAAGCTATTAATATTCTAGAATAGA 6172
               ||  |||||     |||                          ||| |  ||
|
Db       79 GTCCCAGTG------CTG----------------------------
CTTCCAACATGG- 56


Qy      6173
TTAATAAATTGGCTATGTTGTTCCAATGAATGTACAGCACTTCCATTAACTTTTGAAAGC 6232
                                         ||  |||| |||
|
Db       55 ----------------------------
TGATCAGCTCTT----------------C 43


Qy      6233
AACACAGCCTTAAACTCAATGCTTTTGCTTTATGACATGGGAATGTTCTGTCATCAATG 6291
               ||| | |||         | | || |   || |     | || |        | || ||
||
Db       42 AAAATAGC------CACGATCC---TGATAGTAGCCAGTAG--------
GCCAACAGTG 1


RESULT 9
US-10-478-914-57/c
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match            14.1%;  Score 5407;  DB 1;  Length 2336;
  Best Local Similarity   35.5%;  Pred. No. 0;
  Matches 1495;  Conservative    0;  Mismatches  802;  Indels 1914;
Gaps  215;


Qy       351
CTGCCCGAGAAAGGGGTGGCCGCGCTCCAGAACAATTTCTTCATCACAAACCTGATGGAC 410
             | || |||| |   ||||||             ||| || |       |   ||
|
Db     2336 CAGCTCGAGCAC-ATGTGGCC--------------
TTTTTTTTTTTTTTTTTTTTTTGTA- 2293


Qy       411
GTGCTGCAGCGAACTCCAGGCAGCAACGCTGAGGAGTCTTCCATCCTGGAGACAGTCACT 470
                          |||    || ||        |||||   | ||||   ||| | || |
```

```
|
Db       2292 -----------TTCTCAGAGCTGCC------AGGAG---TGCATC---
GAGCCTGTAATT 2256

Qy        471
GCTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCACGATGGGAATGTGATGGAATTT 530
             |    |||         |||||  |||  ||                  ||
|
Db       2255 TC-----CTG---------TTCTCTGAATCCC---CC-------------------
ATCT 2232

Qy        531
TACTGCCAGTCCTGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAGCACGCAGAG 590
             | ||||  |||       || |||||
Db       2231 TTCTGCAGCTCC-------
AAGCTTTGTGT---------------------------- 2209

Qy        591 CACCCCACAGTTCC----
ACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTCCA--G 644
             |||||||  ||    |||||   ||||  ||| |   || |   ||     ||||
|
Db       2208 ---CCCACAG--CCTGTGACTC-----TGTGCT--AACAAATC---
GCTATTGTCCAGTG 2164

Qy        645
GTCCAGCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCAGTTCATC 704
             |  |   ||| ||||  ||| ||||  |  | |        |||| | |||  ||||
Db       2163 GGGCGAATGGTGGCTGG-AACTAAAGAATTGCTG--------TCTGGT-
TTCTATTCAAA 2114

Qy        705
TCTGAAATCATTCATCAGTTAACCAACCAAAAGGCCAGCATCGTGGATGACATTCATTCC 764
             ||          ||| ||          || ||      || |||
Db       2113 TC------------CAGGTA------------
GCGAGATATATGAATG----------- 2090

Qy        765
ACCTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTATGGAATTG 824
             ||||||
Db       2089 --------------------
GACTTT-------------------------------- 2084

Qy        825 GAGGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGATAC--
TCTGCTCC 882
                          || ||    || ||  |     || |||
|||||||
Db       2083 ----------------TCGAA-------TCGTCATG-------
TGAATAACGTCTGCTC- 2055

Qy        883
AGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCCTCAACCATGGCA 942
               |||| ||                                |||| |  | |||||
Db       2054 ---GGCATGA-------------------------------
AGGCTCAGAGCCATG--- 2033

Qy        943
CGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAGCTGGCCG 1002
                          || |   ||||      ||    | | |||  |   |||
|
Db       2032 -----------------CTAG----GAAG--------------
```

```
GATTAACTCGTAGGCTG 2008

Qy        1003
ACCAGGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCATCGTGGAAACCG 1062
                ||||        ||  || ||                  |||    |||| |
||
Db     2007 ACCA---------CTAACATCC--------------------TTT----GTGGGTA--
CG 1984

Qy        1063
AGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCTTAACCACCAACGCCGTTGCCT 1122
                ||||     |||| |  ||| |   ||      || |||   |||
Db     1983 AGGG-----AGAA-ACATTCCCAAGTATC------
ATTTTATTCAC-------------- 1950

Qy        1123
CAGAGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCAGCCCATGTCCG 1182
                                                          | | ||    | ||
Db     1949 -------------------------------------ACTTAAT-----------
TTTCTA 1937

Qy        1183 TCACCCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAA--
AACCGGCAACGCCTACCT 1240
                 || |||| ||| |||     ||| | ||  |||| |  || |   ||| ||| |
||
Db     1936 TC-CCAT-ACCCCCA-----AAATAAGGCTAGCTATTTAATTAGTTGGC--
CGCTTTTCT 1886

Qy        1241 CACCGCCGAACTGAGCACCCCCGACGGGAGCGTGGCAG-
ACGGGGAGATCCTGGACAACA 1299
                |         | | ||      | | |   ||| ||   ||| | || ||     ||
Db     1885 CT---TAATTTTTAGTGTTTCTGTTGATAATGTGTGAGTTTGGGAAAATGCT----
AAGT 1833

Qy        1300
AGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTACCCTGTCTC 1359
                || |     |||        || | |||||||             ||| |
|||
Db     1832 AGCTTTTCAC---------TTAGAACACTGT--------------TATTTTC----
TCTT 1800

Qy        1360
TGAGACTCTATGACCAGCACATCCGAGGCAGCCCGTTTAAGCTGAAAGTGATCCGATCCG 1419
                || |   | | || | |  || |          || ||| | ||| |||
|
Db     1799 TAAAGTTTTCTACCTTACATTT------------ATTATAGC--
ATAGTTATCTTTATAG 1754

Qy        1420
CTGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGGAGCGGCC 1479
                |  | || |          |||| | |||||  | | |   | | | ||
||
Db     1753 CATAGATG----------CAGAAAGTAAGAGAGAGCTTGTTT--
TTTCAAGAAAACAACC 1706

Qy        1480
ACGTCAAGCAGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAACGAAAAG 1539
                || || |||| ||        | | || ||        | |||
|
Db     1705 ----------------CT-TTAAAATAC---------TTTCCAACCC------
```

```
ATGAAGGG 1677

Qy        1540
AGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAAATAAAGGAG 1599
            | ||  || |         |||   ||||         || ||
Db     1676 AAAAATCCTCC--------TTT----TTTC--------
CCCCAAG-------------- 1652

Qy        1600 AGTTTACAAATCTTCAGGGGGTAGCTGCA-
TCTACAAATGGAAAGATATTAATTGCAGAC 1658
                                 |||| |||||  ||          |   |||||
Db     1651 ------------------------TGCATTCTACTTAT---------
TACTTTGCA--- 1629

Qy        1659 AGTAACAACCAATGTGTGCAGATATTTTCCAATG---ATGG---
CCAGTTCAAAAGTCGT 1712
                  |  |  |||| ||    |  | || |  | ||     || |  | |||||||| | |
Db     1628 TTTTTCTCCCAAAGT---CCAAATTTATGCAAAGAAAATAGAAACAAGTTCAAATG-
CAA 1573

Qy        1713
TTTGGCATACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTACAT 1772
                    |  ||||     ||    | |   || |   ||  |  ||              |
|
Db     1572 T---GCAT----------TAAC-----CAAATAAAACAAGTCTC-------------
CTT 1544

Qy        1773
CCCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCTCC 1832
                | | ||| || || |  || |   ||  |     |    | || |    |||| |||    ||
Db     1543 CAAATTAGGAACC-AACCTAAGCATTTGTAAAGTGTAGCAGAATCAGAATT-----
CT-- 1492

Qy        1833 GATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTTCT 1892
                               |||     ||||||| |||         ||| ||| ||
||
Db     1491 ---------TTT-----AAAAATTAGAT-----------TTGGAACCTGAA-------
CT 1464

Qy        1893
GTGGACCGCAATGGGCACATTATTGTTGTGGACAACAAGGCGTGCTGCGTGTTTATCT-- 1950
                 | |  ||   |  | | |    | |||||| || |                  |||||||
Db     1463 ATATAATTCATAATTCTCATTTTT-CTGTGGAAAATTA------------
TTTTATCTTT 1417

Qy        1951 -
TCCAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAG 2009
                 ||| | | ||| | ||||  ||| ||  |  |           |  ||| || ||
Db     1416 CTCCTGTATACCTGAAAAAATGTCCATAGGCTT-------------
AAAGGGTCATGCT- 1371

Qy        2010 TTTGCAGGTCC--CCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTA--
TTACAGA 2065
                ||| ||  || ||   | |||   | |  | |  || | ||||  ||  || |
Db     1370 TTTACA-TTCCTTCCATATCACAG--
GTACTATGAAGTAAGGAGACTTTTAGGTTTCTTT 1314

Qy        2066 TTTCCATAATCATTCTGTCAAGGTGTTTAATCAGGA---
AGGAGAATTCATGTTGAAGTT 2122
```

```
                    ||   |  ||| |   || | | || | ||| ||| |    | ||| | || |
                    ||||
Db     1313 TTGTCTTAAAC--TCAGAC-AGCTTTGTAAGCAGTAGTGTGTAGATTACAAG----
AGTT 1261

Qy     2123
TGGCTCAAATGGAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTC 2182
             |   |||| | ||  | | || | ||         |   |||| | || |
             ||
Db     1260 AG--ACAAAAGCAGGCGCGACTGAGAAG-----------
AGTTGGTGGGGGAGAAGCTT- 1215

Qy     2183
AAATGGAAACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAG 2242
                   ||  || ||  |||  | | |    |  || ||   ||||| |
Db     1214 ---GGGGCACTTC-------CTGTC-----
ACTCAACACATTCCAGAT------------ 1182

Qy     2243
TGGATCATTTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCCT 2302
                            || ||| ||| |  | | |||| || ||     |||
                            |||
Db     1181 ------------------CACTAAAAAATTTCCACACCCTCTGCAT---TCCC----
CCT 1147

Qy     2303
GGCCCTAACTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGT 2362
             ||||   ||| ||| | |              | || |   ||| ||| |
Db     1146 TGCCC--ACTCCAGTT----------------------
CCCGGTATTTTCTGATTCCATAT 1110

Qy     2363
CTATCGATACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCACTAT 2422
             |   | ||| |||| | |                    | | | || |
             |||||
Db     1109 GTTGTGGTATTTACCATACT-----------------TCTCTCCCT--------
CACTAG 1075

Qy     2423
AAACTGGAATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCAGAAG 2482
                  |||                  || ||| |                   |||
Db     1074 GCTCTG----------------GCAAGAC----------------------
TGC------ 1059

Qy     2483
GAATCATTGGTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACT 2542
                           ||| |||    | ||| || ||||||| | ||
Db     1058 ----------------TTCAGAGG--------GGATG---CA--
TTCCTTTAGATTG--- 1031

Qy     2543
TATCCAATTTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAA 2602
                           |||
Db     1030 ------------------
CAC--------------------------------------- 1028

Qy     2603
AACTGCAGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTA 2662
                   |   || |       | ||| |||  |||||||    | ||| ||| | | ||| |
```

```
Db      1027 -AAAGCGG------AGCTGGGAA-AATGGCT-----GGCAG--
TTTCAGAATCTAGTC-- 985

Qy      2663
ATTTTGCAAATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCC 2722
                         | | | ||| |           ||||
||
Db       984 ----------ACGATCGCACGCATG--------AGCA--------------------
CC 964


Qy      2723
TGTGAATGGTAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAAATCTATTGTA 2782
                         |               ||| |   || ||||
|||
Db       963 T-----------------CAC---ACATCCA------------------------
TGT- 950


Qy      2783
GTTATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCTCACTTTTA 2842
                              |||    ||  | |||          || |  |
Db       949 ------------------CCCT-----ACCCGCCCC-------------
CCCGCTC----- 930


Qy      2843
CAGTAGGTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATATAAATTACTTT 2902
              |  |      | ||          || ||
Db       929 CCG--------CCCCTG---------------------
CAGCT--------------- 916


Qy      2903
GGAAAAAGTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCCCTCTGGAGTT 2962
                      ||||| | ||       || ||           ||| |||
Db       915 -----------GGCTGACCTG--------TCTCA--------------
CCCACTG----- 894


Qy      2963
CAGAACTTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGATCCTTTTT 3022
               | | ||  | | |           |     || ||||| ||| |      ||
Db       893 CTGGCCTATCG--AACGG---------CCAGGACTGTCTGGTTTTGGC----- 
TC------ 855


Qy      3023
TGTGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCTTC 3082
               |||  --GTG--------------CCTTTG----TCCATGT-----
Db       854 ---GTG--------------CCTTTG----TCCATGT-----
CTGGCTTAGTTCCTCT-- 823


Qy      3083
AGGGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTT 3142
                       |||   | | ||  ||||||                        |||||
Db       822 --------CTGTCTATGCT--TGCCT------------------------- 
CTACC---- 802


Qy      3143 GGGAAACAAACTGCCCC-GTTAACTCCAGATCATTG--
CACTGGAATGTAATCAAGAAAG 3199
                         |  || ||||| |    | | || ||| |||   ||   | | |||
||
Db       801 ------CCCACCGCCCCAGGCGGCACAAG-TGTTTGGCCACACAAA---
ACTAGAGATAG 752
```

```
Qy        3200
TTAGTCATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTTCCTGAAAG 3259
                |   |  ||  ||   ||      ||||  | | |||     ||| | |||
Db        751 AAA---AGGTGGTAAAAAC------
TTCAAACTTTTCTAAATTCTCCAAC---------- 711


Qy        3260
CGAAAGCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCAGTATCCTAGGACA 3319
                  || ||||  || ||  ||| || | ||| |   |  || ||| |     |
|||
Db        710 ----AG-TTTATTTCTTGTGAATTTCTTC-
CTTCTTTAAATACTCCATTTTAAGAAAACA 657


Qy        3320
GAGAGCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGTGATTGATT 3379
                |     | ||| |||||  ||||         |  |  | |||||||   || ||
Db        656 AA-----AAAATTA---------------------
ATTATCTAAAGGCAAAGAATGGA-- 625


Qy        3380
AATGATTCCCCCTTAGAAAGCAAGTGTTACCAAAGTTGTGTTATCTTGAAAGCATTACAG 3439
                |   |  ||||        |||||  ||  | |||    ||| ||
Db        624 ----AAGCAACCTT--------TGTGTTCC-----TTATAATAAC-
TGACTTCATAAC-- 585


Qy        3440
GTAAGGGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGACT 3499
                                       |  ||                ||  || ||
||
Db        584 -----------------------TCTC------------------------TCCAG---
CT 574


Qy        3500
ATGTATACATGTTAGGGTAAGATAGAATGTATTATATATATATATATATATACACACAC 3559
                       ||  |||----------------   || |||||
Db        573 GCGTT-----------------
ATGGGATGT---------------------------- 560


Qy        3560 ACATATATATAGCTGAATCTTTGGTGTATTGAAATAGGCAGCAC--TCTGAA---
AGACA 3614
                     |||| | ||||   ||| | ||    ||| | | ||||||   | |||
||||
Db        559 --GTATAAAAAGCT---TCTGTTCTG---
AGAACAAAGGAGCACGTGCAGAAATGAGACG 508


Qy        3615
GAAGCTTCGTCCAGCCACTCTTCAGCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTA 3674
                     || || | ||| |||| ||| |   ||||  | || | ||| | ||  ||||    |
||
Db        507 AAAAAATC-CACTGACAGTATTC----CATTAC---ACAAATTACTTAAAAG--
ATTTTA 458


Qy        3675
GTGGAGCAAGCCCTAAAGCAGATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGC 3734
                     ||  |||||||  |   ||         |  ||  ||  |
||||
Db        457 GT----CAAGCCCCTCAACAGATT---------CAATTTTAAAA-------------
TGGC 423


Qy        3735
```

```
TTTTAGTCAGAAAATGGCCTTCTGTGCTTTCAAAAAAAAAACAAAAAAAAAACCACACAC 3794
       ||||||                             |||||||| ||||   |||   |
                                                                ||
Db      422 TTTTAGT-------------------------
TAAAAAAAAAAAATTGAAAGTGCTTAC 389


Qy    3795
ACACATAAAAAACCCAACAGGTCAAAATAAAAGTTGAACTTGAGTTACATTTAATTTAAA 3854
            ||  ||| |||| ||  |||           ||||||   ||||| |
Db      388 CCAGTAAAAGAACCGAAGTAGTCC----------TGAACT---
GTTACGT---------- 352


Qy    3855
TATAAATGCATTTTGAGAAATGTTAAGAACAATTTAGTCAATCGTTCATCTGTCATTGGT 3914
            || | |||| |   | ||| ||| || ||  || ||||| |  || |
||||
Db      351 ----AAGACTTTTT----ACAGTT-GGATC---TTTGTCAAAAGGGGATGGG-----
GGT 309


Qy    3915
ACTGTAAAATAAGCTGTGGTCTATTTCCACTGTTTAATTTTCTACTCAGTTCTACCAAAT 3974
            || | |||||| |   ||  ||||         | ||        |   || |   |||||| | |
Db      308 GATGGGAGA-AAGCAG----------CAAC-----
GACAATCAAAAAAGTTCGAGC---- 269


Qy    3975
AGGATGTCATGTTTGACATTTTTGATAGTGACTTTGGGGTCTTCTTCACTGAAAGCACCT 4034
                                ||| ||| | | || |  ||||  ||
Db      268 -----------------------TGCT-GTGGC-
TAGAGGACAACTTCTGTG--------- 242


Qy    4035
TAGAACTGTACTATAAGAAAACATTTCCCCTATGTATAATTATATGAATGTGATGTTTAT 4094
                                ||||||
Db      241 -----------------------
TTTCC------------------------------ 237


Qy    4095
TGCTTATTAATTTATAATTCAGTCATTCTCTATATAGGACTTCTTAAAATTTAGAAGGGA 4154
                                ||  |||||| |||||     |   |  | ||
|
Db      236 -------------------------------AGATAGGA-
TTCTTGCTGTAGAAATGGAA 209


Qy    4155
AATCTAGCTACTTCAAATTGTCTGTTAAATTTATTATGCCCAAATCAACCTCTGAAAAAA 4214
            ||  |||    ||                    || ||   ||| | |
Db      208 CTTCCAGC-----CA----------------------GCACAG--
CATCC---------- 188


Qy    4215
GGTTTTTCCAGGAAGATTTACATTTAGGTTTAATATTTTTTTAGTTAGGTAGAGTTTTAA 4274
            | ||| ||      ||               ||||||
Db      187 ----TGTCC-----------CA-----------------------
GTAGAG------ 175


Qy    4275
AAAATACTTGAGCCTGTCCGTGATAAAGCTATAAAATTCAATAACTTTTTAGAATGTTAA 4334
            |  ||||  |||| |||| ||  |||| | | ||||      || ||
Db      174 -----AAATGAGTTTGTCAGT--TAAAACAAAAAAA------
```

```
AAATT------------ 141

Qy       4335
ATGAAGACACTGTTTCCTAACATCAGTGAGATACATCTTTGAATTTAAACATTCATATTT 4394
                 ||| |||| |   ||       |||   | || | |   | ||| || |   |
Db        140 ----AGATACTGGAACC------CAG---GCTAGA-
CGAGGTATTGAACCGCGC------ 101

Qy       4395
ACTGAGTACCTACTAGGTACCAAGTACTCTTTTAGGCACTGGAAATACAGTGATGGACAA 4454
             | || | ||| || ||    ||   ||| | || | | | |||   ||
|||
Db        100 -CAGATTTCCTTGCAG---CCCTG---TCTGCTCAGCTC--GCATTCCAGT--
AGGCCAA 52

Qy       4455 AA---
CAGGTAAAAAATCGCTGCCCCCTCAGAGCTGACATTCTGGGGTGGGAATTTCATT 4511
                 |   |   |   ||   ||| ||          || | | |  | | |   ||
|
Db         51 CAGTGCTCGAGGAATTCCGCAGC----------------
TTTTAGAGCAGAAGTAACACT 8

Qy       4512 TTGCCACGTAC 4522
                 |       |||||
Db          7 T----CCGTAC 1


RESULT 10
US-10-478-914-57
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match             14.0%;  Score 5370.5;  DB 1;  Length 2336;
  Best Local Similarity   41.1%;  Pred. No. 0;
  Matches 1464;  Conservative    0;  Mismatches  805;  Indels 1295;
Gaps  219;

Qy         18 TGCGG-GGAGCTAAGTC--
CCCAGATTGGAGGAGGCTGGCTCTGGTCTTCGATGCACAGG 74
                | ||| | | || || | |    | | |  || |  |    || |||| ||||
|
```

```
Db          2 TACGGAAGTGTTACTTCTGCTC----TAAAAGCTGCGGAAT----TCCTCGA-
GCACTG- 51

Qy         75 AGTGGCCGTTATGGAACGC-AGCAGCAGCGTGCAGGGT--
CAAAGACAGCCGGCCCCCCA 131
              ||||| |  ||||| || ||| | |||    |||| ||| |||| || | ||| |
Db         52 -TTGGCC-TACTGGAATGCGAGCTG-
AGCAGACAGGGCTGCAAGGAAATCTGGCGC---- 104

Qy        132 TGTCAGTGGTCTAGGATGGCCAGTGAAGGCACCAACATCCCAAGTCCTGTGGTGCGCCAG 191
                            || | |||| |   ||| | | ||| ||| ||| | ||| |||| |
Db        105 -------------GGTT---CAAT------ACC-TCGT--CTAG-CCTG-
GGTTC----- 132

Qy        192 ATTGACAAGCAGTTTCTGATTTGCAGTATATGCCTGGAACGGTACAAGAATCCCAAGGTT 251
                           |||| ||| ||||   | | |   |  ||| | ||    || || ||
              ||
Db        133 ---------CAGTATCTAATTTTTTTTTTGT---TTTAACTG-AC---AAACTCAT--
TT 174

Qy        252 CTCCCCTGTCTGCACACTTTCTGCGAGAGGTGCCTGCAGAAC--
TACATTCCTGCCCACA 309
                 ||| ||| | |||      |   | | ||||  || | | | ||||| || |
              |
Db        175 CTCTACTG---GGACA------
GGATGCTGTGCTGGCTGGAAGTTCCATTTCTACAGCAA 225

Qy        310 GTTTAACCCTCTCCTG---CCCAG-
TGTGCCGCCAGACCTCCATCCTGCCCGAGAAAGGG 365
                |  || |||| |  |    | |||  ||      | |||| | ||
Db        226 G---AATCCTATCTGGGAAACACAGAAGT------
TGTCCTCTAGCC-------------- 262

Qy        366 GTGGCCGC-
GCTCCAGAACAATTTCTTCATCACAAACCTGATGGACGTGCTGCAGCGAAC 424
                | || ||||  |||| ||| |||            |||| | ||| ||| ||
Db        263 ---ACAGCAGCTC--GAACTTTTT--------------TGATTGTCGT--
TGCTGCTTTC 301

Qy        425 TCCAGGCAGCAACGCTGAGGAGTCTTCCATCCTGGAGAC--
AGTCACTGCTGTGGCTGCG 482
                |||  || || | |       |||| ||| ||| ||   |  ||||
Db        302 TCC---CATCACCCC--------CATCC--
CCTTTTGACAAAGATCCAACTGT------- 341

Qy        483 GGAAAGCCTCTCTCTTGCCCAAACCACGATGGGAATGTGATGGAATTTTACTGCCAGTCC 542
                   ||||  |||      ||||        |||              |  ||||
              |
Db        342 AAAAAG------TCTT---------ACG------------------------
TAACAGTTC 363

Qy        543 TGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAGCACGCAGAGCACCCCCACAGTT 602
                | | |||| | |  | ||      | || |||  |||||
              ||
Db        364 AG---GACTACTTCGGTTC----TTTTAC--TGGGTAAGCAC----------------
```

TT 398

```
Qy         603 CCACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTCCAGGTCCAGCTG----
GATGC 658
                  || |       | |  |       | | || |||    |   |  |  | |||     |
||
Db         399 TCAAT------
TTTTTTTTTTTAACTAAAAGCCATTTTAAAATTGAATCTGTTGAGGGGC 452

Qy         659 -TGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCAGTTC-
ATCTCTGAAATCATT 716
                  | | ||    |     || || ||  || |   | | | |  ||  || | |
||
Db         453 TTGACTAAAA-----
TCTTTTAAGTAATTTGTGTAATGGAATACTGTCAGTGGATTTTTT 507

Qy         717 CATCAGTTAACCAACCAAAAGGCCAGCATCGTGGATGACATTCATTCCACCTTTGATGAG 776
                  | ||        |       || |       | ||| ||||          |  | |||||| |
Db         508 CGTCT----------CATTT---CTGCA-CGTG--------------
CTCCTTTGTT--- 536

Qy         777 CTC----CAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTATG-GAATTG-
GAGGTC 830
                  |||     ||||||  ||||  || |      |   || ||||  | || ||  ||
||||
Db         537 CTCAGAACAGAAG-
CTTTTTATACACATCCCATAACGCAGCTGGAGAGAGTTATGAAGTC 595

Qy         831 AACTATGGCCTCAAACACAAAG--TCC--TCCAGTC---
GCAGCTGGATAC--------- 874
                  | ||| |||||||||| | |  |||| ||   ||     | ||||
Db         596 AGTTATTATAAGGAACACAAAGGTTGCTTTCCATTCTTTGCCTTTAGATAATTAATTTTT 655

Qy         875 ---
TCTGCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCCT 931
                   | | || |   |     ||| ||| |   | | || ||||||
Db         656 TTGTTTTCTTAAAATG-----
GAGTATTTAAAGAAGGAAGAAATTCACA----------- 699

Qy         932
CAACCATGGCACGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAA 991
                                ||| |    |||| | |||| |||         || ||| |
|
Db         700 --------------AGAAATA-----AACTGTTGGAGAATTT------
AGAAAAGTTTGA 734

Qy         992
CGAGCTGGCCGACCAGGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCAT 1051
                  |   |  || |||   || | | |    | | | |     | | | | || || | | |
TGCCG 787
Db         735 AGTTTTTACC-ACCTTTCTATCTCTAGTTT---TGTGTGGCCAAACA-CTTG--

Qy         1052
CGTGGAAACCGAGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCTTAACCACCAA 1111
                  | ||| | ||   |   | | | | | ||   ||  || | || || || | ||
Db         788 CCTGG--GGCGGTGGGG--GTAGAGG--CAAGCATAGAC-
AGAGAGGAACTAAGCC----- 836
```

```
Qy        1112
CGCCGTTGCCTCAGAGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCA 1171
                         ||||| ||| || ||| || |          ||| | | |
||
Db         837 --------------AGACA-TGGACAAAGGCACGAG----------
CCAAAACCAGACA 870

Qy        1172
GCCCATGTCCGTCACCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAA 1231
          || || |||| |||| | |        ||| ||   | ||| ||| |    || ||
Db         871 GTCC-TGGCCGT-TCGAT--------AGGCCA---GCAGTGGG-TGAG----
ACAGG--- 909

Qy        1232
CGCCTACCTCACCGCCGAACTGAGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCCT 1291
                  | |||      ||| |   | |||||||| || ||| |  | |||| ||
Db         910 ----------TCAGCC------AGCTGCAGGGGCGGGAGCGGGG-
GGGCGGGTAG----- 947

Qy        1292
GGACAACAAGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTAC 1351
          ||  ||| ||| |       | |      || |||||  || |   || | ||||
Db         948 GG---ACATGGATG-----TGTGAG-----GTGCTCATGC--
GTGCGATCGTGACT---- 988

Qy        1352 CCTGTCTCTGAGACTCTATGACCAGCACA---TCCGAGGCAGC-
CCGTTTAAGCTGAAAG 1407
                     |  ||||| |||    ||||| ||   |||    |||| ||| ||
|
Db         989 --AGATTCTGAAACT-----GCCAGC-CATTTTCC----CAGCTCCGCTT--------
TG 1028

Qy        1408
TGATCCGATCCGCTGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCC- 1466
          ||   | ||| | || |||   || | | |||                  ||||
Db        1029 TG---CAATCTAAAGGAATGCATCC--CCTCTGAAG-----------------
CAGTCTT 1066

Qy        1467 -
CCGGGGAGCGGCCACGTCAAGCAGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCAC 1525
           || |     ||| || || | |||| | | || ||  | ||||| |
Db        1067 GCCAG-----AGCCTAGTGAGGGAGAGAAGTATGGTAAATACCACAA-
CATAT------- 1113

Qy        1526
TGGAAAAACGAAAAGAGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGG 1585
                  | ||| ||| |||| |  ||   ||  | |        | ||||||| |||
||
Db        1114 --GGAATC----AGAAAATAC---CGGGAAC-----------TGGAGTGGG---
CAAGGG 1150

Qy        1586
AAGAAATAAAGGAGAGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGAT 1645
                  | |||  | ||| ||| | |||| ||  | |         |||      ||||| |
Db        1151 --GGAATGCA-GAGGGTGTGGAAATTTTTTAGTG--------ATC------
TGGAATGTG 1193

Qy        1646
ATTAATTGCAGACAGTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAA 1705
                  | | ||| ||| | |||| ||  || ||| ||           ||| |
```

```
|
Db      1194 TTGAGTGACAGGAAGTGCC--CCAA-----GC-----TTCTCCC-------CCA---
CCA 1231

Qy      1706
AAGTCGTTTGGCATACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGC 1765
                |                  |||| |   ||| || |  ||| |
Db      1232 A----------------------CTCTTC---TCAGTCGC----GCCTGCT------
TT 1255

Qy      1766
TGTACATCCCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTT 1825
             ||| | | ||| | | ||  || | | || | | ||| | ||       || |
|
Db      1256 TGTCTAACTC--TTGTAATCTACACACTACTGCTTA---------------
CAAAGCTGT 1298

Qy      1826
CTCCTCCGATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGG 1885
                ||          | | ||||||||||          |||| || |   ||  |
Db      1299 CT-----------GAGTTTAAGACAAAAA---------
GAAACCTAAAAGTCTCCTTA-- 1336

Qy      1886 AGTTTCTGTGGACCGCAATGGGCACATTATTGTTGTGGACAACAAGGCGTG---
CTGCGT 1942
                 ||| | ||| ||     || | ||| |   ||||  ||     ||
|
Db      1337 --CTTCATAGTACC----TG----------TGATATGG-----
AAGGAATGTAAAAGCAT 1375

Qy      1943
GTTTATCTTCCAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGA 2002
              |     ||| |||| |  ||| | |  |  ||||| |          | | |  ||
||
Db      1376 G--ACCCTTTAAGCCTAT--GGACATT--TTTTCAGGTAT------------
ACAGGAGA 1417

Qy      2003 CAGGCAGTTTGCAGGTCCCCATTTTGCAGCTGTAAATAGC-
AATAATGAGATTATTATTA 2061
                ||  |    |        | ||| | | ||| |  ||| |||| |   ||
|
Db      1418 AAGATAAAAT----------
AATTTTCCACAGAAAAATGAGAATTATGAATTATATAGTT 1467

Qy      2062
CAGATTTCCATAATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGT 2121
              ||| || | |   | |||      |||||   ||||||      ||
|
Db      1468 CAGGTTCCAAATCTAATT-----------TTTAA--------AAGAATTC----
TGA--T 1502

Qy      2122 TTGGCTCAAATGGAGAAGGAAATGGGCAGTTT---
AATGCTCCAACAGGTGTAGCAGTGG 2178
              |  ||| |              || |||  ||||||    ||||
|||
Db      1503 TCTGCT------------------ACACTTTACAAATGCT----TAGGT-------
TGG 1532

Qy      2179
ATTCAAATGGAAACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATG 2238
```

```
                   |  |  |||        |||   |   ||||  |                        ||||
 |
Db      1533 TTCCTAAT---------TTGAAGGAGACTTG--------------------
TTTTATTT 1562

Qy      2239
GGAGTGGATCATTTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAG 2298
                  ||            |||       ||       |  |         ||| ||
Db      1563 GG---------TTAATGCATTGCATTTGAACT--
TGTTTCTATTTTCTTTG--------- 1602

Qy      2299
GCCTGGCCCTAACTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCA 2358
                  |  |||  ||     |||  |        |||       ||| | ||  |||
 ||
Db      1603 -------CATAAATT----TGGACT--------TTG--------GGAGAAAAATG---
CA 1632

Qy      2359
AAGTCTATCGATACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCA 2418
                  ||||      |      |  | |        ||||      |||
Db      1633 AAGTAATAAGTAGAATGCACT-----TGGG-----
GGA---------------------- 1660

Qy      2419
CTATAAACTGGAATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCA 2478
                  |||  |||  |||||| ||        ||      |   |  ||||
Db      1661 ----AAAAAGGA--GGATTTTTC---------CCT-------
TCATGGGTT--------- 1689

Qy      2479 GAAGGAATCATTGGTGAACTTTCCAAGGTT-
ATTTCTGAATGTAACAATTTCCTTAAAAA 2537
                  ||||       |   | |  |  ||||  |||||   |    ||||| ||
Db      1690 ---GGAA-------
AGTATTTTAAAGGGTTGTTTTCTTGAAAAAACAAGCTC-------- 1731

Qy      2538
TGACTTATCCAATTTCTGTATTTCACCTTTAGGGTTAAAAAAAAACTCTTCTACTGAATCT 2597
                  ||  |  |  ||||| | |   || ||  | |||            ||| ||
 ||
Db      1732 --TCTCTTAC--TTTCTGCATCTATGCTATAAAGATAA-----------CTA-TG---
CT 1772

Qy      2598
ATAAAAACTGCAGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTA 2657
                  ||||  || ||         ||           ||||        ||||
 |
Db      1773 ATAATAAATG------------------------TAAG-------------GTAG-
AA 1792

Qy      2658
AACTAATTTTGCAAATCAAACAGACACTTAAAAAAAACTAGCATATGTAAAGGTATTCGTT 2717
                  ||||                     ||||| | |     |  ||| || |||
 |
Db      1793 AACT-----------------------TTAAAGAGA-------
AAATAACAGTGTTC--T 1820

Qy      2718 AATCCTGTGAATGG-----
TAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAA 2772
                  ||     ||||| |     ||||  ||| | || ||| || |     |||| |||||
```

```
Db      1821 AA----GTGAAAAGCTACTTAGCATTTTCCCA-
AACTCACACATTATCAACAGAAACACT 1875

Qy      2773
ATCTATTGTAGTTATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAAC 2832
             |   ||| || |  |  |    | |||  |  ||                    |||
  |
Db      1876 AAAAATT-AAGAGAAAAGCGGC----CAACTAATTAAATAG--------------
CTAGC 1916

Qy      2833
CTCACTTTTACAGTAGGTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATAT 2892
             || | |||    |  | |||||             |  ||  |  || ||| | |
  |
Db      1917 CTTATTTT----GGGGGTAT---------------------
GGGATAGAAAATTAAGTGT 1951

Qy      2893
AAATTACTTTGGAAAAAGTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCC 2952
                ||| |       |||| |   |      |||| | |||| |       |||
  ||
Db      1952 GAAT--------AAAATGATA------CTTG-GGAATGTT------TCT---------
CC 1981

Qy      2953 CTCTGGAGTTCAGAACTTAAG-
TATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAA 3011
             |||     || |   || |   |  | |   | ||||       ||| ||   |   | ||||
Db      1982 CTC----GTAC--CACAAAGGATGTTAGTG-------GTCAGCC--
TACGAGTTA----- 2021

Qy      3012
AGATCCTTTTTTGTGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAA 3071
             ||||||| | |       ||||| |  | |    |  |  |  |      |||| ||
Db      2022 --ATCCTTCCTAG------CATGGCTCTGAGCCTT---CATGCCG------
AGCAGAC-- 2062

Qy      3072
AGTACTTCTTCAGGGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAA 3131
             |  ||| |   ||  || ||| |    |        ||||||  ||| || |  |
Db      2063 -GTTATTC---------ACATGACGATTC---------GAAAAGTCCATT-
CATATATCT 2102

Qy      3132
TGCTACCTTTTGGGAAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAAT 3191
             ||||||                                  || | | ||||
  ||
Db      2103 CGCTACC-----------------------------------
TGGATTTGAATAGAAA 2125

Qy      3192
CAAGAAAGTTAGTCATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTT 3251
             | |||  || || | | ||   || | || || ||||             |   |||| |
Db      2126 CCAGACAG-----CAATTCTTTAGTTCCA-----------------
GCCACCATTCGCCCC 2164

Qy      3252
CCTGAAAGCGAAAGCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCAGTATC 3311
             ||| | | | ||| |        ||| ||||                ||| |||
  ||
Db      2165 ACTGGA--CAATAGCGAT-----------TTGTTAGCA---------------
```

CAGAGTC 2196

Qy   3312
CTAGGACAGAGAGCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGCATGT 3371
                ||| | | | | || || ||| |||||| || |||
Db   2197 ACAGG-CTGTGGGACACAA--AGC---TTGGAG--CT----------------
GCA--- 2228

Qy   3372
GATTGATTAATGATTCCCCCTTAGAAAGCAAGTGTTACCAAAGTTGTGTTATCTTGAAAG 3431
                || ||| ||||| ||| | || | | || || | |
|
Db   2229 GAAAGATGGGGGATTC------AGAGAACAGGAAATTACAGG----------CTCG-
ATG 2271

Qy   3432
CATTACAGGTAAGGGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTC 3491
                || | || || | || || | || || | | |
Db   2272 CACTCCTGGCA---GC----------------
TCTGAGAATACAAAAAAAAAAAAAAAAAA 2312

Qy   3492 AAGGGACTATGTATACATGATTAG 3515
                || | || | | || | || |
Db   2313 AAAAGGCCACATGTGCTCGAGCTG 2336

RESULT 11
US-10-478-914-64/c
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE: 2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

   Query Match   14.0%; Score 5350; DB 1; Length 2120;
   Best Local Similarity 39.1%; Pred. No. 0;
   Matches 1348; Conservative   0; Mismatches 718; Indels 1378;
Gaps 206;

Qy   59 GTCTTCGATGCACAGGAGTGGCCGTTATGGAACG--
CAGCAGCAGCGTGCAGGGTCAAAG 116
                ||||| || ||||| || | ||||| || ||
Db   2120 GTCT------------AGCGGCCG--------CGACCTGCAGCT-
CGAGC---------- 2092

```
Qy         117
ACAGCCGGCCCCCCATGTCAGTGGTCTAGGATGGCCAGTGAAGGCACCAACATCCCAAGT 176
              |||  ||||   | |   |    |               |  | | ||
Db      2091 ACATGTGGCCTTTTTTTTTTTTTTTT-------------
TAAAAGAA-------------- 2059

Qy         177
CCTGTGGTGCGCCAGATTGACAAGCAGTTTCTGATTTGCAGTATATGCCTGGAACGGTAC 236
                  || | |    ||||| |  |||| | |  |||| |  ||   ||||        || |||
|
Db      2058 --TGAGTTACATTT-ATTGATATG--GTTTGTCATATGCTTTATA-------
AATGGT-C 2012

Qy         237
AAGAATCCCAAGGTTCTCCCCTGTCTGCACACTTTCTGCGAGAGGTGCCTGCAGAACTAC 296
              |     |||    ||     | |    | | |      ||| ||  | ||  |      |     | |||
Db      2011 A-----CCCT---TTGAAACATGTATTATTACTATTTGGGGGAGAGG-----
GGGACT-- 1967

Qy         297 ATTCCTGCCCACAGTTTAACCCTCTCCTGCCCAGTGTGC-
CGCCAGACCTCCATCCTGCC 355
              |||  |         ||||             |||  |   || |||       |
||
Db      1966 GTTCAT--------TTTA-------------CAGGGGACAAGCAAGA-------
CAGGCT 1935

Qy         356
CGAGAAAGGGGTGGCCGCGCTCCAGAACAATTTCTTCATCACAAACCTGATGGACGTGCT 415
              | || ||  || | |||| | |||| |           |||||||||            |||
Db      1934 CAAGGAGGGAAAGGACAGGCTCAAAG---------TCATCACA------------
GTGTG 1896

Qy         416
GCAGCGAACTCCAGGCAGCAACGCTGAGGAGTCTTCCATCCTGGAGACAGTCACTGCTGT 475
              |              ||| | || ||      |||   || ||||
Db      1895 G-----------GGCTGGAATGC-----
AGTTGCCCTTCCT------------------ 1871

Qy         476
GGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCACGATGGGAATGTGATGGAATTTTACTG 535
                                  ||| ||             |||| |  |
Db      1870 ----------------TCTTTCT-----------------------------
TTTTGC-- 1858

Qy         536
CCAGTCCTGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAGCACGCAGAGCACCC 595
                         | |         || ||  || ||  | |||    |||||||         ||||
Db      1857 ----ACAT------CTTCC--GTCTCTAGGGTG--AGGAGGGG-----
TGCAGG------ 1823

Qy         596
CACAGTTCCACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTCCAGGTCCAGCTGGA 655
                       |||||   ||| ||||        |||||         ||   |||||||||
Db      1822 CACAGG--CACCCAAG-----------ACAGCT---------GC----
GGTCCAGC---- 1793

Qy         656
TGCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGCTCTTCAGTTCATCTCTGAAATCAT 715
                             |||             || |   |          |||    ||
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```
Db       1792 -----------------CCCG-----------GCCCCAC---------
CTGTGGTC-- 1774

Qy        716
TCATCAGTTAACCAACCAAAAGGCCAGCATCGTGGATGACATTCATTCCACCTTTGATGA 775
              ||||| |  |  || | ||||| ||||              |||| |    |
|||
Db       1773 ---TCAGTGA--CGCCCCAGAGGCCC-CATC--------------
TTCCCCACATAATGA 1734

Qy        776 ----
GCTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTATGGAATTGGAGGTCA 831
                    ||||||                          | || || |   |
Db       1733 GGCTGCTCCA--------------------------
TCCTCCTCAAAG----------- 1712

Qy        832
ACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGATACTCTGCTCCAGGGG---C 888
                 |  | |||  || || | |||| | |             || | || |||
|
Db       1711 -CCCAGACCTATTTCATAAG---CCCCAGACCCCAC--------
CTTCACCCAGGGCCCC 1664

Qy        889 AGGAGAGCATTAAGAGCTGCAGCAACTTC-AC----AGCGCAG---
GCCCTCAACCATGG 940
              | |||| |  |||||||| ||  ||||| ||     ||| | |   |||||| |
Db       1663 AAGAGAAC----
AGAGCTGGAGACACTTCTACTCCTAGCACTGGATGCCCTCTCC----- 1613

Qy        941
CACGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAGCTGGC 1000
                               ||| || ||||| | || ||                | |
|||
Db       1612 ---------------CCTCCT-GTGAAGCTGTAGGTGG--------------
GGGGTGG- 1584

Qy       1001 CGACCAGGACTTCCCCTT---GCA--
CCCGCGGGAGAACGACCAGCTGGATTTCATCGTG 1055
                    ||||| ||| || |||| || | || |||   | || |  | || |
||
Db       1583 -----AGGACACCCCTTTAAGGCAGGCTCGGGGGGCTATGAACTCCAAGACTCC----
TG 1533

Qy       1056
GAAACCGAGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCTTAACCACCAACGCC 1115
                     ||| ||    | | | |    | |||| | |  ||  ||| || |
Db       1532 GAAGCCAGTAAGAAGTGGGAAGGTAGGCACACCATTTGG--
GATTTTTAT---------- 1485

Qy       1116
GTTGCCTCAGAGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCAGCCC 1175
                    ||  | | ||| |               | |||| | |  ||| | || | |
||
Db       1484 -TTTTCACTGAGCTA---------AGAGAGGAGATTC--CAG-CTAT-----
GGAATCCA 1443

Qy       1176
ATGTCCGTCACCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAACGCC 1235
                   | |||            |  || | |||      ||| | |   ||| |||
|||
```

```
Db       1442 GAGAGCGT--------TCTACAGGAACA--------GAACAG----
AAATTGGCTGGGCC 1403

Qy       1236
TACCTCACCGCCGAACTGAGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCCTGGAC 1295
                         ||| |  ||| ||                  ||||
|||||||
Db       1402 ----------------CTGGG---CCCAGA------------------GGAGG-
CCTGGA- 1381

Qy       1296 AACAAGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTA-
CCCT 1354
                          ||  |       ||  ||| || || ||||         ||| | ||
|
Db       1380 ----------GCCGC------TTACTGTTCAGTG-CCAG-----------
CTTCATCCTT 1349

Qy       1355 GTCTCTGAGACTCTATGAC--
CAGCACATCCGAGGCAGCCCGTTTAAGCTGAAAGTGATC 1412
                | | ||  | |||| ||  |  |  | || |  | ||| ||| || |    |||
Db       1348 GGCACTCTGCCTCTCACACAGCATCGC-TCC--GGCTCCCAG----
AGC----------- 1307

Qy       1413
CGATCCGCTGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGG 1472
                 || | |  |        |  || | |||| || |  ||| |  | | |    |||
Db       1306 ----CCACAGTGG------CAGCCGCTGGAGGC-TGTGGCAGC-
AGCTGCTGCCCT---- 1263

Qy       1473
AGCGGCCACGTCAAGCAGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAA 1532
                  |||   |||| |||  || | |||| |   | |  || | ||||  |   ||
Db       1262 ----GCC----CAAG--GAGGGATGTG----GGCTTG---GCTCTGACAGTTC---
AAGC 1223

Qy       1533
CGAAAAGAGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAAAT 1592
                 |  |||||| |   || || |||| |  |  | | |||  |  | |    || | ||
|||||
Db       1222 CAGAAAGAG----CCTTAGAAGTCATTCAGGACATTCCCAT--
TTTACAGATGATGAAAT 1169

Qy       1593 AAAG----
GAGAGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGATATT 1648
                || |  |||||         |||||| |  |    | | ||| |     ||
Db       1168 AAGGCTCAGAGAG----------
AGCAGGGGCTTTCAAGAACAATAAAGGTGGAG----- 1124

Qy       1649 AATTGCAGACAGTAACAACCAATGTGTGCAGA---TATTTTCCAATGATGGC---C--
AG 1700
                | | | ||| |  |  | |  |||  ||| ||   | | | ||  ||| |   |    |
||
Db       1123 ACTGGAACTCAG--GCCTCC--
TGTCTGCTGAGGGTGTCTGCCCATGCTCTCTCTCAGAG 1068

Qy       1701 TTCAAAAGTCGTTTTGGCATACGGGGACG--
CTCTCCGGGGCAGCTGCAGCGGCCCACAG 1758
                || |  ||| || || || |    |||| |  | | | |   |||        ||| | || |
Db       1067 TTTCTGAGTGGTGGTGTCTGGAGGGGCTGGACACGCAAGGG-------
AGCTGGCCTCGT 1015
```

```
Qy        1759
GAGTGGCTGTACATCCCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCA 1818
            |  ||| |||| |  ||    |||| |  || |  | |  || |    | || | |
||
Db        1014 GTGTGTCTGTCTGTGCC----GGGATGT-GTCTGTG--
GCTTCTGTCTCTGAACGTGCCA 962


Qy        1819
GCATTTTCTCCTCCGATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGAC 1878
            |   |||    ||| || |                     || ||      ||| ||
|
Db         961 GGGGTTTTGTGTCCTGTGTG-----------------TGTCTCT------
CTGTGGGTGC 925


Qy        1879 CCAAAGGAGTTTCTGTGGACCGCAA--
TGGGCACATTATTGTTGTGGACAACAAGGCGTG 1936
             |       |||||  | | ||   |||| ||        ||| ||    |||
||
Db         924 TC---------CTGTGTGCAGGAACTTGGGGCCA---------
TGGCCAGAGAGGGATG 884


Qy        1937
CTGCGTGTTTATCTTCCAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAA 1996
               ||      |  ||||   ||| | |  |    ||  |||         || |||
Db         883 -GGC------CTATTCCT-ACAATCTTGGGAGGCCTCCACAG--------
GCTGAGCTGG 840


Qy        1997
TGGGGACAGGCAGTTTGCAGGTCCCCATTTTGCAGCTGTAAATAGCAATAATGAGATTAT 2056
             ||||||     |||||| ||| ||   || | || | ||| |  | | | || |
Db         839 TGGGGA------------GGGTCC------TGAAG-GGTAGAGTG-
AAGATGGGGACT-- 802


Qy        2057 TATTACAGATTTCCATAATCATTCTGTCAAGGTGTTTAATCAG-
GAAGGAGAATTCATGT 2115
             ||||     |||        | |             |  || | |||| ||
Db         801 --TTAC-----TCC---------CAG--------------
CGGAGAGGAAGAAACCA--- 775


Qy        2116
TGAAGTTTGGCTCAAATGGAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAG 2175
             |||| | |||||    ||| | | |||||               | |||| | |
Db         774 -GAAGATAGGCT----TGGGGCATG-GATGGG---------------
AAAGGTCTTG--- 739


Qy        2176
TGGATTCAAATGGAAACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTG 2235
             | |   ||||        | |  |||||||||| | |  |||
Db         738 -GAACTAGGATGG----------------GGCAAGGGAAACA--
AAGCCCCA-------A 705


Qy        2236 ATGG-
GAGTGGATCATTTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCC 2294
             |||| |  ||| ||       ||| |        |  |||| ||||| ||
||||
Db         704 ATGGAGTATGGGTC--------CCTGGA----------AGTTGACACACTCT-
TAGCCCT 664


Qy        2295 CAAGGCCTGGCCCTAACTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAAT--
```

```
CACT 2352
            || ||   |||||    |   |||  ||| |      | ||  |  | | |  || |
||||
Db        663 CATGG--GGGCCCAGCC--
CAGTGGGTAACCCCGGGGAAGTGGTCACATGACGTGACACT 608


Qy        2353
GTTTCAAAGTCTATCGATACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGT 2412
              | |||        |  |   || |              ||   |||    |||
||
Db        607 -TCTCA---------GCTGATTGCT----------------TGAGATCCC----CCA--
GT 579


Qy        2413 CTTGCACTATAAACTGGAATGGATTTCTCAATGCGGGA--
CCAGATTATGACTAGAGTTT 2470
               | ||        |||    ||  || ||  || | ||  |||| ||
Db        578 GTGGC--------CTG----
GGCCTTGTCCTTGAGTGAGCCCAGGTTC------------ 543


Qy        2471
TTATGCCAGAAGGAATCATTGGTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCC 2530
               | |||||| |       |||    | || |  ||||||    ||||
Db        542 --AAGCCAGGAAGGC----TGGCCAGCTGCCCAAGG-----
ACTGAG------------- 507


Qy        2531
TTAAAAATGACTTATCCAATTTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTAC 2590
                  | ||| |||          ||            ||            ||| ||
|
Db        506 --------GCCTTCTCC------------TC---------------------
CTCCTCCTC 487


Qy        2591
TGAATCTATAAAAACTGCAGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTAT 2650
               || ||        ||| |    || |  |  ||||| ||  |  ||| ||| |
Db        486 TGTGTC--------CTCC---TCGATCATCT-TGGCC---
AGCTCCCGGGGC--------- 450


Qy        2651 GTAGCTAAACTAATTTTGCAAATCAAACAGACA-
CTTAAAAAAACTAGCATATGTAAAGG 2709
               |||| |         |   | | | | ||| |      || |  ||| |||
Db        449 --AGCTCCA---------
CGTCTCCACCTGCCATCTGGATCTGGCTCTCATCTGTC---- 405


Qy        2710
TATTCGTTAATCCTGTGAATGGTAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAAC 2769
               ||||  || ||  ||||||      | | ||
Db        404 ---TCGT---TCTTG-----GGTAGC-------
CGGTATTT------------------- 382


Qy        2770
AAAATCTATTGTAGTTATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCT 2829
               ||   || |      ||           ||        | |||      |||
|
Db        381 -GTCTCGGAAGTGG-------CT--------CCGCAGT---GTGGCCC----
GCTCTGCC 345


Qy        2830 AACCTCACT-
TTTACAGTAGGTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAA 2888
               ||||  | |  || ||  || | ||  | ||     |||      || ||  | ||
```

```
Db        344 TTCCTCTGTGTGAACTGT--GCATCCCGCT----CCATC------
TTCTCTTCCAC--- 301

Qy       2889
ATATAAATTACTTTGGAAAAAGTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGC 2948
           |  ||  |||  || |            ||  |   |  |  ||||  ||||
Db        300 ----GAGTTGCTTCTGATAC----------TCCT-
CGTACTCCTCCCGGCTC-------A 263

Qy       2949
AGCCCTCTGGAGTTCAGAACTTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGA 3008
             |||||            ||  ||| |   |   |||  | || ||  ||   |||
Db        262 TGCCCT----------GAGCTTCGG---C--TGCCGACTTGTC--
CCCATCT-------- 228

Qy       3009
CAAAGATCCTTTTTTGTGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAA 3068
           |   ||||          ||  || || |  ||||| |   ||
Db        227 CCCTTATCC-----------------
TCGCCGCCTCCCAGGCTCCCAGTG---------- 195

Qy       3069
CAAAGTACTTCTTCAGGGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAG 3128
            | |  ||||||||    |||         |||          |||        ||
Db        194 --AGG---TTCTTCAG------CTG-----------GCC-------
GC------------ 176

Qy       3129 TAATGCTACCTTTTGGGAAACAAACTGCCCCGTTAACTCCA-
GATCATTGCACTGGAATG 3187
               | |||  |   ||        || | || | ||| ||| | || |   | | ||
                                                                         |
Db        175 -----CCACCAT---GG------TCTTCACCATGAACGCCATGGTCTT--
CGCCGGCCGG 132

Qy       3188
TAATCAAGAAAGTTAGTCATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCG 3247
            | |                       |  || || |  ||| |||
Db        131 GGCACCGG-------------------GCGCC-
TGCTACCACGCG--------------- 107

Qy       3248
ACTTCCTGAAAGCGAAAGCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCAG 3307
             || | ||  | | ||   |  |  | ||  |      |||||        ||
                                                                      ||||
Db        106 ----CCAGGCACCGGGCACGTCCGCGCCTACT----TCAGC------------
ACTCCAG 67

Qy       3308
TATCCTAGGACAGAGAGAGCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCAACCAAAGGC 3367
              ||            ||||  ||| || |    |||||
Db         66 TA------------GGCCAACAGT-GCTC----
GAGGA---------------------- 46

Qy       3368 ATGTGATTGATTAATGATTCCCC--
CTTAGAAAGCAAGTGTTACCAAAGTTGTGTTATCT 3425
                                 ||||| | ||| | |||| || ||
                                                                          ||
Db         45 -----------------ATTCCGCAGCTTTTAGAGCAGAAGTAAC-------------
ACT 15
```

```
Qy      3426 TGAAAGCATTACAGGTAAGGGCAT 3449
             |    |  ||||     ||| |
Db        14 T-----CCGTACA------GGCCT 2
```


RESULT 12
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match   13.9%; Score 5309; DB 1; Length 2120;
  Best Local Similarity   39.3%; Pred. No. 0;
  Matches 1311; Conservative   0; Mismatches 726; Indels 1302;
Gaps 201;

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Qy        14 GGGCTGCGGGGAGCTAAGTCCCCAGAT-
TGGAGGAGGCTGGCTCTGGTCTTCGATGCACA 72
             || |||   |||  |   | | | | | | |  || |   || ||||
||||
Db         3 GGCCTGTACGGAAGTGTTACTTCTGCTCTAAAAGCTGCGGAAT----TCCTCGA-
GCACT 57

Qy        73 GGAGTGGCCGTTATGGAACGCAGCAGCAG-------
CGTGCAGGGTCAAAGAC------- 118
             |   |||||| |  |||| || | || ||      ||||| |||    | |
Db        58 G--TTGGCC-
TACTGGAGTGCTGAAGTAGGCGCGGACGTGCCCGGTGCCTGGCGCGTGGT 114

Qy       119
AGCCGGCCCCCCATGTCAGTGGTCTAGGATGGCCAGTGAAGGCACCAACATCCC-----A 173
             ||| ||| |||  || |                |||| | |||| |    | | |
|
Db       115 AGCAGGCGCCCGGTGCC-----------
CCGGCCGGCGAAGACCATGGCGTTCATGGTGA 163

Qy       174
AGTCCTGTGGTGCGCCAGATTGACAAGCAGTTTCTGATTTGCAGTATATGCCTGGAA--C 231
             || || ||||| ||     | ||| |    ||     || ||  |||||| |
|
Db       164 AGACC-ATGGTGGGC------GGCCAGCTG---
AAGAACCTCACTGGGAGCCTGGGAGGC 213
```

```
Qy        232 GGTACAAGAATCCCAAGGTTCTCCCCTGTCTGCACACTTTCTGCGAGAGGTGC----
CTG 287
              ||  | || ||  ||||                         |  || || |    |
|
Db        214 GG--CGAGGAT---AAGG------------------------
GAGATGGGGACAAGTCGG 244

Qy        288
CAGAACTACATTCCTGCCCACAGTTTAACCCTCTCCTGCCCAGTGTGCCGCCAGACCTCC 347
              |||                 ||  ||      ||| | |  |||||||  ||   |
|
Db        245 CAG--------------CCGAAG---------CTCAGGGC--
ATGAGCCGGGAGGAGTAC 279

Qy        348 -------ATC-----CTGCCCGAGAAAGGGGTGGCCGCGCTCCA-
GAACAATTTCTTCAT 394
                      |||     |  | ||  ||| |  |  | ||  | | |||  |
|
Db        280
GAGGAGTATCAGAAGCAACTCGTGGAAGAGAAGATGGAGCGGGATGCACAGT-------T 332

Qy        395 CACAAACCTGATGGACGTGCTGCAGCGAACTCCAGGCAGCAACGCTGAGGAGTCTTCCAT 454
              ||||  | ||  || ||  | | |||          || | ||||  |   |
|
Db        333 CACA---CAGA-GGAAG-GCAG-AGCG----------GGCCACACTGCGGAGCC--
ACTT 374

Qy        455 CCTGGAGACAGTCACTGCTGTGGCTGCGGGAAAGCCTCTCTCTTGC---
CCAAACCACGA 511
              ||  ||||||  ||     |||| |  | | |    |  ||   ||| | |
||
Db        375 CC--GAGACAAATAC-----
CGGCTACCCAAGAACGAGACAGATGAGAGCCAGATCCAGA 427

Qy        512
TGGGAATGTGATGGAATTTTACTGCCAGTCCTGTGAGACTGCCATGTGTCGGGAGTGCAC 571
              | | | ||| |  |||  |   ||||  | |    |||| |               ||
|
Db        428 T-GGCAGGTGGAGACGTGGAGCTGC----CCCGGGAGCTGGCCAAG--------
ATGATC 474

Qy        572 GGAGGGGGAGCACGCAGAGCACCCCACAGTTCCACTCAAGGATGTGGTGGAACAGCACAA 631
              ||||  |||             |||||        |||| | || |||
||
Db        475 -GAGGAGGA---------------CACAG---------AGGAGGAGGAGGAG------
AA 503

Qy        632
GGCCTCGCTCCAGGTCCAGCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGATTCTGC 691
              ||||||  ||| |  |||||||         ||    |  || |
||
Db        504 GGCCTCAGTCCTTGGGCAGCTGGC------CAGC------CTTCCTG-----------
GC 540

Qy        692
TCTTCAGTTCATCTCTGAAATCATTCATCAGTTAACCAACCAAAAGGCCAGCATCGTGGA 751
              ||  | | |||   ||| ||| || |||     ||  ||||||
```

```
Db        541 -------TTGAAC-CTGGGCTCACTCA--AG------GAC---
AAGGCC----------- 570

Qy        752
TGACATTCATTCCACCTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCT 811
                     ||  ||||  |  |  |||  |||  |         ||  |  ||||| 
Db        571 -------CAGGCCACACTGGGGGATCTCAAGCAATC--------
AGCTGAGAAGTGT--- 612

Qy        812
GCTTATGGAATTGGAGGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAGCTGGA 871
                    |                |  |||| | || ||    | |   ||   ||| | |
|||||
Db        613 -C------------ACGTCA--TGTGACCACTTCCCCGGGGTTACCCACTGG--
GCTGG- 654

Qy        872
TACTCTGCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCC- 930
                        || ||    || ||| ||  |||||| | |||||||| |||    |
|||
Db        655 ------GCCCC-----CATGAGGGC--TAAGAG-TGTGTCAACTTC-CAG---
GGACCCA 696

Qy        931 TCAACCAT----GGCACGGAGACCGAGGTCC--
TACTGGTGAAGAAGCAGATGAGCGAGA 984
                | ||||   ||| |   ||  | || | || ||
Db        697
TACTCCATTTGGGGCTTTGTTTCCCTTGCCCCATCCTAGT-------------------- 736

Qy        985 AGCTGAACGAGCTGGCCGACCAGGAC--TTCC---
CCTTGCACCCGCGGGAGAACGACCA 1039
                             ||| ||| |||| || ||| |||  |      | |
|
Db        737 ------------------TCCAAGACCTTTCCCATCCATGC-CCCAAG-----
CCTATCT 772

Qy        1040 GCTGGGATTTCATCGTGGAAACCGAGGGGCTGAAGAAGTCCATC----CACAACC--
TCGG 1093
                  ||||  ||||  |  |   ||| |||  ||    |||||   |  | ||| ||
|
Db        773 TCTGG-TTTCTTCCT---
CTCCGCTGGGAGTAAAGTCCCCATCTTCACTCTACCCTTCAG 828

Qy        1094 GACGATCTTAACCACCAAC---GCC----
GTTGCCTCAGAGACAGTGGCCACGGGCGAGG 1146
                  |||   |  | |||||| |   |||      |  ||||||         ||| |   |
|
Db        829 GAC---CCTCCCCACCAGCTCAGCCTGTGGAGGCCTC-----------
CCAAGATTGTAG 874

Qy        1147
GGCTGCGGCAGACCATCATCGGGCAGCCCATGTCCGTCACCATCACCACCAAGGACAAAG 1206
                | | || |  || ||| ||   |  |||||| ||          ||||| |
Db        875 GAATAGGCCCCATCCCTC-TCTGG----CCATGGCC--------------
CCAAGTTC---- 912

Qy        1207
ACGGTGAGCTGTGCAAAACCGGCAACGCCTACCTCACCGCCGAACTGAGCACCCCCGACG 1266
                     |||                    |  ||| | |||||||||| |
Db        913 --------CTG----------------------CACACAG------- 
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```
GAGCACCCAC---- 932


Qy        1267
GGAGCGTGGCAGACGGGGAGATCCTGGACAACAAGAACGGCACCTATGAGTTTTTGTACA 1326
                  ||  |  |  || ||          |  |||| |||| |    |  |||
||
Db         933 --AGAGAGACACAC--------ACAGGAC-ACAAAA----CCCCTG-----------
GCA 966


Qy        1327
CTGTCCAGAAGGAAGGGGACTTTACCCTGTCTCTGAGACTCTATGACCAGCACATCCGAG 1386
                  |  || ||| ||  ||  |  |    |  |  ||  |  | |   |||    ||||
||||
Db         967 C-GTTCAG-AGACAGAAGCCACAGACACATCCC---GGCAC--
AGACAGACACACACGAG 1019


Qy        1387 G-CAGCCCGTTTAAGCTGAAAGTGATCCGATCCGCTGATGTGTCTCC-
CACCACAGAAGG 1444
                  | |||| |  || ||    ||| | || |   | | |  | ||| |  |||||
Db        1020 GCCAGCTCCCTT--GC-----GTGTCCAGCCCCTCC----
AGACACCACCACTCAGAAAC 1068


Qy        1445 CGTGAAGAGGCGCGTTAAGTCCCCGGGGAG-CGGCCACGTCAAGCAGAAAG-CTGTG-
AA 1501
                  |||    | || |        ||| || |  ||  | ||  ||| | ||| |
Db        1069 TCTGAGAGAGAGCAT--------
GGGCAGACACCCTCAGCAGACAGGAGGCCTGAGTTC 1119


Qy        1502
AAGACCCGCAAGCATGTACAGCACTGGAAAACGAAAAGAGAATCCCATCGAAGACGATTT 1561
                  || | || | ||  | | | | |               |||
|
Db        1120 CAGTCTC-CA--CCTTTATTGTTCTTGAAAGC-----------
CCC-------------T 1152


Qy        1562
GATCTTTCGAGTGGGTACCAAAGGAAGAAATAAAGGAGAGTTTACAAATCTTCAGGGGGT 1621
                  |  ||| ||  || |  || |    |                 || |  ||| ||  |
Db        1153 GCTCTCTC---TGAG--CCTTA-------------------TTTC--
ATCATCTG----- 1181


Qy        1622
AGCTGCATCTACAAATGGAAAGATATTAATTGCAGACAGTAACAACCAATGTGTGCAGAT 1681
                  ||||||  ||                                         ||| |
||
Db        1182 ----------TAAAATGGGAA-----------------------------
TGTCCTGA- 1200


Qy        1682 ATTTTCCAATGATGGCCAGTTCAAAAG-
TCGTTTTGGCATACGGGGACGCTCTCCGGGGC 1740
                  ||| |  ||| | | | ||  | |||| |         ||  || |
|
Db        1201 -----------ATGAC---TTCTAAGGCTCTTTCTGGCTT------
GAACTGTCAGAGCC 1240


Qy        1741 AGCTGCAGCGGCCCACAGGAGTGGCTGTACATCCCAGTG-
GGGACATAATCATTGCCGAT 1799
                  |        |||||||        |  |  |||  | |  || ||        || |
|
Db        1241 A--------AGCCCACA----------TCCCTCCTTGGGCAGGGCA--------
```

```
GCAGCT 1274

Qy        1800
TATGATAATAAATGGGTCAGCATTTTCTCCTCCGATGGGAAATTTAAGACAAAAATTGGA 1859
              ||  |            ||||     ||||  ||
Db        1275 GCTGCCA----------CAGC-----
CTCCAGCG------------------------- 1293

Qy        1860
TCAGGAAAGCTGATGGGACCCAAAGGAGTTTCTGTGGACCGCAATGGGCACATTATTGTT 1919
                    ||||        |||  |  ||||  ||  ||        ||  |  |  ||
|
Db        1294 -------GCTG-------CCACTGTGGGCTCTGGGAGCC------
GGAGCGATGCTG-T 1331

Qy        1920
GTGGACAACAAGGCGTGCTGCGTGTTTATCTTCCAGCCAAACGGGAAAATAGTCACCAGG 1979
                   |||        ||  | ||||  |     |  ||  ||| |  ||| |   ||  |
|||||
Db        1332 GTGAGAGGCA--GAGTGCCAAGGATGAAGCTGGCA-CTGAACAG--
TAAGCGGCTCCAGG 1386

Qy        1980
TTTGGTAGCCGAGGAAATGGGGACAGGCAGTTTGCAGGTCCCCATTTTGCAGCTGTAAAT 2039
                 |    ||        |||  |        ||||  ||        ||||
Db        1387 CCT-----CC------TCTGGGCC----------CAGGGCC--------
CAGC------- 1410

Qy        2040
AGCAATAATGAGATTATTATTACAGATTTCCATAATCATTCTGTCAAGGTGTTTAATCAG 2099
                 ||||                                  ||||||           ||
|
Db        1411 --CAAT--------------------------------TTCTGT------------
TCTG 1424

Qy        2100
GAAGGAGAATTCATGTTGAAGTTTGGCTCAAATGGAGAAGGAAATGGGCAGTTTAATGCT 2159
                       |||  |||  |||       ||||     ||||
|
Db        1425 ---------TTCCTGTAGAA----CGCTC-TCTGGA---------------------
TT 1448

Qy        2160
CCAACAGGTGTAGCAGTGGATTCAAATGGAAACATCATTGTGGCCGACTGGGGAAACAGC 2219
                        ||||  ||||  ||||  ||           |  |  ||||  |  |  |  | | |||
Db        1449 CCA-------TAGC--TGGAATC--------TCCTCTCT-TAGC--
TCAGTGAAAAATAA 1488

Qy        2220
AGGATCCAGGTTTTTGATGGGAGTGGATCATTTTTGTCCTACATTAACACATCTGCTGAC 2279
                |   |||  |    ||        || ||           |||||| ||  ||| |||
Db        1489 AAATCCCAAAT--------GGTGTG------------
CCTACCTTCCCACTTCT------ 1522

Qy        2280
CCACTCTATGGCCCCCAAGGCCTGGCCCTAACTTCAGATGGTCATGTTGTGGTTGCAGAC 2339
                ||    ||||  |||  |                                        ||
|
Db        1523 -TAC----TGGCTTCCAGG----------------------------------
AGTC 1540
```

```
Qy        2340
TCTGGAAATCACTGTTTCAAAGTCTATCGATACTTACAGTAATGGTGGGCAGGTGGATAC 2399
            |  ||||        |||  ||   | |||  |  |||  |          |||| |
                                                                    |
Db        1541 T-TGGAG--------TTCATAGCCCCCGA-GCCTGCCTTAAAGG------GGTG--
TCC 1582

Qy        2400 -
CCGCTTCCATGGTCTTGCACTATAAACTGGAATGGATTTCTCAATGCGGGACCAGATTA 2458
               ||  ||     |||  ||       |||        ||| ||  | |||
Db        1583 TCCACCCCC---------CACCTACAGC----------TTCACAG-
GAGGGG-------- 1614

Qy        2459
TGACTAGAGTTTTTATGCCAGAAGGAATCATTGGTGAACTTTCCAAGGTTATTTCTGAAT 2518
                                  ||| || |||         |   | |||  |
Db        1615 -------------------AGAGGGCATC---------
CAGTGCTAGG-----------A 1635

Qy        2519
GTAACAATTTCCTTAAAAATGACTTATCCAATTTCTGTATTTCACCTTTAGGGTTAAAAA 2578
              |||  |  | ||               ||||  |||| |||  ||  || |||
Db        1636 GTAGAAGTGTC---------------TCCAG-CTCTG---TTCTC--
TTGGGG------- 1667

Qy        2579
AAACTCTTCTACTGAATCTATAAAAACTGCAGTTTTACATCTGTGAACTATGGCTTAAGG 2638
              | ||                           |            || |  ||  ||||||
                                                                      |
Db        1668 ---CCCT-----------------GGGTGAAGG--------
TGGGGTCTGGGGCTTATGA 1699

Qy        2639
GACAGGATTTATGTAGCTAAACTAATTTTGCAAATCAAACAGACACTTAAAAAAACTAGC 2698
              | ||||           || || |     |  || ||||| | |
Db        1700 AATAGGT---------CTGGGCT-
TTGAGGAGGATGGAGCAGCCTCAT------------ 1737

Qy        2699
ATATGTAAAGGTATTCGTTAATCCTGTGAATGGTAGCTTTTGCACAGAACTTCCAAAAGC 2758
              |||||   |   |         ||| |  || |||   |  | |  ||| ||   ||| |
                                                                       |
Db        1738 -TATGTGGGGAAGATGG---GGCCTCTG---GG--GCGT---CACTGAG--
ACCACAGGT 1783

Qy        2759
AAAACAAAAACAAAATCTATTGTAGTTATATACTTCATTTAACCTAGGTCACAAGACCCA 2818
              |      |    |  | | | |  | |||     | | || ||  ||  |   |
              ||
Db        1784 GGGGCCGGGGCTGGACC----GCAGCTGT--------------
CTTGGGTGCCTGTGCCT 1825

Qy        2819
GGGAATCTTCTAACCTCACTTTTACAGTAGGTATTACTCTTGTGACATTTTTTTGGTTAT 2878
              |     |   |   ||||              || ||| |||  |
              ||
Db        1826 G-----CACCCCTCCTC------------------ACCCTAGAGACG-------
GAAGAT 1855
```

```
Qy        2879
CAACAACTAAATATAAATTACTTTGGAAAAAGTAAGGCTGTCTTGCAAAATGATCCCAGC 2938
                  ||| |                   | || ||| ||||      ||||    ||
|||||
Db        1856 GTGCAAAAA--------------GAAAGAAGGAAGG-------
GCAACTGCATTCCAGC 1893

Qy        2939
TCTGATTAGCAGCCCTCTGGAGTTCAGAACTTAAGTATCAGTGCAAATTTCTC------A 2992
                  |       | | |||    | | |||| |  | ||| ||||| |
|
Db        1894 CC----------CACACTG----TGATGACTT-TGAGCCTGTCC---
TTTCCCTCCTTGA 1935

Qy        2993
ACCTTTCTGGGTTAGACAAAGATCCTTTTTGTGTGTTCTTTTCACCACCCCTTTGGCTC 3052
                  ||| ||| | ||         ||| | |    || | | ||| | ||        |
|
Db        1936 GCCTGTCTTGCTT--------GTCCCCTGTAAAATGAACAGTCCCCCTCTCC-----
CCC 1982

Qy        3053
ACCTTGTATCAGCAAACAAAGTACTTCTTCAGGGAAACCTGAAATTTCTAATGCCTTGAA 3112
                  | | ||| | | |||   | ||| |||| |||    |||| |
|
Db        1983 AAATAGTAATA--ATACA---TGTTTC-AAAGGGTGACC----
ATTTAT----------A 2022

Qy        3113
AAGCATATTACAAAAGTAATGCTACCTTTTGGGAAACAAACTGCCCCGTTAACTCCAGAT 3172
                  ||||||||| ||||        ||| | |  | || ||||||
|
Db        2023 AAGCATATGACAA----------ACCATAT----CAATAAATG------TAACTC--
ATT 2060

Qy        3173
CATTGCACTGGAATGTAATCAAGAAAGTTAGTCATGTTTTATGTACCATGTTTTCACACG 3232
                  | ||         | || || ||| || |                    ||||
|
Db        2061 CTTT---------TAAAAAAAAAAAAAAAAAGGC--------------------
CACATG 2090

Qy        3233 TGTCTCTTCTCTTCGACTTCCTGAAAGCGAAAGCTTTAC 3271
                  ||         |||| | | |  ||| ||| ||
Db        2091 TG---------CTCGAGCTGCAGGTCGCGGCCGCTAGAC 2120
```

RESULT 13
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775

```
  Query Match           13.8%;  Score 5280.5;  DB 1;  Length 2198;
  Best Local Similarity   37.3%;  Pred. No. 0;
  Matches 1415;  Conservative    0;  Mismatches  748;  Indels 1633;
Gaps  205;

Qy        54 CT-
CTGGTCTTCGATGCACAGGAGTGGCCGTTATGGAACGCAGCAGCAGCGTGCAGGGTC 112
             || |||||||        |  ||||  ||| |     |  ||||| || | |
|||
Db         2 CTACTGGTCTT----------GTGTGGGTGTTTT------C--CAGCA-CG-
GAAAAGTC 41

Qy       113 AAAGACAGCCGGCCCCCCATGTCAGTGGTCTAGGATGGCCAGTGAAGGCACCAACATCCC 172
               |    |        || || || || |||    ||    | ||||
||
Db        42 GAGATAA-----------TTGCCAATGATC-AGGGAAACC-------GAACCAC---
TCC 79

Qy       173 AAGTCCTGTGGTGCGCCAGATTGACAAGCAGT-
TTCTGATTTGCAGTATATGCCTGGAAC 231
              |||   |||   |||| || ||   || |   | | |   | || ||||| |
||
Db        80 AAGCTATGT----CGCC---TTTACGGACACTGAACGGTTGATCGGTG-ATGCC-
GCAAA 130

Qy       232 GGTACAAGAATCCCAAGGTTCTCCCCTGTCTGCACACTTTCTGCGAGAGGTGCCTGCAGA 291
               |   ||||  |  ||| | || | || |   | |||| ||| ||        |||
|
Db       131 GAATCAAG--TTGCAATGAACCCCAC---CAACACAGTTTTTG---------
ATGCCAA 175

Qy       292 ACTACATTCCTGCCCACAG-TTTAACCCT-
CTCCTGCCCAGTGTGCCGCCAGACCTCCAT 349
              || | | || | ||| |    | || || |||||            | || |
|
Db       176 ACGTC-TGATTGGACGCAGATTTGATGATGCTGTTGTCCAGT-------
CTGATATGAAA 227

Qy       350 CCT--GCCCGAGAAAGGGGTGGCCGC-GCT-
CCAGAACAATTTCTTCATCACAAACCTGA 405
              | |  ||||    |  | |||||    |  ||| ||| |          ||    ||
Db       228 CATTGGCCCTTTATGGTGGTGAATGATGCTGGCAGGCC-----------
CAAGGTCC--- 273

Qy       406
TGGACGTGCTGCAGCGAACTCCAGGCAGCAACGCTGAGGAGTCTTCCATCCTGGAGACAG 465
              | ||        ||| | ||| || || | |  |   |||| |||| |||
```

```
|
Db       274 ---AAGT-------AGAATACAAGGGAGAGAC-CAAAAG---CTTCTATCC-
AGAGGAGG 318


Qy       466
TCACTGCTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCACGATGGGAATGTGATGG 525
             | || || ||| |                      |  | || ||  |       |||
||
Db       319 TGTCTTCTATGGTT---------------------CTGACAAAGA--------
TGAAGG 348


Qy       526
AATTTTACTGCCAGTCCTGTGAGACTGCCATGTGTCGGGAGTGCACGGAGGGGGAGCACG 585
             || ||      ||| |      || || || |              ||| ||
Db       349 AAATTG-----CAG------AAGCCTACCTT-------------------
GGGAAG---- 374


Qy       586
CAGAGCACCCCACAGTTCCACTCAAGGATGTGGTGGAACAGCACAAGGCCTCGCTCCAGG 645
                     || ||| |  ||| || | |||||     |||| ||| |     |||
Db       375 -----------ACTGTTAC---CAATGCTGTGGT-------CACAGTGCC-
AGCT----- 407


Qy       646 TCCAGCTGGATG-CTGTCAACAAAAGGCTCCCAGAAATAGATTCT-
GCTCTTCAGTTCAT 703
                  | |   |  ||| || ||| |   ||||| ||    | |||| ||| |  ||   | |
|
Db       408 TACT--TTAATGACTCTCAGCGTCAGGCTACC----
AAAGATGCTGGAACTATTGCTGGT 461


Qy       704
CTCTGAAATCATTCATCAGTTAACCAACCAAAAGGCCAGCATCGTGGATGACATTCATTC 763
                 ||| | |  |||| | |||| ||   | ||  |    ||  |||
||
Db       462 CTCAATGTACTTAGAATTATTAATGAGCCAA-----CTGCTGC-----
TGCTATTGCTTA 511


Qy       764
CACCTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAGTGTGCTGCTTATGGAATT 823
                 | |||  || |         | | ||| | |  |   || ||| |  | |   ||| ||
|
Db       512 CGGCTTAGA------CAAAAAGGTTGGAGCAGAAAG-AAACGTGCTCATCTT-
TGACCTG 563


Qy       824 GGAGGT--CAACTATG--GCCTCAAACACAAAGTCCTC-
CAGTCGCAGCTGGATACTCTG 878
                 |||||| ||  | | ||||      |||||  | | |  | |||| ||
||
Db       564 GGAGGTGGCACTTTTGATGTGTCAA--------
TCCTCACTATTGAGGATGGAATCTTTG 615


Qy       879
CTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGCAGGCCCTCAACCAT 938
                        || || |              || ||||
Db       616 -----AGGTCAAGT------------
CTACAGCT------------------------- 632


Qy       939 GGCACGGGAGACCGAGGTCCTACT--
GGTGAAGAAGCAGATGAGCGAGAAGCTGAACGAGC 996
                 ||||||        || |||  ||||  |||||     |||        | | |||
```

```
Db       633 -----GGAGAC-----ACCCACTTGGGTGGAGAAGATTTTGA-----
CAACCGAA----- 672

Qy       997
TGGCCGACCAGGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCTGGATTTCATCGTGG 1056
             ||| | |||| |      |   ||           |||| ||| | ||
Db       673 TGGTCAACCA-----TTTTATT--------------------
GCTGAGTTTAAGCG--- 703

Qy       1057
AAACCGAGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCTTAACCACCAACGCCG 1116
             | |   ||  |||||| |||
Db       704 ----CAA---
GCATAAGAAGGACAT-------------------------------- 721

Qy       1117
TTGCCTCAGAGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATCATCGGGCAGCCCA 1176
                       ||||| || | ||  ||||    |||         |||
Db       722 -----------CAGTGAGAACAAGAGA---GCTGT--AAGAC------------
GCC-- 750

Qy       1177
TGTCCGTCACCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAAAACCGGCAACGCCT 1236
             |||||        || |       |||| | |||| || |    |
Db       751 --TCCGT-------ACTGCTT------------GTGAAC-
GTGCTAAGCGTAC------- 781

Qy       1237
ACCTCACCGCCGAACTGAGCACCCCCGACGGGAGCGTGGCAGACGGGGAGATCCTGGACA 1296
             |||| |  ||      ||||||| | |||         ||||||
Db       782 -CCTCTCTTCC------AGCACCCAGGCCAGTATT------------
GAGATC------- 815

Qy       1297
ACAAGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGGGACTTTACCCTGT 1356
                          | ||| | |||  | | | ||||||   ||||
Db       816 -------------------GATTCT---CTCTAT---GAAGGAA-
TCGACT--------- 840

Qy       1357 CTCTGAGACTCTATGACCAGCACATCCGAGGCAGCCCGTTT----AAGCTGAAAG-
TGAT 1411
                  |||    ||| || ||| |        ||||| ||   | ||||| |
|||
Db       841 -TCTATACCTCCATTACCCG------------
TGCCCGATTTGAAGAACTGAATGCTGAC 887

Qy       1412
CCGATCCGCTGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGG 1471
             |  | |||     ||| | |||           ||                 | ||| |
Db       888 CTGTTCC------GTGGCACCC-------------TG--------------
GACCCAGTA 914

Qy       1472 GAGCGGCCACGTCAAGCAGAAAGCTGTGAAAAGACCCGCAAGCATG-
TACAGCACTGGAA 1530
             |||    | | || ||  | |        || |||| | |   | |||| |   ||||
Db       915 GAGAAAGCCCTTCGAGATGCCAAACTAGACAAGTCACAGATTCATGATATTGTCCTGG-- 972

Qy       1531
AACGAAAAGAGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTACCAAAGGAAGAA 1590
```

```
                              |  |   ||    |||  |                   |  ||  |||
Db      973  -----TTGGTGGTTCTACTCGTA-----------------------
TCCCCAAG------ 998

Qy      1591
ATAAAGGAGAGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGGAAAGATATTAA 1650
               ||  ||  ||  |  |  |||  ||            |||  |||   |  |||||  |
||
Db       999 ATTCAGAAGCTTCTCCAAGACT----------------
TCTTCAATGGAAAAGAACTGAA 1042

Qy      1651
TTGCAGACAGTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTC 1710
             |    |  || |  ||||||             |   ||||  |  |  |||
Db      1043 T----AAGAGCATCAACC------------------CTGATGAAG--
CTGTT-------- 1070

Qy      1711
GTTTTGGCATACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGGAGTGGCTGTAC 1770
                 ||  ||  ||  |   |||  |||  |       |||||
Db      1071 ------GCTTATGGTGCAGCTGTCCAG-------
GCAGC--------------------C 1097

Qy      1771
ATCCCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCT 1830
               |||            |||  |
Db      1098 ATC------------------
TTGTC---------------------------------- 1105

Qy      1831
CCGATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTT 1890
               |||                      ||||||
Db      1106 ----TGG--------
AGACAAG----------------------------------------T 1116

Qy      1891
CTGTGGACCGCAATGGGCACATTATTGTTGTGGACAACAAGGCGTGCTGCGTGTTTATCT 1950
               |||  |                  |  |||||         ||||    ||||||
Db      1117 CTGAG------------------AATGTT--------CAAGATTTGCTGC-------
TCT 1143

Qy      1951
TCCAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGT 2010
               |            |||    ||||||
Db      1144 T-----------GGA----
TGTCAC---------------------------------- 1153

Qy      2011
TTGCAGGTCCCCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTATTACAGATTTCC 2070
                           |||  |
|||||
Db      1154 -------TCCTC--------------------------------------------
TTTCC 1163

Qy      2071
ATAATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGGCTCAA 2130
                                 |  |||  || ||  |   |   ||  |  | ||||
```

```
Db      1164 ------------CTTGGTATTGAAACT-
GCTGGTGGAGTCAT----------------- 1192

Qy      2131
ATGGAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAATGGAA 2190
                              | | ||    | |||| | | |  | |||        || |
Db      1193 ---------------GACTGT------CCTCATCAAGCGTA-------
ATAC-------- 1216

Qy      2191
ACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAGTGGATCAT 2250
             || |||| ||| ||        ||||| |
Db      1217 -CACCATT----CCTAC-------
CAAGCAGACAC------------------------- 1239

Qy      2251
TTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCCTGGCCCTAA 2310
              | |||| ||           || |||| | |   | |  | |  ||| |||||
Db      1240 ---AGACCTTCA------------CT-ACCTATTC--TGACAACCA--
GCCTG------- 1272

Qy      2311
CTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTATCGAT 2370
                              ||| ||| | ||| |   ||   ||| | | ||
Db      1273 ------------------GTG--TGCTTATTCAGGT--------
TTATGAAGGCGAGCGTG 1305

Qy      2371
ACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCACTATAAACTGGA 2430
              | |      | ||     | || ||||| |  | | ||| |   |  | | ||||
Db      1306 CCAT-----------GACA-AAGGATAACAACCTGCTTGG-CAAG---
TTTGAACTCAC 1348

Qy      2431
ATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCAGAAGGAATCATT 2490
              | | || ||| |||                 ||              || ||
Db      1349 AGGCATACCTC-CTGC--------------AC--------------
CCCGA---------- 1370

Qy      2491
GGTGAACTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACTTATCCAAT 2550
               ||||    ||||         || || ||               || | |||| |
||
Db      1371 GGTG----TTCC---------TCAGATTG---------------
AAGTCACTTTTGACAT 1402

Qy      2551
TTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAAAACTGCAG 2610
              |  ||       || | ||| |               |  ||           |||
Db      1403 TGATG-------CCAAT--GGT------ATACTC----AATG--TCT-------
CTG--- 1431

Qy      2611
TTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATTTTGCA 2670
                        ||||| | |  | |  ||||| | |        ||| |   ||
Db      1432 -------CTGTGGACAA--GAGTACGGGAAAAGA-----------
GAACAAGATT---- 1466

Qy      2671
AATCAAACAGACACTTAAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGTGAATG 2730
```

```
                  ||   ||||              |||  ||||    ||||    || | |
              |
Db      1467  ------ACTATCACT------------AATGACAAGGGC--CGTT-----
TGAGCAAG 1499

Qy      2731 GTAGCTTTTGCACAGAACTTCCA-
AAAGCAAAACAAAAACAAAATCTATTGTAGTTATAT 2789
             | ||  ||| || |  |||| |||| |  | ||  ||||| ||   |   |  |
Db      1500 GAAGACATTGAACGTATGGTCCAGGAAGCTGAG-AAGTACAAAG-
CTGAAGATGAGA--- 1554

Qy      2790
ACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCTCACTTTTACAGTAGG 2849
                     | | |||   || || || || || ||
              |
Db      1555 ---------AGCAGAGG------GA--
CAAGGTGTCATCCAA----------------G 1580

Qy      2850
TATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATATAAATTACTTTGGAAAAA 2909
                 ||| | |||| | | |     |   |||||    || ||  ||| | |||
              |
Db      1581 AATT-CACTTGAGTCCTAT-----GCCTTCAAC------
ATGAAAGCAACTGTTGAAGAT 1628

Qy      2910 GTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCCCTCTGGAG-
TTCAGAAC 2968
                 |  |  ||    |||| || || |    ||| || ||  | | || ||| |
              ||
Db      1629 GAGAAACTTCAAGGCAAGATTAAC--------GATGAGGA-
CAAACAGAAGATTCTGGAC 1679

Qy      2969
TTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGATCCTTTTTTGTGTG 3028
                 |||| | ||||| | ||  | || || | |||   |||
Db      1680 --AAGTGT-AATGAAATTATC---
AACTGGCTTGATAAGAATCAGA-------------- 1719

Qy      3029
TTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAACAAAGTACTTCTTCAGGGAA 3088
                     || ||    ||   || | | |   | || ||  |||
              |
Db      1720 ---------------CT---GC------
TGAGAAGGAAGAATTTGAACATCAACAGAAAG 1755

Qy      3089
ACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTTGGGAAA 3148
                 | |||| |                             ||||           ||||
Db      1756 AGCTGGA-------------------------GAAAG-----------
TTTG----- 1771

Qy      3149
CAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGTTAGTCATG 3208
                 |  |||| | |||| | |||| | || ||  ||  || | |   ||
              ||||
Db      1772 ----CAACCCCATCATCACCA-AGC--TGTACCAGAGTG----CAGG------
AGGCATG 1814

Qy      3209 TTTTATGTACCA--
TGTTTTCACACGTGTCTCTTCTCTTCGACTTCCTGAAAGCGAAAGC 3266
```

```
                    |||     |    |   |  |             ||  ||||||   |  |
Db     1815  ---------CCAGGAGGAATGCCTGGGG------------GATTTCCTGGTGGTG-
GAGC 1852

Qy     3267
TTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACCAGTATCCTAGGACAGAGAGCC 3326
           |   |||||              |  |   || ||      |    | ||||    ||| |
Db     1853  T---CCTCC------------CTCTGGTGGT---------GCTTCCT----CAGGGC-
CC 1883

Qy     3327 ATAAGTAGCCCTTTGGAG-
GACTGATGGTGTCAACCAAAGGCATGTGATTGATTAATGAT 3385
            |        ||  |||  || |    || |  | |||||||     |||    ||     ||
Db     1884  A--------CCATTGAAGAGGTTGATTAAGCCAACCAA----
GTGTAGATGTAGCATTGT 1931

Qy     3386 TCC--CCCTTAGAAAGCAAGTGTT--
ACCAAAGTTGTGTTATCTTGAAAGCATTACAGGTA 3442
            |||  || | |   ||| || ||   ||| || ||               | |
Db     1932  TCCACACATTTAAAACATTTGAAGGACCTAAATT---------------
CGT-------- 1968

Qy     3443
AGGGCATGTTATGGTTATTTATCATTGTTTAATGAATAGTAGAGGTGTCAAGGGACTATG 3502
                |||  || ||      |   | ||  |||| | || |||  || ||
Db     1969  --AGCAAATTCTG------TGGCA--GTTT--TAAAAAGTTAAGCTG--------
CTAT- 2007

Qy     3503
TATACATGATTAGGGTAAGATAGAATGTATTATATATATATATATATACACACACACA 3562
                          ||||| ||    | ||| | |||   | ||| |||| |
Db     2008  -------------AGTAAGTTACTGGGCATTCTCAATACTTGAATATGGA-------
ACA 2047

Qy     3563
TATATATAGCTGAATCTTTGGTGTATTGAAATAGGCAGCACTCTGAAAGACAGAAGCTTC 3622
              |||                                  |||| | |||  |   |  | |
Db     2048  TAT----------------------------------
GCACAGGGGAAGGAAATAACATT 2073

Qy     3623 GTCCAGCCACTCT-
TCAGCACATTCCTTTACTAAGCAGTTTAAAGCCGTCCTAGTGGAGC 3681
            |      |||| | | ||| | || |   ||                      |||||||
Db     2074  G------CACTTTATAAACACTGTATTGTA----------------------
AGTGGAAA 2105

Qy     3682
AAGCCCTAAAGCAGATTTAATTTTTGCCATTTTCCAAGAATGACGGTGGTGGCTTTTAGT 3741
             | || |      |  |||| |     | |||| |
Db     2106  ATGCAAT------
GTCTTAAATAAAACTATTT--------------------------- 2131

Qy     3742
CAGAAAATGGCCTTCTGTGCTTTCAAAAAAAAAACAAAAAAAAAAACCACACACACACATA 3801
```

```
                 |||  ||||   |  |      ||||||||||  ||||||||  |||||    |  |
Db     2132 --AAAATTGGC--
ACCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCCACATGTGCTCGAG 2187


Qy     3802 AAAAACCCAACAGGTC 3817
                  |  ||||||
Db     2188 -------CTGCAGGTC 2196
```

RESULT 14
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

  Query Match   13.8%; Score 5272.5; DB 1; Length 2198;
  Best Local Similarity   39.2%; Pred. No. 0;
  Matches 1330; Conservative   0; Mismatches 762; Indels 1303;
Gaps 187;

```
Qy        12
GCGGGCTGCGGGGAGCTAAGTCCCCAGATTGGAGGAGGCTGGCTCTGGTCTTCGATGCAC 71
            |||  ||||    ||||   |  | |      | ||| | |  |  | |||    |
Db     2198 GCGACCTGC----AGCTCGAGCAC--------ATGTGGC---
CTTTTTTTTTTTTTTTT 2154

Qy        72 AGGAGTGGCCGTTATGGAACGCAGCAGCAGCGTGCAGGGTCAAAGACA--
GCCGGCCCCC 129
                  |  ||||||  | ||    |    |    |  ||||||  ||
||
Db     2153 TTTTTT-----TTATGGTGC-
CAATTTTAAATAGTTTTATTTAAGACATTGCATTTTCCA 2100

Qy       130 CATG----TCAGTGGTCTAGGATGGCCAGTGAAGGCACCAAC-------------
ATCC- 171
             | |     |||| || ||  | |  || ||       || |
|||
Db     2099 CTTACAATACAGT-
GTTTATAAAGTGCAATGTTATTTCCTTCCCCTGTGCATATGTTCCA 2041

Qy       172 ----CAAGTCCTGTG-
GTGCGCCAGATTGACAAGCAGTTTCTGATTTGCAGTATATGCCT 226
```

```
                    ||||  || |  ||| ||||  | ||    |  |  | || |  |  | ||
Db      2040 TATTCAAGTATTGAGAATGC-CCAG--
TAACTTACTATAGCAGCTTAACTTTTTAAAACT 1984

Qy       227 GGAACGGTACAAGAATCCCA---AGGTTC-
TCCCCTGTCTGCACACTTTCTGCGAGAGGT 282
                 |  | || |   |   |  ||||| ||   |||      ||| |   | |
                 ||
Db      1983 GCCACAGAATTTGCTACGAATTTAGGTCCTTCAAATGT--------
TTTAAATGTGTGG- 1933

Qy       283 GCCTGCAGAACTACATTCCTGCCCACAGTT-------TAACCCTCTCCT-------
GCCC 328
                    ||  |||||| || | |||       | | |||| |
                ||||
Db      1932 ---AACAATGCTACAT--
CTACACTTGGTTGGCTTAATCAACCTCTTCAATGGTGGGCCC 1878

Qy       329
AGTGTGCCGCCAGACCTCCATCCTGCCCGAGAAAGGGGTGGCCGCGCTCCAGAACAATTT 388
                 | |  || |||  |||||       ||| ||| |   || | |||| | |
                |
Db      1877 TGAG-GAAGC---ACCACCA--------GAGGGAGGAGC-TCCAC-
CACCAGGAAA---T 1835

Qy       389
CTTCATCACAAACCTGATGGACGTGCTGCAGCGAACTCCAGGCAGCAACGCTGAGGAGTC 448
                 | |    || |||  ||| ||| ||||      ||| |  | || |
Db      1834 CCCCCAGGCATTCCTCCTGG-CATGC---------CTCCTG-------
CACTCTGG---- 1796

Qy       449
TTCCATCCTGGAGACAGTCACTGCTGTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAACCA 508
                 | || |||| |           || | |||| |    |  | |||| || |     |
Db      1795 -TACAGCTTGGTGA-------TGATGGGGTTGC-----
AAACTTTCTCCAGCTCTTTC-- 1751

Qy       509
CGATGGGAATGTGATGGAATTTTACTGCCAGTCCTGTGAGACTGCCATGTGTCGGGAGTG 568
                 || || |  ||||||          |||       || |
Db      1750 -----------TGTTGATGTT------CAAAT--------
TCTTCCTT------------ 1728

Qy       569 CACGGAGGGGGGAGCACGCAGAGCACCCCACAGTTCCACTCAAGGATGTGGTGGA--
ACAG 626
                 | |        |||| |              ||| ||||| || |    |
                ||
Db      1727 CTC--------AGCAGTCTGA-----------
TTCTTATCAAGCCAGTTGATAATTTCAT 1687

Qy       627
CACAAGGCCTCGCTCCAGGTCCAGCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGAT 686
                 |||    || |   |  |||    |  ||| ||   ||| |  | ||
Db      1686 TACA----CTTG-
TCCAGAATCTTCTGTTTGTCCTCATCGTTAATCT------------ 1645

Qy       687
TCTGCTCTTCAGTTCATCTCTGAAATCATTCATCAGTTAACCAACCAAAAGGCCAGCATC 746
                 |||  |  ||||  ||||   ||| |||| |||||                  ||
```

```
                     |||
Db       1644 --TGCCTTGAAGTT--TCTC----ATC-TTCAACAGTT------------
GCTTTCAT- 1608


Qy        747
GTGGATGACATTCATTCCACCTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAGT 806
                  || || | |||                       |  ||||          ||||
|
Db       1607 GTTGAAGGCAT------------------------AGGACT-----------
CAAGTGA 1584


Qy        807
GTGCTGCTTATGGAATTGGAGGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCAG 866
              | |           ||||| | || ||                       ||||
Db       1583 ATTC-----------TTGGATGACACCT-----------------
TGTCC----------- 1562


Qy        867 CTGGATACTCTGCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGC----
AACTTCACAGC 922
                   |||||||| |                    |||      || ||||      |||||
||||
Db       1561 -------CTCTGCTTCT------------CAT------
CTTCAGCTTTGTACTTCTCAGC 1527


Qy        923
GCAGGCCCTCAACCATGGCACGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGA 982
                      ||| |||||  ||    |  | ||| | ||
Db       1526 ----TTCCTGGACCAT---AC---
GTTCAATGTCTTCCT--------------------- 1498


Qy        983 GAAGCTGAACGAGCTGGCCGACCAGGACTTCCCCTTG-
CACCCGCGGGAGAACGACCAGC 1041
                     |||   | | | |       |||||| ||   | | || |       |
|
Db       1497 -----------TGCT---CAAACGG------CCCTTGTCATTAGTGATAGTA-----
ATC 1463


Qy       1042
TGGATTTCATCGTGGAAACCGAGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCT 1101
                  | | | ||| | | |          |||      ||  |      |||||| |    | ||| ||
Db       1462 TTGTTCTCTT-----TTCCCGT---ACTCTTG-------TCCACAGC--AGAGAC-
ATTG 1421


Qy       1102 TAACCACCAACGCCGTTGCCTCAGAGAC---
AGTGGCCACGGGCGAGGGGCTGCGGCAGA 1158
                     |||| |    || ||| | |  |||| | |        ||| || |
|
Db       1420 AGTATACCATTG-----GCATCAATGTCAAAAGTGACTTC-------
AATCTGAGGAACA 1373


Qy       1159 CCATCATCGGGCAGCC-----CATGTCCGTCA--
CCATCACCACCAAGGACAAAGACGGT 1211
                     ||    ||||| ||    ||| | || |    ||        ||||||      | |  |
|
Db       1372 CC----TCGGGGTGCAGGAGGTATGCCTGTGAGTTCAAACTTGCCAAG---
CAGGTTGTT 1320


Qy       1212 GAGCTGTG-
CAAAACCGGCAACGCCTACCTCACCGCCGAACTGAGCACCCCCGACGGGAG 1270
                     || || ||    |  ||  |||||| | | | | ||| | ||| || | | ||
```

```
Db      1319 ATCCTTTGTCATGGCACGC-TCGCCTTCATAAAC-CTGAA-
TAAGCACACCAGGCTGGT- 1264

Qy      1271 CGTGGCAGA------
CGGGGAGATCCTGGACAACAAGAACGGCACCTATGAGTTTTTGTA 1324
                   || |||| |   | ||| || | | |  | ||    ||| || |
||
Db      1263 --TGTCAGAATAGGTAGTGAAGGTCTGTGTCTGCTTGGTAGG----AATG-
GTGGTATTA 1211


Qy      1325 CACTGTCCAGAAGGAAGGGGACTTTACCCTGTCTCTG-----
AGACTCTATGACCAG--- 1376
                  | ||        || | |||| | | || |||      || | || || | ||
Db      1210 CGCT-------TGATGAGGACAGT--
CATGACTCCACCAGCAGTTTCAATACCAAGGGA 1161


Qy      1377 ---------CACATCCGAG-
GCAGCCCGTTTAAGCTGAAAGTGATCCGATCCGCTGATGT 1426
                  |||||| | ||||   || ||   ||| | || | ||
                                                                       |
Db      1160 AAGAGGAGTGACATCCAAGAGCAGC-----AAATCT-----TGAAC--
ATTCTCAGACTT 1113


Qy      1427
GTCTCCCACCACAGAAGGCGTGAAGAGGCGCGTTAAGTCCCCGGGGAGCGGCCACGTCAA 1486
             ||||||  || ||| |||                  | || |||  ||| ||
Db      1112 GTCTCCAGACA-AGATGGC-------------------
TGCCTGGACAGCTGC-------- 1080


Qy      1487
GCAGAAAGCTGTGAAAAGACCCGCAAGCATGTACAGCACTGGAAAACGAAAAGAGAATCC 1546
                                   || |||||| |||||
Db      1079 -------------------ACCATAAGCA---
ACAGCT---------------------T 1063


Qy      1547 CATCGAAGACGATTTGATCT--TTCGAGTGGGTACCAAAGGAAGAAATAAAGGAG-
AGTT 1603
                 ||||   |  || || ||| ||| |||   | | |||||| |   |||| ||
                                                                       |
Db      1062 CATCAGGGTTGA--TGCTCTTATTC-
AGTTCTTTCCATTGAAGAAGTCTTGGAGAAGCT 1006


Qy      1604 TACAAATCTTCAGG----
GGGTAGCTGCATCTACAAATGGAAAGATATTAATTGCAGACA 1659
                 |  |||||| ||    | |||| | || || |
             ||||
Db      1005 TCTGAATCTTGGGGATACGAGTAGAACCACCAACCA-------------------
GGACA 965


Qy      1660
GTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCAGTTCAAAAGTCGTTTTGGCA 1719
                || ||   ||| ||||      || || | | ||| |||| || || | || || |
Db       964 ATATCAT-GAATCTGTG----ACTTGTCTA--
GTTTGGCATCTCGAAGGGCTTTCT---C 915


Qy      1720 TACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCA---
CAGGAGTGGCTGTACATCCCA 1776
                ||| |||        ||| ||| |||   ||| || ||  | ||| | | | || |
                                                                       |
Db       914 TACTGGG------TCCAGGG----TGCCACGGAACAGGTCAGCATT--
```

```
CAGTTCTTCAAA 867

Qy        1777
GTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAGCATTTTCTCCTCCGATG 1836
              ||| ||              | | |||     || |  |||         |||| |
|
Db       866 TCGGGCACG-----------GGTAATGGAGGTATAGAAGTCG------
ATTCCTTCATAG 824

Qy        1837
GGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACCCAAAGGAGTTTCTGTGG 1896
              || | |    || | ||| | ||      || |||      || |||
||
Db       823 AGAGAATCGATCTCAATACTGGC-CTGGG----TGCTGG-----AAGAGAG-------
GG 781

Qy        1897
ACCGCAATGGGCACATTATTGTTGTGGACAACAAGGCGTGCTGCGTGTTTATCTTCCAGC 1956
              ||| |  ||||| ||            ||||| || | |         ||||
||||
Db       780 TACGC--TTAGCACGTT------------CACAAGCAGTACGGAG---
GCGTCTTACAGC 738

Qy        1957
CAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGGGGACAGGCAGTTTGCAG 2016
                              || |     ||| | |             || |
|
Db       737 ---------------TCTC-----TTGTTCTC-------------ACTG---------
AT 720

Qy        2017 GTCCCCATTTTGC---AGCTGTAAAT-
AGCAATAATGAGATTATTATTACAGATTTCCAT 2072
               |||| || |||   ||| || | ||||||||  | ||     | | | |
||
Db       719 GTCCTTCTTATGCTTGCGCTTAAACTCAGCAATAAAATGGTTGACCATTCGGTTGT-
CAA 661

Qy        2073 AATCAT-TCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAAGTTTGG--
CTCA 2129
               |||| | ||    | | |||            || |  | || | || ||  | |
||||
Db       660 AATCTTCTCCACCCAAGTG------------GGTGTCTCCA-
GCTGTAGACTTGACCTCA 614

Qy        2130
AATGGAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGATTCAAATGGA 2189
              |                   || |     |||| |   | ||| |  ||| |
||
Db       613 A------------------AGAT------TCCATCCTCAATAG-TGAGGATT------
GA 585

Qy        2190
AACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCAGGTTTTTGATGGGAGTGGATCA 2249
               ||||||     ||| ||      |||||| |   |||| |    |
||
Db       584 CACATCAAAAGTGCCACCT---------------
CCCAGGTCAAAGATGAGCACGTTTCT 540

Qy        2250
TTTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCAAGGCCTGGCCCTA 2309
```

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                  || |  ||| || ||       | ||        |||| |  ||  |||   | ||
|
Db        539 TTCTGCTCCAACCTT------TTTG---------TCTAAG--
CCGTAAGCAATAGC---A 500

Qy       2310
ACTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTTCAAAGTCTATCGA 2369
              |  ||| |||           |||       || | |  ||| |||| ||
||
Db        499 GCAGCAGTTGG------------------CTC-----
ATTAATAATTCTAAGTACATTGA 463

Qy       2370
TACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTGCACTATAAACTGG 2429
                 ||  ||| ||| |       | ||| || |  ||| | || ||  |
|||
Db        462 GAC---CAGCAATAG------------TTCCAGCATCTTTGG--TAGC-CTG-
ACGCTGA 422

Qy       2430
AATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGCCAGAAGGAATCAT 2489
              |  |||   | | || ||  |  ||||  |            |||
|||
Db        421 GAGTCATTAAAGTAAGCTGGCACTG----TGACCA------------CAG-------
CAT 385

Qy       2490 TGGTGA---
ACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAAATGACTTATC 2546
              |||| |    ||| |||||||                        | |||
|
Db        384 TGGTAACAGTCTTCCCAAGGT----------------------------
AGGCTTCTG 355

Qy       2547
CAATTTCTGTATTTCACCTTTAGGGTTAAAAAAAACTCTTCTACTGAATCTATAAAAACT 2606
              |||||||                        |||| ||   ||
Db        354 CAATTTC------------------------------
CTTCATCTTTGTC---------- 335

Qy       2607
GCAGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTTATGTAGCTAAACTAATTT 2666
                                |||| || |
Db        334 ---------------
AGAACCATAG---------------------------------- 325

Qy       2667
TGCAAATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTATTCGTTAATCCTGTG 2726
                          ||||||                                  ||||
||
Db        324 -----------AAGACAC----------------------------------
CTCCTCTG 310

Qy       2727
AATGGTAGCTTTTGCACAGAACTTCCAAAAGCAAAACAAAAACAAAATCTATTGTAGTTA 2786
               || | |||||||| |     || ||
Db        309 GATAGAAGCTTTTGGTC---TCTCCC------------------------------
TTG 284

Qy       2787
```

```
TATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAACCTCACTTTTACAGT 2846
           ||| || | || |||| ||| || |  |    ||| | ||| | | ||| | | | |
|
Db       283 TATTCTAC-TTGGACCTTGGGC-CTG---CCA--GCATCAT-TCACCAC-
CATAAAGGGC 233


Qy      2847
AGGTATTACTCTTGTGACATTTTTTGGTTATCAACAACTAAATATAAATTACTTTGGAA 2906
             | || |    |  |||      ||| | || ||| |   | ||
Db       232 CAATGTTTCATATCAGAC-------
TGGACAACAGCATCATCAAAT-------------- 194


Qy      2907
AAAGTAAGGCTGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGCCCTCTGGAGTTCAGA 2966
               ||| | |              |||         | ||| | ||| | |
|
Db       193 ---------CTG-CGT-----------CCA---------
ATCAGACGTTTGGCATCAAAA 164


Qy      2967
ACTTAAGTATCAGTGCAAATTTCTCAACCTTTCTGGGTTAGACAAAGATCCTTTTTTGTG 3026
             ||| ||  |||    ||          |||||  || |   |||
Db       163 ACT---GTGTTGGTG-------------------GGGTT---
CATTGCAACTT------- 136


Qy      3027 TGTTCTTTTCACCACCCCTTTGGC-
TCACCTTGTATCAGCAAACAAAGTACTTCTTCAGG 3085
               |||||| |             ||| |||||     |||| |
|||||
Db       135 GATTCTTTGC-----------GGCATCACC---GATCAACCG------------
TTCAGT 102


Qy      3086
GAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGTAATGCTACCTTTTGGG 3145
             |                   || | ||| |   ||| |    ||
||||
Db       101 GT------------------CCGT-AAAGGCG----ACATA------GC------
TTGG- 78


Qy      3146
AAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATGTAATCAAGAAAGTTAGTC 3205
                   | ||    || |  | | || ||||||||
Db        77 ------AGTGGTTCGGTTTC-
CCTGATCATTG-------------------------- 53


Qy      3206
ATGTTTTATGTACCATGTTTTCACACGTGTCTCTTCTCTTCGACTTCCTGAAAGCGAAAG 3265
                                ||  | |||| || ||| | | ||| ||
Db        52 ----------------------GCAATTATCTCGACTTTTC--
CGTGCTGGAA------- 24


Qy      3266 CTTTACCTCCTGCAAATGTCAGCACATGTAGTAGG 3300
             | | || || | | |        ||||||
Db        23 ----AACACCCACACAAGACC--------AGTAGG 1


RESULT 15
US-10-478-914-3/c
; Sequence 3, Application US/10478914
; Patent No. 7335755
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  Query Match          12.8%;  Score 4899.5;  DB 1;  Length 2083;
  Best Local Similarity   38.0%;  Pred. No. 0;
  Matches 1319;  Conservative   0;  Mismatches  729;  Indels 1421;
Gaps  187;

Qy       327
CCAGTGTGCCGCCAGACCTCCATCCTGCCCGAGAAAGGGGTGGCCGCGCTCCAGAACAAT 386
            | || | ||||| ||||| ||    || |||| |   ||||||    |
|
Db     2083 CTAGCG-GCCGC--GACCTGCA----GCTCGAGCAC-ATGTGGCCTTTTT------
TTTT 2038

Qy       387
TTCTTCATCACAAACCTGATGGACGTGCTGCAGCGAACTCCAGGCAGCAACGCTGAGGAG 446
            || || |    ||| | |||| | |||| |          | ||         ||
||
Db     2037 TTTTTTTTTATTTTGCCT-----TCTTGCT-----------CTGG---------
TGGTTAG 2003

Qy       447
TCTTCCATCCTGGAGACAGTCACTGCTGTGGCTGCGGGAAAGCCTCTCTCTTGCCCAAAC 506
            ||| | | || | ||| || | |    || | | ||              || |||| |||
Db     2002 TCT--CCTACTATAAACA-----TGATTT---------------TCCTTCTT-
CCC---- 1970

Qy       507
CACGATGGGAATGTGATGGAATTTTACTGCCAGTCCTGTGAGACTGCCATGTGTCGGGAG 566
                                    | | |  |||||||||     | ||
Db     1969 ------------------------TTCAG--AGTCCTGT-------
CAAT---------- 1953

Qy       567
TGCACGGAGGGGGAGCACGCAGAGCACCCCACAGTTCCACTCAAGGATGTGGTGGAACAG 626
                                    |   || ||  |||| || |
||||
Db     1952 --------------------------CTTTACTTTTTTTCTCATTAATAT------
ACAG 1925

Qy       627 CACAAGGCCTCGCTCCAGGTCCA-
GCTGGATGCTGTCAACAAAAGGCTCCCAGAAATAGA 685
```

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              |  |      ||  ||| | ||   |   | |   || |  | |||   || || |||||
Db     1924 ----
AAGTTATACTACAGATACATTCAAGCTCATGACTGCTAAAAACTTCCTGAAATG-- 1871

Qy      686
TTCTGCTCTTCAGTTCATCTCTGAAATCATTCATCAGTTAACCAACCAAAAGGCCAGCAT 745
                   ||                     || || |||| |                        |
||
Db     1870 ---AGC--------------CTTAATTCATAC-----------------------
GAAT 1852

Qy      746
CGTGGATGACATTCATTCCACCTTTGATGAGCTCCAGAAGACTTTAAATGTGCGCAAGAG 805
                | |          ||| | |||| |   ||          |||   | || |
|||
Db     1851 CAT------------TTCTA--TTTGTT---CT---------
TTTTTTTTTGAGACAGA- 1819

Qy      806
TGTGCTGCTTATGGAATTGGAGGTCAACTATGGCCTCAAACACAAAGTCCTCCAGTCGCA 865
                                                ||| || |   ||| ||||
Db     1818 -----------------------------------CTCTTACTC--
TGTCGCCCAG----- 1800

Qy      866 GCTGGA-
TACTCTGCTCCAGGGGCAGGAGAGCATTAAGAGCTGCAGCAACTTCACAGCGC 924
                  |||||| |  | |||              |||| || ||  | ||    |||| ||
Db     1799 GCTGGAGTGCACTG----------------GCAT---GATCT-CGGC----
TCACTGC-- 1766

Qy      925
AGGCCCTCAACCATGGCACGGAGACCGAGGTCCTACTGGTGAAGAAGCAGATGAGCGAGA 984
                    |||| ||   ||| | |  ||| | |||||               ||||| |
Db     1765 --AACCTCTGCCT---CAC-GAGTT--AGGTC------------
AAGCAATT-------- 1734

Qy      985
AGCTGAACGAGCTGGCCGACCAGGACTTCCCCTTGCACCCGCGGGAGAACGACCAGCT-G 1043
                         ||          || ||  |  ||| ||               ||||
|
Db     1733 -----------CT----------TCTGCCTCAGCCTCCCGAGG----------
AGCTAG 1706

Qy      1044
GATTTCATCGTGGAAACCGAGGGGCTGAAGAAGTCCATCCACAACCTCGGGACGATCTTA 1103
                  |||| |                      | |||| |
Db     1705 GATTAC------------------------
AGGTCCCT---------------------- 1692

Qy      1104
ACCACCAACGCCGTTGCCTCAGAGACAGTGGCCACGGGCGAGGGGCTGCGGCAGACCATC 1163
                    ||||||      ||||| ||   |   | |             |  | |||| |
||
Db     1691 GCCACCA-------TGCCTGAGTAATTTTTGTATTTTTAGTAGAGATGGGG-----
TTTC 1644

Qy      1164
ATCGGGCAGCCCATGTCCGTCACCATCACCACCAAGGACAAAGACGGTGAGCTGTGCAAA 1223
                  | |  |   ||| |   ||| |   ||  ||          |||  ||  |
|
```

```
Db       1643 ACCATGTTAGCCAAGCTGGTCTCGAATTCC-----------------
TGACCTCAGGTGA 1601

Qy       1224
ACCGGCAACGCCTACCTCACCGCCGAACTGAGCACCCCCGACGGGAGCGTGGCAGACGGG 1283
                 ||| | || |  | |||| || |  | ||| |    ||||| | || |
 ||||
Db       1600 TCCGCCCACCTCAGCCTC-CCAAAGTGCTGGGATT-----ACGGGCGTGAGCC--
ACGGT 1549

Qy       1284
GAGATCCTGGACAACAAGAACGGCACCTATGAGTTTTTGTACACTGTCCAGAAGGAAGGG 1343
                 |   ||||| |        ||| |   |||| | |    ||
Db       1548 G----CCTGG---------------
CCTCTATTTTTTATTTTAAATACCT---------- 1518

Qy       1344 GACTTTACCCTG---TCTCTGAGACTCT-
ATGACCAGCACATCCGAGGCAGCCCGTTTAA 1399
                 ||| |||||  ||| ||   |||| || | || ||| |  |      || ||||
 |
Db       1517 ---TTTGCCCTGAAATCTATGT-CCTCTGATTATCAACACTGCTTA-----
CCAGTTTTA 1467

Qy       1400
GCTGAAAGTGATCCGATCCGCTGATGTGTCTCCCACCACAGAAGGCGTGAAGAGGCGCGT 1459
                         |  | || ||| |  ||
 |
Db       1466 --------------
TTTTTGTTGGTATTTATTTCA-------------------------T 1445

Qy       1460
TAAGTCCCCGGGGAGCGGCCACGTCAAGCAGAAAGCTGTGAAAAGACCCGCAAGCATGTA 1519
                 | | ||||| |     || |    || |||        ||    ||| |       |
 ||
Db       1444 TCAATCCCAG---------CTCTACAA--------CT-------TACCAG------
TATA 1415

Qy       1520
CAGCACTGGAAAACGAAAAGAGAATCCCATCGAAGACGATTTGATCTTTCGAGTGGGTAC 1579
                 |  | |||                   ||| ||   || |||||| |
Db       1414 AAAATTTGG-------------------ATCAGTTAC---
TTAATCTTGC---------- 1387

Qy       1580
CAAAGGAAGAAATAAAGGAGAGTTTACAAATCTTCAGGGGGTAGCTGCATCTACAAATGG 1639
                             ||||      |||||          | | ||
 ||||||
Db       1386 --------------------AGTT------TCTTC------------
CTTTTAAAAATGG 1365

Qy       1640
AAAGATATTAATTGCAGACAGTAACAACCAATGTGTGCAGATATTTTCCAATGATGGCCA 1699
                 || ||||          || |   ||    |||| |   | |||
 |||
Db       1364 AATAATAT-------------TATCTATC-----------ATAT------
AAAATGCCCA 1335

Qy       1700
GTTCAAAAGTCGTTTTGGCATACGGGGACGCTCTCCGGGGCAGCTGCAGCGGCCCACAGG 1759
                 ||| |             || | | || | |      || || | |||
```

```
Db      1334 GTTAA------------CAAATATGAACTAACAC--------
CTACAATGTGCCA---- 1300

Qy      1760
AGTGGCTGTACATCCCAGTGGGGACATAATCATTGCCGATTATGATAATAAATGGGTCAG 1819
               |||          |||
Db      1299 ---GGC-------
ACCA------------------------------------------ 1293

Qy      1820
CATTTTCTCCTCCGATGGGAAATTTAAGACAAAAATTGGATCAGGAAAGCTGATGGGACC 1879
              ||||        |||||    || |    |||| |||| |           ||
 ||||
Db      1292 ----TTCT-------AGGGAA---TAGAATGTAAATAAGTTCAAGTT--CT----
TGACC 1253

Qy      1880
CAAAGGAGTTTCTGTGGACCGCAATGGGCACATTATTGTTGTGGACAACAAGGCGTGCTG 1939
                 ||  ||||||         |||||        ||||| | ||         | |
 |
Db      1252 TGAATAAGTTT------------------ACATTTTAGT----------------
GAGAAG 1226

Qy      1940
CGTGTTTATCTTCCAGCCAAACGGGAAAATAGTCACCAGGTTTGGTAGCCGAGGAAATGG 1999
                         ||| |||     |||| |  | ||| |
Db      1225 ------------ACAGACAA-----
TAAATCAATAACATGT------------------- 1202

Qy      2000
GGACAGGCAGTTTGCAGGTCCCCATTTTGCAGCTGTAAATAGCAATAATGAGATTATTAT 2059
                            ||||| |||  | |   ||||             |
 |
Db      1201 ---------------------CCATTATGC--CAG---ATAG---------------
TTT 1183

Qy      2060
TACAGATTTCCATAATCATTCTGTCAAGGTGTTTAATCAGGAAGGAGAATTCATGTTGAA 2119
               || |  | | ||     | ||   |||  ||||||  ||     | |||
 |||
Db      1182 TAAATGTCACAAAGAAAA-------AGGGGGAGCAATCAGATAG------TGATG--
GAA 1138

Qy      2120
GTTTGGCTCAAATGGAGAAGGAAATGGGCAGTTTAATGCTCCAACAGGTGTAGCAGTGGA 2179
               |||    ||| |  | |||| ||   ||| |||  ||    ||     ||| |  |
Db      1137 GTTACACTC---TAGAGAGGG---
TGGACAGAAAAAGTTTCTCTTAGGAGATG------- 1091

Qy      2180
TTCAAATGGAAACATCATTGTGGCCGACTGGGGAAACAGCAGGATCCA---
GGTTTTTGA 2236
               ||  ||  ||||    | |    |||||| | | | |    ||| |
 |||
Db      1090 -ACATCTG--AACAGAGATCTAAATGACTGAGTACAAACC-----
CCAATGGAAAAGTGA 1039

Qy      2237
TGGGAGTGGATCATTTTTGTCCTACATTAACACATCTGCTGACCCACTCTATGGCCCCCA 2296
               | || |||       |||    |||   ||||||| | |    ||| |||
Db      1038 TTGGTGTG--------TTGTGAAACAGCAACACAGC--
```

```
CAGTTTGACTAGATG------- 996


Qy       2297
AGGCCTGGCCCTAACTTCAGATGGTCATGTTGTGGTTGCAGACTCTGGAAATCACTGTTT 2356
              ||             |  ||||| | |   ||  ||| |  |||| |||   |||
|
Db        995 AG----------TAGATCAGAATGAC----TGAGGTGG--GACTGTGG---
TCA-----T 960


Qy       2357
CAAAGTCTATCGATACTTACAGTAATGGTGGGCAGGTGGATACCCGCTTCCATGGTCTTG 2416
              |||||     |||       |||  ||| | |||  |  || ||  |   || | ||   |
||
Db        959 CAAAG-----AGAT-----CAG-AGAGGTAGCCTG--GGAAGGCCACATCACAG--
AATG 915


Qy       2417
CACTATAAACTGGAATGGATTTCTCAATGCGGGACCAGATTATGACTAGAGTTTTTATGC 2476
                 || |    |         ||| |  |              || |||||
Db        914 TCCTTTGGGC------------CTCTGTAAG----------------
AGCGTTTT----- 888


Qy       2477
CAGAAGGAATCATTGGTGAACTTTCCAAGGTTATTTCTGAATGTAACAATTTCCTTAAAA 2536
               |  || ||| |||  |      | |||||||               || ||
||
Db        887 ---GAAAAAACAGTTCTGAG----CAAAGGTTA-----------------
GTCATTTAAC 852


Qy       2537 ATGACTTATCCAATTTCTGTATTTCACCTTTAGGGTTAAAAAAAAACTCTT---
CTACTGA 2593
                |||||||          ||         ||||||      || | | |||    |||
|||
Db        851 TTGACTTA--------CT---------CTTTAG------
AAGGATCACTTTGGCTATTGA 815


Qy       2594 ATCTATAAAAACTGCAGTTTTACATCTGTGAACTATGGCTTAAGGGACAGGATTT-
ATGT 2652
                |   || ||||| |   | |  | |  ||| |            || ||||| |  |
|
Db        814 GTGGCAAACAACTGGAGAAGTGGTTAGGGGAGCACTG------
TGGGCAGGAATAGAAGG 761


Qy       2653
AGCTAAACTAATTTTGCAAATCAAACAGACACTTAAAAAAACTAGCATATGTAAAGGTAT 2712
                 ||             | ||| || || |                |||
Db        760 AG-------------GAAAAGCAGACTGG--------------
AGCC-------------  741


Qy       2713
TCGTTAATCCTGTGAATGGTAGCTTTTGCACAGAACTTCCAAAAGCAAACAAAAACAAA 2772
                ||||||| ||                         |||||   ||  | | ||   |||
|
Db        740 ----TAATCCAGT----------------------ACTTC----
AGATGAGAAATGACAGA 710


Qy       2773
ATCTATTGTAGTTATATACTTCATTTAACCTAGGTCACAAGACCCAGGGAATCTTCTAAC 2832
                |   ||         ||| |||||| ||||              |||
Db        709 TTTGCCTG-------GTACATCATTT--CCTA---------
```

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TCCC-------------- 683

Qy       2833
CTCACTTTTACAGTAGGTATTACTCTTGTGACATTTTTTTGGTTATCAACAACTAAATAT 2892
                    |||||    ||| |||  | ||   | ||||| ||       ||| |
|
Db       682 ------TTTACT-----TATAACTTAT-TGGTGTATTTTTATTT---------
TAAGTGT 644

Qy       2893 AAATTACTTTGGAAAAAGTAAGGC-
TGTCTTGCAAAATGATCCCAGCTCTGATTAGCAGC 2951
              ||||| |||  | || | ||| |   ||| | |||||    | || |||
Db       643 AAATT--TTT---ATAAATGAAGCATAATTTGAAGATTGAT--
ATGTTCGGA-------- 599

Qy       2952 CCTCTGGAGTTCAGAACTTAAGTATCA--
GTGCAAATTTCTCAACCTTTCTGGGTTAGAC 3009
                  || | |||   || | ||||| |||    | |||| ||| | |   ||
Db       598 ---CTTGTGTT---TTCT--ATTATCATGGTG----TCTCTCCACATACCT---
TT---- 558

Qy       3010
AAAGATCCTTTTTTGTGTGTTCTTTTCACCACCCCTTTGGCTCACCTTGTATCAGCAAAC 3069
               ||| |||   ||||||    |    || |||| | ||    | |
Db       557 -----TCCCTTT-----AGTTCT----GCTTCTTATTGTGCTCCTCAAGT-----
CTATT 517

Qy       3070
AAAGTACTTCTTCAGGGAAACCTGAAATTTCTAATGCCTTGAAAAGCATATTACAAAAGT 3129
               || ||| |||  ||||   | ||||| ||  |||||  | ||
Db       516 TTTGTTCTT-TTC-------CCT-
CTACTTCTACTGTTTTGAACTGTAT----------- 477

Qy       3130 AATGCTA--
CCTTTTGGGAAACAAACTGCCCCGTTAACTCCAGATCATTGCACTGGAATG 3187
              ||||||   || ||  | |   |   | ||||||  |         || ||| |||
Db       476 -ATGCTATTTCTATTTTGCCAGGAGTTACCCCCTTCAATT---
TTCGTTGTACT------ 427

Qy       3188 TAATCAAGAAAGTTAGTCATGTTTTATGTACCATGTTTTCACACGT--
GTCTCTTCTCTT 3245
              ||       | ||||            ||||| | ||    ||   |||||||
|
Db       426 --CTC-------
TCAGTCTCAAACACATACCCATGCTCTCTTCTGTCCTTCTCTTCATAT 376

Qy       3246
CGACTTCCTGAAAGCGAAAGCTTTACCTCCTGCAAATGTCAGCACATGTAGTAGGACACC 3305
              |   |||| |||  ||   |   | || | | ||||   |  || || |
||
Db       375 CATCTTCTAGAA----TTAGTTCTAC--CC--
CGATTTTCTACCAATTTATTTTATTTCC 324

Qy       3306 AGTATCCTAGGACAGAGAGCCATAAGTAGCCCTTTGGAGGACTGATGGTGTCA-----
AC 3360
              |   ||| || ||| || |||| || || |   ||  ||  | |||
Db       323 A--ATC--
AGTACATTGATTCAGATTTATCAATATGTTTTACCAATTTTATCATTTTTTT 268

Qy       3361 CAAAGGCATGTGATT---
```

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GATTAATGATTCCCCCTTAGAAAGCAAGTGTTACCAAAGTTG 3417
                 |||| ||| |||  | || ||  ||   ||| ||   ||     | |   ||
|
Db       267 TGGAGGCTTGTTATTTAAGGTTCATTTTT----CTTGGAGTACA-----
TCCTTCAGAAG 217


Qy       3418
TGTTATCTTGAAAGCATTACAGGTAAGGGCATGTTATGGTTATTTATCATTGTTTAATGA 3477
            |  |  || |     |||        ||| |   | | |||||| || ||| ||
Db       216 TTCTTTC-----AGC---------AAGAAC---
TCATGGTTGTTAATCTTT--------- 183


Qy       3478
ATAGTAGAGGTGTCAAGGGACTATGTATACATGATTAGGGTAAGATAGAATGTATTATAT 3537
                  | |||        || |||        || ||         |||
Db       182 ---------GAGTC------CTTTGT--------TTCTGG----------
TGT------- 163


Qy       3538
ATATATATATATATACACACACACATATATATAGCTGAATCTTTGGTGTATTGAAATAGG 3597
            | ||  | | | | |||  |       ||| | | |   || |   |
||
Db       162 ---TTTAACTTTTTCCCCTCACTCT----------TGAGTAATAG-----
TTTAGCTGGG 121


Qy       3598 CAGCAC---
TCTGAAAGACAGAAGCTTCGTCCAGCCACTCTTCAGCACATTCCTTTACTA 3654
            ||  |   || ||  | |||   |||         || |  ||||      |||
Db       120 CATAAAATTTCAGATTGGCAGTTACTT----------TTCCTTGGCAC-------
TACGA 78


Qy       3655 AGCAGTTTAAAGCCG-TCCTAGTGGAGCAAGC--
CCTAAAGCAGATTTAATTTTTGCCAT 3711
            ||    | |||| ||   | |     || |||  || | | | |||
Db        77 AG-------ATGCCGCTCC-------
GTTATCTTATTACAGCCAATATTACTATTG---- 36


Qy       3712 TTTCCAAGAATGACGGTGGTGGCTTTTAGTCAGAAAATGGCCTTCTGTG 3760
            ||||       || |||  | |          ||| |  |||| | |||
Db        35 -TTCC---TTTGTAGGTAATCTC-------CAGTA---GGCCAACAGTG 1



Search completed: March  9, 2010, 15:52:48
Job time : 29.9458 secs

                          GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on:        March  9, 2010, 15:51:16 ; Search time 1 Seconds
                                          (without alignments)
                                          1134.946 Million cell
updates/sec

Title:         US-10-572-905-34
Perfect score: 19464
Sequence:      1 gcggcgcgcccgagcctagt..........taatttgttccggttaagga
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Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       417 seqs, 79705 residues

Total number of hits satisfying chosen parameters:     834

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      7335755.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6914.5	35.5	3210	1	US-10-478-914-4	Sequence 4, Appli
c 2	6808.5	35.0	3210	1	US-10-478-914-4	Sequence 4, Appli
3	6790.5	34.9	3589	1	US-10-478-914-21	Sequence 21, Appl
c 4	6758.5	34.7	3589	1	US-10-478-914-21	Sequence 21, Appl
5	5876	30.2	2437	1	US-10-478-914-61	Sequence 61, Appl
c 6	5713	29.4	2437	1	US-10-478-914-61	Sequence 61, Appl
c 7	5535.5	28.4	2495	1	US-10-478-914-20	Sequence 20, Appl
8	5468.5	28.1	2120	1	US-10-478-914-64	Sequence 64, Appl
9	5459	28.0	2495	1	US-10-478-914-20	Sequence 20, Appl
10	5299	27.2	2198	1	US-10-478-914-17	Sequence 17, Appl
c 11	5270.5	27.1	2336	1	US-10-478-914-57	Sequence 57, Appl
c 12	5184	26.6	2120	1	US-10-478-914-64	Sequence 64, Appl
c 13	5132.5	26.4	2198	1	US-10-478-914-17	Sequence 17, Appl
14	5110.5	26.3	2336	1	US-10-478-914-57	Sequence 57, Appl
c 15	4714	24.2	2083	1	US-10-478-914-3	Sequence 3, Appli

16	4679.5	24.0	2083	1	US-10-478-914-3	Sequence 3,
Appli c 17	4670.5	24.0	2022	1	US-10-478-914-60	Sequence 60,
Appl 18	4552	23.4	1946	1	US-10-478-914-62	Sequence 62,
Appl c 19	4537.5	23.3	1946	1	US-10-478-914-62	Sequence 62,
Appl 20	4447.5	22.8	2022	1	US-10-478-914-60	Sequence 60,
Appl c 21	4104.5	21.1	1813	1	US-10-478-914-63	Sequence 63,
Appl 22	4002.5	20.6	1813	1	US-10-478-914-63	Sequence 63,
Appl 23	2263.5	11.6	889	1	US-10-478-914-5	Sequence 5,
Appli 24	2249	11.6	1020	1	US-10-478-914-68	Sequence 68,
Appl c 25	2230	11.5	1020	1	US-10-478-914-68	Sequence 68,
Appl 26	2223	11.4	867	1	US-10-478-914-6	Sequence 6,
Appli c 27	2198.5	11.3	867	1	US-10-478-914-6	Sequence 6,
Appli 28	2146.5	11.0	938	1	US-10-478-914-69	Sequence 69,
Appl c 29	2120.5	10.9	938	1	US-10-478-914-69	Sequence 69,
Appl 30	2119	10.9	889	1	US-10-478-914-9	Sequence 9,
Appli c 31	2117	10.9	816	1	US-10-478-914-15	Sequence 15,
Appl c 32	2115	10.9	839	1	US-10-478-914-16	Sequence 16,
Appl 33	2114.5	10.9	816	1	US-10-478-914-15	Sequence 15,
Appl c 34	2102.5	10.8	889	1	US-10-478-914-5	Sequence 5,
Appli c 35	2082	10.7	889	1	US-10-478-914-9	Sequence 9,
Appli c 36	2078.5	10.7	909	1	US-10-478-914-67	Sequence 67,
Appl 37	2066	10.6	839	1	US-10-478-914-16	Sequence 16,
Appl 38	2054.5	10.6	717	1	US-10-478-914-42	Sequence 42,
Appl c 39	2051.5	10.5	816	1	US-10-478-914-38	Sequence 38,
Appl c 40	2050.5	10.5	794	1	US-10-478-914-13	Sequence 13,
Appl 41	2028	10.4	794	1	US-10-478-914-13	Sequence 13,
Appl 42	2024	10.4	816	1	US-10-478-914-38	Sequence 38,
Appl c 43	2023.5	10.4	811	1	US-10-478-914-37	Sequence 37,
Appl 44	2007.5	10.3	909	1	US-10-478-914-66	Sequence 66,
Appl c 45	1997.5	10.3	820	1	US-10-478-914-39	Sequence 39,
Appl						

ALIGNMENTS

RESULT 1
US-10-478-914-4
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
; FILE REFERENCE: 7388-80899
; CURRENT APPLICATION NUMBER: US/10/478,914
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/JP02/05294
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-162775
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-255226
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match   35.5%; Score 6914.5; DB 1; Length 3210;
  Best Local Similarity 45.9%; Pred. No. 0;
  Matches 1677; Conservative   0; Mismatches 1161; Indels 815;
Gaps 225;

Qy   4 GCGCGCCCGAGCCTAGT-CCCCACGCC--GCGGCGCGCCCGGGCTCCCTGC-
TGATCCCA 59
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Db   1 GCACTGTTG-GCCTACTGGCCCAGGCCTTGC-
ACACGCAGGTGCTCTCTTAGTGCTCCCT 58

Qy   60 GAACAATCAACCATGACGACCGAATCTGGATCAG-
ACTCGGAATCCAAGCCGGACCAGGA 118
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Db   59 GG-----CAAGGATGG-GAAGGCAT---GTTCAGTCCTAGGAGT--
AGGAAGGGCAGAG 107

Qy   119 G-GCCGA--GCCCCAGGAG-GCGGCGGGGGCGCAGGGGCGGCGGG-------
GGCCGTGC 167
            | | || ||||| || ||||| || ||| || || | ||| |
|
Db   108 GTGTTGATGGCCCCTACAGAGCGGCCAAGGACAAGGAGCTGCTGTTCGAAACAGCC-
TTC 166

Qy   168 CGG----------AGCCGCCCA---AGGAGGAGCAGCAGCAGGCC--CTGG--
AGCAGTT 210
            | | ||| |||| | ||| ||| | |||| || |
Db   167 CTGCTCCCCAACCTGCCTCCCACCCAACAGGTTTTGCATATACTCTACTGGGAAGAGGGA 226

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Qy        211 CGCCGCCG-CTGCAGCGCACAGCACCCCGGTGCGAGGGAGGTCACTGACAAGGA-
ACAGG 268
              |  |  ||| |||||  ||| || |  ||     |   |  ||| |  || |
||||
Db        227 CACACCCGACTGCA--TCACTGCCCTCCAAGTCTCTCCCTG-
CCCTGTCCAGCATCCAGG 283

Qy        269 AGTTTGCTGCC------AGGGCTGC----
AAAACAGCTCGAATATCAGCAATTAGAAGAC 318
              |     ||  ||   |  ||||  ||    || | |  |  ||||  |  || |
Db        284 A----GCACCCCTAGTTGGGGAAGCTTCTGTGACTCCCCCTACAACAGC-
CTAGGATGGA 338

Qy        319 G--------ATAAACTTTCTCAGAAATCA-TCT---
AGCAGTAAACTCTCTCGGTCTCCA 366
              |        |  | |||  |||||  || ||   |  || || |  ||  |
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Db        339 GTGGGGTTTGTGAACAAATGCAGAAGGCAGTCTTAGGGAGGTCAGCTGACATG--
CCCC- 395

Qy        367 TTAAAGATTGTCAAAAAGCCTAAAAGCATGCAGT-
GCAAAGTGATACTTCTCGATGGATC 425
                          || |   || |    ||| | ||  |  || | ||  | ||||  |  |
||
Db        396 --------TGGCCTGTGGCTGGGAAGTA-GCAGAGGCTAA--GGTTCTTCCC---
CGCTC 441

Qy        426 AGAATATACCTGTGATGTAGAGAAACGCT-------CCAGAGGACAAG------
TGCTGT 472
              |   |  || |        ||| |  ||          |||  |||| |
||
Db        442 TGGGGTTGCCAG-------
GAGTAGCACTGGATCAGTCAGGTGACAGGGCTCTCCTCTCT 494

Qy        473 TTGATAAAGT---
GTGTGAACACTTGAACTTGCTAGAGAAAGACTACTTTGGGCTTACGT 529
                        |||  || |  ||| | |  | ||    |   | | ||      |
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Db        495 CTGAGCAGGTCCGGTGGCAGCCTTCAAGGTCGCC--
ACGCCGTATTCCCTGTATGTCTGT 552

Qy        530 ATCGAGATGCTGAA---------AACCAGAAGAATTGGTTGGACCCTG----
CTAAGGAA 576
                |||| || |||       ||| | ||  |  |||| |||||    | ||||
Db        553 CCCGAGGGGCAGAACGTCACCCTCACCTGCAGGCTC--
TTGGGCCCTGTGTGGACAAAGGGC 610

Qy        577 ATAAAAAAACAGGTTC-----GAAGTGGTGCTTGGCACTTTTCATTTAATGTG----
AAA 627
              |   |     ||   |||    || ||||| |  |  |   ||     | |   |
|
Db        611 ACGATGTGACC--TTCTACAAGACGTGGTAC----
CGCAGCTCGAGGGGGCGAGGTCAGA 664

Qy        628 TTTTATC----
CACCAGACCCTGCCCAACTATCTGAAGATATCACCAGGTACTACCTCTG 683
              |  ||    | || ||| | |||||  ||||| ||    |     |||||  || |
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CCAGGACCTTCACCTG 717
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Qy        684
CTTGCAGTTGCGAGATGACATCGTGTCCGGAAGGCTGCCCTGCTCCTTTGTTACCCTGGC 743
          |                 ||| | ||   |||||| || |  |         || |
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Db        718 C--------------ACCATGGAGGCCACCAGGCTG-CCAACACC-----
AGCCACGAC 756

Qy        744
CTTGCTGGGCTCCTACACTGTCCAGTCAGAGCTCGGAGACTATGACCCAGATGAATGTGG 803
          || ||| || ||      | | |   ||| | || ||||    |
|||
Db        757 CTGGCTCAGCGCC--------ACGGGCTGGAGTCG--GCCTCCGACC------
ACCATGG 800

Qy        804 GAGCGATTACATTAGTGAGTTCCGCTTTGC---
ACCAAACCACACTAAAGAACTG----- 855
          | |  | |||         | | |||   ||| |||   ||  | ||| |
Db        801 CAACTTCTCCAT----------
CACCCATGCGCAACCTGACCCTGCTGGATAGCGGCCTCT 850

Qy        856 ---GAAGAC-----AAAGTGATCGAGCTGCACAA----GAGCCACAGAGG-
AATGACGCC 902
             | | |         | |||| || ||| |   ||| ||||| |    |||
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Db        851 ACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAG-
CACAGGGTCCATGGTGCC 909

Qy        903 A-------
GCAGAAGCAGAGATGCATTTCTTGGAAAATGCCAAAAAATTATCAATGTATG 955
          |        |||| ||||| ||| |        || |||   |   | |||
||
Db        910 ATGGAGCTGCAGGTGCAGACAGGCA--------AAGATGC----
ACCATCCAACTGTGTG 957

Qy        956
GGGTAGATTTACATCATGCTAAGGACTCAGAAGGGGTAGAAATTATGTTAGGAGTTTGTG 1015
          | |||       |||| | ||    | ||| | |    |||| || ||| ||
Db        958 GTGTA----CCCATCCTCCT-----CCCAGGAGAG--TGAAA----
GTAAGG-------- 994

Qy        1016 CAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGATTTGCCTGGCC--
CAA 1073
                             |||| | |       ||||| ||
Db        995 -----------------------GACCAACCTC------------TTGCC---
CCTTTTG 1016

Qy        1074
GGTTCTAAAGATTTCATACAAACGGAACAACTTTTACATTAAGATCCGGCCGGGAGAGTT 1133
          ||||||  | |||| |   | |  |  |  ||| |  ||| ||   ||| |
|
Db        1017 GGTTCT-CTGTTTTCTT-----CTGTCCTCATCCTGCACCCAGACCCTGTTTGGA-
ACTC 1069

Qy        1134 TGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCCAAACCATC-
GAGCTGCCAAGCGTT 1192
          ||  |   |      ||||              |||| || || || |  ||   ||
|
Db        1070 TGGCCTCAT------CACC---------------CCAAGCCCTCAGAACCCCC---
CGGT 1105
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Qy        1193 TATGGAAAGTATGTGTTG-AGCATCATACATTTTTCAGACTACT-------
GTTACCAGA 1244
               |     | | | | |   ||| ||| | | |    || ||         |
|||||
Db        1106 CCTCCTCCTTTTCTGCTGCTGCA-
CATCCCTTCTGCTTCCTCCTTGGTGCAATCCCCAGA 1164

Qy        1245 AGCAC-CTCCCAAGAAATTCCTAACCTTGGGT------TC--
CAAGTTTCGTTATAGTGG 1295
               ||| | ||| |       || ||   || || ||     || | | || |
|||||
Db        1165 AGCCCACTCTCCTTCCAT--
CTGCTCTGGAGTCTCTGCTCCTCTTGACTCTCTGGAGTGG 1222

Qy        1296 CAGGACACAAGCGCAAAC----GAGAAGAGCCAGTGCGT--TGATAGAT--------
CGC 1341
               | | |   ||     ||     | || ||||||| |  ||| || |          |
|
Db        1223
CTGTGCCTTGGCAGTGACCTTTGGCCAGGGCAAGTGCCTCATGACAGGTACTGGGTGCCC 1282

Qy        1342 CCAGCACCTTACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCG---
CAGCTTG 1398
               | ||| ||| |      ||| |  || | |  | ||| || |      |||
|
Db        1283 CAGGCAGCTAAGT---GCCGCCCTGCCCACCAGC---
CCCCTATGGCTTGGGAAGGCTGG 1336

Qy        1399 G------
ATGGAGCATCAGTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCT 1452
               |     | | || ||| |  ||||| ||   | | ||| | ||     | |
Db        1337 GGGTCCTCTTGGCCAACAGGG--TGAAACCCC--ATCTCTAC-
TAAAAACACAAAAATTA 1391

Qy        1453 GCTGCAG--AGGTTGGTACTGGCCAGTACGCCACAACAAAAGGCATCTCTC-
AGACCAA- 1508
               || ||| |  | |||| | ||| ||| | ||        || ||| || |
|
Db        1392 GC--CAGGCATGGTGGTGCGCGCCTGTA-GTCCCA-------
GCTACTCAAGAGGCTGAG 1441

Qy        1509 -CTTGATCACCACTGTGACTCCGGAGAAGAAGGCTGAGGAGGAGCGGGA-
CGAGGAAGAG 1566
               | || | | ||   || | |||||    ||| || | |   || || || |
|
Db        1442
GCAAGAGAATCGCTTGAACCCGGGAGTCAGAGGTTGCAGTGAGCCGAGATCGCGCCACTG 1501

Qy        1567 GACAAACGGAGGAAGGGGGAAGAAGTCACGCCCATCTC-
GGCCATCCAGCACGAGGGAAA 1625
               ||    |  | |    || |||  |   |||||||     | || | |
Db        1502 CACTCCAGCCTGCTGATAGAGCAAGACT---CCATCTCAAAAAAAAACAACCC-
AAAATTT 1557

Qy        1626 GACTGACA--GTGAGC--GCA-
CGGACACCGCAGCCGACGGGGAGACCACTGCCACTGAG 1680
               | ||| || |  ||| || ||| | |   | |||||      |||||      ||| ||
Db        1558 GCCTGGCATGGTG-GCAGGCATCTGTAATCCCAGCTACTCGGGAG---
GCTGAGACATGA 1613
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Qy        1681
GAGCTAGAAAAAACTCAAGATGACCTGATGAAACATCAAACCAACATTAGCGAGCTGAAA 1740
         |||||  |    |||   || | | ||  ||   | || ||  ||  |        |||
|
Db        1614 GAGCT-GCTTGAACCTGGGAGG--
CAGAAGTTGCAGTGAGCCGAGATCACACCACTGCA- 1669


Qy        1741 AGAACCTTCTTAGAAACCTCAAC-AGACACTG--CCGTAA---CGAATGAA------
TGG 1788
              || | | |   |   | | ||||  ||| || || | | ||  ||          |
|
Db        1670 --
CTCCAGCCTGGGTGACAGAGCGAGACTCTGTCCCAAAAAATCAAAAAAATCACTTTTG 1727


Qy        1789 GAGAAGAGGCTTTCCACCTCC----CCCGTGC--GAC-
TGGCCGCCAGGCAGGAGGATGC 1841
              |   ||| || ||   ||     ||| || | | || | || ||
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Db        1728 GTAGAGATGCACTCTCGCTATGTTGCCCAGGCTGGTCTTGAACTCCTGG---------
GC 1778


Qy        1842 CCCCATGATCGAACCA-
CTTGTCCCTGAAGAGAAAATGGAAACCAAGACGGAGTCCAGTG 1900
              |   ||||| ||| ||| | ||               ||||     ||| | |
|
Db        1779 TCAATTGATCTTCCCACCTTGACC-----------------TCCAA-----
AGTGCTGGG 1816


Qy        1901 GATAGAGACGGAACCCACCGTGCACCACCTGCCG------CTT-----
AGCACTGAGAAG 1949
              || || |  | ||||| |||   ||| | |     |||      | | ||
||||
Db        1817 ATTACAGGTGTGAGCCACCATGCCTAGCCT-
CAGGGAATTCTTATAAGAACTCTATGAAG 1875


Qy        1950 GTGGTGCAGGAGACC---------GTGTTGGTGG-AGGAGCGGCGT-
GTGGTGCACGCGA 1998
              |  |||   |||      || |  ||| | ||| |||| | | || | ||
|
Db        1876 TAG--GCA--
TCACCATCTTCTCTGTATCCATGGAAAGAGAGGCCTAGAGATGTATGCTA 1931


Qy        1999 GTGGGGATGC---TTCTTACTCGGC---GGGAGAC--
AGCGGGGATGCTGCAGCACAGCC 2050
              ||| || || || | ||     | ||| |||||| || |||   ||
|
Db        1932 AC----TTGCCCAAGCTCACATAGCCCAGGGTAGCATAGCTGGGATGTTG-
AGCTGAGGC 1986


Qy        2051 C-----------GCATTCACAGGCATTAAAGGGAAAGAGG--GCTCTGCTTGACG-
GAG 2095
              |            ||| || |||     | | ||| ||||||   || | |
|
Db        1987 CGGAGGAGAAGTAGCAGTCGCTGGC----
AGAGCACACAGGCTGCTCTGGGGGATGAGCT 2042


Qy        2096 GGGGC--TAAAGAGGAAGG--
AGGGGAGGAGGTCGCTAAAGCTGTCCTGGAACAGGAAGA 2151
              || ||  | |||     ||| ||    ||    |||| |||| ||   || |  ||
|||
```

```
Db       2043 GGTGCGTTTAAGGAACAGGCCAGCACTGGCATTCGC--AAGCAGT--
GGGGAAGGGGAGA 2098

Qy       2152 GACAGCCGCTGCTTCCCGTGAGCGACAAGAGGAGCAGAGTGCAGCC-----------
ATC 2200
                  ||  ||||  |      ||  |    | |   ||||   |||
|
Db       2099 GA-TGCCGAGGTG----GTCAGTATCCTGACTTTCAGAG----
GCCTTTTTTTGTTTGTT 2149


Qy       2201 CACATTTCAGAAACTTTGGAACAAAAACCTCATTTTGA-
GTCCTCAACGGTGAAGACGGA 2259
                   ||||  |  |  |||  |   |||| |||||| | | |  ||||| |         |
|
Db       2150 TTAATTTTTGCTAGATTGATATTAAAAACTCATGTGGAGGAACTCAAGGAATGTTTAGAA 2209


Qy       2260 AACCATCAGTTTTGGCAGTGTTTCACCGGGAGGAGTAAAGCTAGAAAT-------
TTCCA 2312
                   ||||  |||     || ||   || |   | | | |||||  |  |||        ||
|
Db       2210 GACCAAAAGTCCC--CAATG----ACAG---
GAACAAAAGCAACCAATTTTTAACTTTCT 2260


Qy       2313 CAAGAAGTGCCAGTAGTTCACACCGAAACCAAAACCATCACATATGAATCAT---
CACAG 2369
                  |     |  ||    |||  |        |   |  ||  ||||| ||    | | |
|||
Db       2261 CTTCTCATTCC---TGTTTTCATTG-----ATTTCC--
CACATGTAGTCCTTTTGCTCAG 2310


Qy       2370 GTCG-----------ATCCAGGCAC-----
AGATCTGGAGCCAGGCGTGCTGATGAGTGC 2413
                  | |          ||  |||  |       || ||| ||   ||| |  | ||
||||
Db       2311 GAAGTCTTTGGGGAAATTAAGGATCTTTGAAGCTCT-
GAAATAGGTGATCAGGTTAGTG- 2368


Qy       2414 ACAGACGATCACATCTGAAACCACCAG--TACCACCACCACTACCCA----
CATCACCAA 2467
                   | | ||   |   || |  |  || |   |    |||||| ||      ||||
||
Db       2369 -GTGTCTGT--CAGCTG--
TCTAAGAGGTTGGAAAATGAACTACTCAAGATAGTCACGAA 2423


Qy       2468 AACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAATAGTCATCACGG---- 2523
                  || |  |||||||   |  ||||        | | |||||       | | | |   | |
Db       2424 AATACTGAAAGTTTG-ATTTTTCTTTCCATATTTGA------
ATTAATTTTTTCTGTTTG 2476


Qy       2524 --GGGATGCAGACATTG----ACCATGACC-
AGGCGCTGGCTCAGGCAATTAAAGAGGCC 2576
                   ||| |  |||    || |  |||   |||           || || |||
Db       2477 ACTGGAAGGGGTTTTTGTATAACTAAAACCTCAGCGC-----------
ATAAAGGAGATT 2525


Qy       2577 AAAGAGCAGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAGAC-
AGAGAT 2635
                  || || |||| | ||| |   ||||        |||| |||| || ||
```

```
||||||
Db      2526 TAAAAGGAGCA-CATGATTT---AGTG--------GGTGGGCCAT---
GAAACTAGAGAT 2570

Qy      2636 CACACCAGAAGATGGAGAGGA--
TTGACCAGAGGAATAACTTAGCTTGCACATGAATGCA 2693
               |  |  |||  |  ||  |||  |      ||||  |      || |  | |||
||
Db      2571 ------GGGATTTGGGGGTGAATTTGTC------AATATC------
TGGATTTTAATCCA 2612

Qy      2694 GTCA----TGCAAAC---
CGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCTTCTAAC 2746
               | ||    ||| |||  | || || ||   ||    |  |||      |||| ||| |
||
Db      2613 GACATCTCTGCTAACGAGCCTTTGGTAAGTCACTTCAGATAC--
TTTTCCTCCTTTTTAC 2670

Qy      2747 CCA------
ACTGTACTTGTATCTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTT 2800
               |     |||    |  | |    |  |  |    ||  || ||| ||    ||||| |
Db      2671 AAAGAGAGGGCTGGCTTAGTTATTTGCCAAAGCCCCTTCCAGGCC---
TGAATTCCACAA 2727

Qy      2801 GACC--ATTAATAAAGACACTGGCAGAGAGATCTTCC----CATAATA-----
AAGCAAT 2849
               | |   ||| |  ||    || |  |  |    |||| |   ||| ||      ||||
|
Db      2728 GTACGATTTACTGTAG----
TGTCTTATCACTCTTTCATGTCACAATAGCGTGGAGCATT 2783

Qy      2850 CTGATTCAGCATCACTAAACCGATAATGCATGA-
AGCAACGATAAAATTACAAAAGAGCA 2908
                 |||   ||| || ||  || |   ||| ||| | | | |||| ||
Db      2784 AGAGAAAAGC----CTAGACTTTTAGT---TGATAGCCA-
GTTGAAATATCATTGAT--A 2833

Qy      2909 GCATTTTTAATTTTCACAAAATGTCTCAGTTTTC-AGC--
TATACCTGCTCGTTCATAAC 2965
               | ||||| |||  ||||| |  | | || |||  |   || | | |
Db      2834
GAATTTTAGTTTTAGGAAAAATTGGTTTGATTTCTAGCTTTATTACTATTAGGT------ 2887

Qy      2966 CAACAATATAAACCGTGGTCTCATGTAACACATAAACAAT---TCATGCCTT-
TCATAGT 3021
                      || | | ||| | ||  | |||| | |  ||  |  || ||  |
Db      2888 -----ATGTGAGCT-TGGGCAAAT----
CGCTTAATCTTTGAGTCTAGTTTTCTCTCAAA 2937

Qy      3022 TTATTATTATTAAAGTCTAAA-------CAAAATTGCAATT--
TCTTAGGTAACCTTATA 3072
               |   | |||  || |||||    | | |  | ||  |  || ||| |
|||
Db      2938 ATGAGAACATT--
AGGCTAAATGATTTCCGAGTTTCCAGCTAGTCCTAGAGTTCTATATT 2995

Qy      3073 TTTACAATAAATGA---AGATTACCCT-CAAATGCT--
AGAAGCTGTCTAGGTCCGTCCG 3126
               | ||| ||| ||| |  |  ||||| | |     ||| |  ||  | |||     || |
```

```
                 |
Db      2996 TCTAC-ATAGTTGAATTATTTTATCATGCTGTTGCTGGGGAATATGACTA-
ACCCTTTTG 3053

Qy      3127 GTGTGTCAGATTTCC--TC-AGATTAGATGTGCCAATAACCAAGTT-
TATTCAGTAAACA 3182
                 |   |   ||||    || || ||  | ||  | |||||     ||| | ||||| |||
                 |
Db      3054 AAGCTACTAATTTTATGTCGAGCTTTAAAGT--CCATAA--
TTGTTATCTTCAGAAAATA 3109

Qy      3183 --ACTTGTACT----TGTTTC---
ATCTGGTTTATTACTCTCACCCATAAACAGTAATGA 3233
                 | ||| ||   | | ||  |||   |||| ||  || |     ||||| ||
                 |
Db      3110 TTATTTGACCTACAGTATGTCCAAATC-
AATTTAATAAAATCGCTTTATAACAGGAAAAA 3168

Qy      3234 CTCTCTGACCCTCTGGAAATATGTAATGCTTCCAATCTTGCTTTGTGTATCTC 3286
                 |         ||| |  || ||  |           |||| |||
Db      3169 AAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCCAC----------ATGTG---CTC 3208


RESULT 2
US-10-478-914-4/c
; Sequence 4, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 3210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-4

  Query Match             35.0%;  Score 6808.5;  DB 1;  Length 3210;
  Best Local Similarity   44.2%;  Pred. No. 0;
  Matches 1634;  Conservative    0;  Mismatches 1170;  Indels  895;
Gaps  222;

Qy         5 CGCGCCCG---AGCC-------------------------
TAGTCCCCACGCGCGGCG 35
             || || |    |||                            |  | ||
  |||
Db      3209
CGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTGTTATAAAGCG 3150

Qy        36 C-------------GCCCGGGCTCCCTGCTGATCCCAGAACAATCAACCATGACG--
```

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ACC 80
                                    || |   ||| | ||    || |||      ||| | |
                                                                          |
Db       3149 ATTTTATTAAATTGATTTGGACATACTGTAGGTC---
AAATAATATTTTCTGAAGATAAC 3093

Qy         81 GAATCTGGA---TCAGACTCGGAATCCA------AGCCGGACCAGG---
AGGCCGAGCCC 128
                     | | |||| | | |||| || |      ||| | | ||| || | |
||
Db       3092
AATTATGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCC 3033

Qy        129 CAGGAGGCGGCGGGGGCGCA-GGGGCGGC--
GGGGGCCGTGCCGGAGCCGCCCAAGGAGG 185
              | |   | | ||| | |    | | | | | | |    | | |||
Db       3032 CCAGCAACAGCATGATAAAATAATTCAACTATGTAGAAATATAGAA----
CTCTAGGA-- 2979

Qy        186 AGC-AGCAGCAGGCCCTGGAG-
CAGTTCGCCGCCGCTGCAGCGCACAGCACCCCGGTGCG 243
                    | ||| | | || | |    || || ||   || | | ||         |
Db       2978 --CTAGCTGGAAACTCGGAAATCATTTAGC-----CTAATGTTCTCA--------
TTTTG 2934

Qy        244 AGGGAGGTC---ACTGACAAGGAACAGGAGTTTGCTGCCAGGGCT-
GCAAAACAGCTCGA 299
              || ||   |  ||| ||| ||||||| |    ||| || | | |
                                                                          |
Db       2933 AGAGAAAACTAGACT--CAAAGATTAAGCGATT--
TGCCCAAGCTCACATACCTAATAGT 2878

Qy        300 ATATCAGCAATTAGAAGACGATAAACTTTCTCAGAAATC-----
ATCTAGCAGTAAACTC 354
              |    |||  ||||| | |   | ||| ||  ||| |      |||| || | |
Db       2877 AATAAAGC---
TAGAAATCAAACCAATTTTTCCTAAAACTAAAATTCTATCAATGATATT 2821

Qy        355 T---CTCGGTCTCCATTAAA-------GATTGTCAAAAAGCCTAAAAGC----
ATGCAGT 400
              |   || | | ||| | ||||      | || ||   || || | ||        ||
Db       2820
TCAACTGGCTATCAACTAAAAGTCTAGGCTTTCTCTAATGCTCCACGCTATTGTGACAT 2761

Qy        401 GCAA-AGTGAT-----ACTTC------TCG-----ATGGA--
TCAGAATATACCT----- 436
              | || |||||||     ||| |    |||      |||| ||||        |||
Db       2760 GAAAGAGTGATAAGACACTACAGTAAATCGTACTTGTGGAATTCAG-----
GCCTGGAAG 2706

Qy        437 GTGATGTAGAGAAACGCT---
CCAGAGGACAAGTGCTGTTTGATAAAGTGTGTGAACACT 493
              | | | | | | | || ||   || |   |  |||| |    || | | | || | |    | |
Db       2705 GGGCTTTGGCAAATAACTAAGCCAG----
CCCTCTCTTTGTAAAAAGGAGGAAAAGTATC 2650

Qy        494
```

```
TGAACTTGCTAGAGAAAGACTACTTTGGGCTTACGTATCGAGATGCTGAAAACCAGAAGA 553
         ||||  |   ||     ||||  |  || |   |  |  || ||| | |||  |||||
Db      2649 TGAAGTGACTTACCAAAGGCT-CGTT-AGCAGAGATGTCTGGAT--
TAAAATCCAGA--T 2596

Qy      554 ATTG----GTTGGACCCTGCTAAGGAAATAAAAAAACAGGTT----------
CGAAGTGG 599
         ||||    |  |||| |  |   |||| | |  |||        | | |
Db      2595 ATTGACAAATTCACCCC--C-----
AAATCCCATCTCTAGTTTCATGGCCCACCCACTAA 2543

Qy      600 TGCTTG-GCACTTT-------TCATTTA----ATGTGAAATT--
TTATCCACCAGACCCT 645
               | || || |  ||       || ||||    ||| |   ||  |||| || |
         ||||
Db      2542
ATCATGTGCTCCTTTTAAATCTCCTTTATGCGCTGAGGTTTTAGTTATACAAAAACCCCT 2483

Qy      646
GCCCAACTATCTGAAGATATCACCAGGTACTACCTCTGCTTGCAGTTGCGAGATGACATC 705
               ||   | | ||| |||| || |   | | |  |||  | |   | |  || |  ||
Db      2482 TCCAGTCAAACAGAAAAAATTA----
ATTCAAATATGGAAAGAAAAATCAAACTTTCAGT 2427

Qy      706 GTGTCCGGAAGGCTGCCCTGC-----TCCTTTGTTACCCTGGCCTT-----
GCTGGGCTC 755
               | | ||    | | | ||      || ||| | ||| |||       ||||
Db      2426 ATTTTCG--TGACTATCTTGAGTAGTTCATTTTCCAACCT---
CTTAGACAGCTGACAGA 2372

Qy      756 CTACACTGTCCAG----------TCAGAGC-TCGGAGA--CT--
ATGACCCAGATGAATG 800
               |  |||| ||  |         |||||||| ||  |||  || |  ||| | ||
         |
Db      2371
CACCCACTAACCTGATCACCTATTTCAGAGCTTCAAAGATCCTTAATTTCCCCAAAGACTT 2312

Qy      801 TGGGAGC-----
GATTACATTAGTGAGTTCCGCTTTGCACCAAACCACACTAAAGAACTG 855
               ||||     || |||||  | || |           ||| | || | |||
Db      2311 CCTGAGCAAAAGGACTACATGTGGGAAAT-----------CAATGAAAAC--
AGGAATGA 2265

Qy      856 GAAGACAAAGTGATCGA---GCTGCACAAGAGCC--ACAGAGGAATGAC-----
GCCAGC 905
               ||||| ||||| |   |   | ||| |  || || || ||   ||| | |
         |
Db      2264 GAAGAGAAAGTTAAAAATTGGTTGCTTTTGTTCCTGTCATTGGG--
GACTTTTGGTCTTC 2207

Qy      906 AGAAGCAGAGATGCATTTCTTGGGAAAATGCCAAA-------
AAATTATCAATGTATGGGG 958
               ||        |||| |||   ||| |  | | | | | |||||| ||
         |
Db      2206 TAAA---------CATTCCTTGAGTTCCTCCACATGAGTTTTTAATATCAATCTA---
GC 2159

Qy      959 TAGATTTACATCATGC----
TAAGGACTCAGAAGGGGTAGAAATTATGTTAGGAGTTTGT 1014
               | | ||| || |      |||| ||| ||          | || ||||
```

```
 ||
Db        2158 AAAAATTAAAACAAACAAAAAAAGGCCTCTGA-------------
AAGTCAGGATACTGA 2112


Qy        1015 GCAAGT-
GGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGATTTGCCTGGCCCAA 1073
                    ||  | || | |       || | || | ||||||       |  | |||||  ||
Db        2111
CCACCTCGGCATCTCTCCCCTTCCCCACTGCTTGCGAATGCCAGTGCTGGCCTGTTCCTT 2052


Qy        1074
GGTTCTAAAGATTTCATACAAACGGAACAACTTTTACATTAAGATCCGGCCGGGAGAGTT 1133
                | | | |||| | | || || |    | | | | || |||   || |
Db        2051 -AAACGCACCAGCTCAT-CCCCCAGAGCAGC-----CTGTGTGCTCT-GCC---
AGCGAC 2003


Qy        1134 TGAACAATTTGAAAGCACCATTGGGTTTAAGCT-GCCAAACCATCGA-
GCTGCCAAGCGT 1191
                    || | | ||     | ||  ||  | |||    ||  ||| | ||| ||
Db        2002 TG--CTACTT-----CTCC-
TCCGGCCTCAGCTCAACATCCCAGCTATGCTACC------ 1957


Qy        1192 TTATGGAAAGTATGTG-TTGAGCAT-----CATACATTTTCAGACTACTGTTACCA-
GA 1244
                      |||     | || | ||| |||      |||||| | | | || | || |||
|
Db        1956 --CTGGGCTATGTGAGCTTGGGCAAGTTAGCATACATCTCTAGGCCT-
CTCTTTCCATGG 1900


Qy        1245 AGCACCTCCCAAGAA-------ATTCCTA--ACCTTGGGTTC----
CAAGTTTCGTTATA 1291
                    |  | |  ||||        || |||| | | | ||||     |    ||| |
Db        1899 A-----
TACAGAGAAGATGGTGATGCCTACTTCATAGAGTTCTTATAAGAATTCCCT--- 1848


Qy        1292 GTGGCAGGACAC--
AAGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCACC 1349
                    |  |||  | ||      || || || | |  |||| | ||| || ||
Db        1847 GAGGCTAGGCATGGTGGCTCACACCTGTAATCCCAGCACTTTGG-
AGGTC---------- 1799


Qy        1350 TTACTTTGAACGCTCAT-----CCAGCAAACGTTATACCATGTCTCGCAGCTTGG---
AT 1401
                    |  | | | | ||||     || || ||| ||| | | ||||| |||
|
Db        1798 -AAGGTGGGAAGATCAATTGAGCC--CAGGAGTT----CAAGAC---
CAGCCTGGGCAAC 1749


Qy        1402 GGAGCATCAGTGAATGAAAACC--
ATGAAATATACATGAAGGATT--------------C 1445
                    |||   |||| ||    ||| | | || |   |||     ||
Db        1748
ATAGCGAGAGTGCATCTCTACCAAAAGTGATTTTTTTGATTTTTTGGGACAGAGTCTCGC 1689


Qy        1446 TATGTCTGC----------
TGCAGAGGTTGGTACTGGCCAGTACGCCACAACAAAAGGCA 1495
                    | ||||  |          |||||  |||  |  ||   |  |  |  |  ||||     |
Db        1688 TCTGTCACCCAGGCTGGAGTGCAGTGGTGTGATCT---
CGGCTCACTGCAACTTCTG--- 1635
```

```
Qy       1496 TCTCTCA-GACCAACTTGATCACC--
ACTGTGACTCCGGAGAAGAAGGCTGAGGAGGAGC 1552
              ||| || | ||| | | |   ||  | |||| ||| || ||        ||
||
Db       1634
CCTCCCAGGTTCAAGCAGCTCTCATGTCTCAGCCTCCCGAGTAGCTGGGATTACAGATGC 1575


Qy       1553 GGGACGAGGAAGAGGACAAACGGAGGAAGG--------
GGGAAGAAGTCACGCCCATCTC 1604
                 | |           | |||| ||  |      | || |||| || | |
||
Db       1574 CTGCCACCATGCCAGGCAAATTTTGGGTTGTTTTTTTTGAGATGGAGTCTTGCTC-
TATC 1516


Qy       1605
GGCCATCCAGCACGAGGGAAAGACTGACAGTGAGCGCACGGACACCGCAGCCGACGGGGA 1664
              |   | || ||| |         ||||| || ||  | || | |   | |
Db       1515 AG----CAGGCTGGAGTG---------CAGTG---
GCGCGATCTCGGCTCACTGC----- 1477


Qy       1665
GACCACTGCCACTGAGGAGCTAGAAAAAACTCAAGATGACCTGATGAAACATCAAACCAA 1724
              ||| ||| | | || | |   | | |||  | || |      |||       || |
Db       1476 AACCTCTGACTCCCGGGTTCAAG-CGATTCTCTTG----CCT-------
CAGC------- 1436


Qy       1725 CATTAGCG-AGCTGAAAAGAACCTTCTTAGAAAC-
CTCAACAGACACTGCCGTAACGAAT 1782
              | | | | ||||| |   || |   | | |  || || |  |||| | |
|||
Db       1435 CTCTTGAGTAGCTGGGA-----CTAC----AGGCGCGCACC--ACCATGCC-
TGGCTAAT 1388


Qy       1783 GAATGGG-----AGAAGA----GGCTTTCCACCT--------------
CCCCCGTGCGAC 1819
               || |     || |||    || |||  |||            |||||     |
|
Db       1387 TTTTGTGTTTTTAGTAGAGATGGGGTTTCACCCTGTTGGCCAAGAGGACCCCC---
AGCC 1331


Qy       1820 TGGCC--GCCA-----GGCAGGAGGATGCCCCCATGATCGAACCACTTGTC--
CCTGAAG 1870
              | || |||| |       ||| || ||  ||       |  || ||||| |  | ||||
Db       1330 TTCCCAAGCCATAGGGGGCTGGTGG--GC-----AGGGCGG--
CACTTAGCTGCCTG--- 1283


Qy       1871
AGAAAATGGAAACCAAGACGGAGTCCAGTGGATAGAGACGGAACCCACCGTGCACCAC-- 1928
                          || ||| ||     ||| | ||      || |  ||  ||  || ||| |
Db       1282 -------GGGCACCCAGTACCTGTCATGAGGCACTTGCCCTGGCCAAAGGT-
CACTGCCA 1231


Qy       1929 -----CTGCCGCTTAGCACTGAGA---AGGTGGTGCAG-GAGACC-
GTGTTGGTGGAGGA 1978
                   | |||| ||       | ||||    | | |  |||| ||  || | |  | ||||
Db       1230 AGGCACAGCCACT----
CCAGAGAGTCAAGAGGAGCAGAGACTCCAGAGCAGATGGA--- 1178


Qy       1979 GCGGCGTGTGGTGCACGCGAGTGGGGA-
```

```
TGCTTCTTACTCGGCGGGAGACAGCGGGGATG 2037
                     ||  | ||||    |||  | |||| |||      |  || ||  || |||
                     ||||||
Db     1177 -AGGAGAGTGG-----GCTTCTGGGGATTGC----ACCAAGGAGGAAG-
CAGAAGGGATG 1129


Qy      2038 CTGCAGCACAGCCCGCATTCACAGGCATTAAAGGGAAAGAGGGCTCTGCTTGACGGAGGG 2097
                       ||||||                   ||| |||||  | |||| |          |||
             |||
Db     1128 -TGCAGCA----------------GCAGAAAAGG--AGGAGGAC---------
CGGGGGG 1097


Qy      2098 GGCTAAAGAGGAAGGAGGGGAGGAGGTCG------
CTAAAGCTGTCCTGGAACAGGAAGA 2151
                       || |   ||    | || || |||| |      |  ||     |||  ||  |||||
             ||
Db     1096 TTCTGA--
GGGCTTGGGGTGATGAGGCCAGAGTTCCAAACAGGGTCTGGGTGCAGGATGA 1039


Qy      2152 GACAGCCGCTGCTTCCCGTGAGCGACAAGAGGAGC-AGAG--
TGCAGCCATCCACATTTC 2208
                        |   | |   |   | ||  | |||  ||| ||  |||| ||   || |  |
             ||||
Db     1038 G--GACAGAAGAAAACAGAGAAC-CCAAAAGGGGCAAGAGGTTGGTCCCTTAC---
TTTC 985


Qy      2209
AGAAACTTTGGAACAAAAACCTCATTTTGAGTCCTCAACGGTGAAGACGGAAACCATCAG 2268
                        |   |  | |||| | |             || || | ||   |  |     |
             ||||
Db      984 ACTCTCCTGGGAGGAGGA---------TGGGTACACCACACAGTTGGATGGTG-
CATC-- 937


Qy      2269
TTTTGGCAGTGTTTCACCGGGAGGAGTAAAGCTAGAAATTTCCACAAGAAGTGCCAGTAG 2328
                         |||| ||| || | ||||        |  |||| || | ||| |    || ||
Db      936 -TTTGCCTGT-CTGCACC--------TGCAGCT--CCATGGCACCATG--
GACCCTGT-- 893


Qy      2329 TTCACACCGA-------AACC--AAAACCATCACATATGAATCATCACAGGTCG--
ATCC 2377
                         | ||||        ||  |   ||| |||  | | ||  | ||| ||
             ||||
Db      892 ---GCTCCGAGTGGTGGTGCCTGATCTCCACCACC-
AGGCAGCAGTAGAGGCCGCTATCC 837


Qy      2378 AGGCACAGATCTGGAGCCAGGCGTGCTGATGAGTGCACAGACGATCACA------
TCTGA 2431
                         | |||  ||| |    ||  || |  ||        ||| | |  ||          ||
             ||
Db      836 A-GCA-GGGTCAGGTTGC--GCATGGTGATGG------
AGAAGTTGCCATGGTGGTCGGA 787


Qy      2432 AACCACCAGTACCACCACCACTACCCACATCACCAAAACTGTGAAAGG---
GGGCATTTC 2488
                         ||       | |||| |    | |    ||| | |||    ||    ||||
Db      786 GGCC------GACTCCAGCCCGTGGCGCTGAGCCAGGTC-
GTGGCTGGTGTTGGCAGCCT 734


Qy      2489 AGAGACAAGAATTGAGAAGCGAATAGTCAT--CACG-
```

```
GGGGATGCAGACATTGACCATGA 2545
                        | | |   || | || |   |  ||| |   ||| | || ||| |
                     |||
Db       733 GGTGGCCTCCATGGTGCAGGTGAAGGTCCTGGAACGTGAGGTTGCGG---------
ATGG 683


Qy      2546 CCAGGCGCT-GGCTCAGGCAATTAAAGAGGCCAAAGAGCAGC---
ACCCTGACATGTCAG 2601
             | ||||||  |  ||||     |    | ||  |||| ||  ||| | | |||
Db       682 GCCGGCGCTCTGAGCAGGTCTGCACCTCGCCCCTCGAGCTGCGGTACCACGTCTTGTAGA 623


Qy      2602 TGACCAAAGTAGTG------
GTCCATAAAGAGACAGAGATCACACCAGAAGATGGAGAGG 2655
             |  || | ||  | ||||   |||  | | |  | | |  ||| | |  ||| || || ||
             |
Db       622 AGGTCACA-TCGTGCCCTTTGTCC--ACAGGGCCCAAGAGC-
CTGCAGGTGAGGGTGACG 567


Qy      2656 AT-
TGACCAGAGGAATAACTTAGCTTGCACATGAATGCAGTCATGCAAACCGTTAGGAAA 2714
             | || ||   || ||   |    |  ||| |||| | || |  |||  ||| | | |
Db       566 TTCTGCCCCTCGGGACA----GACATACA-GGGAATACGG-
CGTGGCGACCTTGAAGGCT 513


Qy      2715 ACCA--GAGCCT-------
ATATGGAGTTCCCTCTTCTAACCCAACTGTACTTGTATCTG 2765
               ||| |  |||            |||| |||   | | ||| |||| |  ||
               ||
Db       512 GCCACCGGACCTGCTCAGAGAGGAGGAGCCC---TGTCACCTGACTGATCCAGTG-
CTA 457


Qy      2766 TCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCATTAATA-----
AAGACACTG 2820
             |  ||| ||   ||| | | || | ||   ||||| || |  ||    || |||
             |
Db       456 CTCCTGGCAAC-CCCAGAGCGG--
GGAAGAACCTTAGCCTCTGCTACTTCCCAGCCACAG 400


Qy      2821
GCAGAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTAAACCGATAATGCAT 2880
             ||  | |  |       ||| |   | | |  |||||     | || |||| |      |||
             |
Db       399 GCCAGGGG-------CAT------GTCAGCTGA-----CCTCCCTAAGAC-----
TGCCT 363


Qy      2881
GAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACAAAATGTCTCAGTTT 2940
             | |||||    | |||||||||
Db       362 -------------------------TCTGCATT-----
TGTTCACAAA------------ 345


Qy      2941
TCAGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACACATAA 3000
             ||  |||  ||  || |  ||   || | || ||   |    ||||
             ||
Db       344 --------CCCCACTC---CAT--CC-------
TAGGCTGTTGTAGGGGGAGTCACAGAA 305


Qy      3001 ACAATTCATGCCTTTCATAGTTTATTATT--
```

```
ATTAAAGTCTAAACAAAATTGCAATTTCT 3058
                  |  |||  ||  |  | |  | |  ||   | |    ||     | |
                                                                      ||
Db       304 GC--TTC---CCCAACTAGGGGTGCTCCTGGATGCTGGACAGGGCAG----
GGAGAGACT 254


Qy      3059
TAGGTAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCTAGAAGCTGTCTAGG 3118
               |  |   |  |      | ||  |    |    |  |||||  | || ||  || ||
                                                                      |
Db       253 TGGAGGGCAGTG---ATGCAGTC---GGGTGTGTCCCTC--TTCCCAGTAG-
AGTATATG 203


Qy      3119 TCCGTCCGGT---
GTGTCAGATTTCCTCAGATTAGATGTGCCAATAACCAAGTTTATTCA 3175
                       || ||   ||| ||      ||| || |  | ||    |  |    ||
                                                                      ||
Db       202 CAAAACCTGTTGGGTGGGAGG------CAGGTTGGG-
GAGCAGGAAGGCTGTTTCGAACA 150


Qy      3176
GTAAACAACTTGTACTTGTTTCATCTGGTTTATTACTCTCACCCATAAACAGTAATGACT 3235
               |  | |  ||||| ||||      ||||        |    |||| ||||
Db       149 G-CAGCTCCTTGTCCTTGGCCGCTCTG---------
TAGGGGCCATCAACA--------C 108


Qy      3236 CTCTGACCCT--------CTGGAAATATGTAATGCTTCCAAT-
CTTGCTT---------- 3276
              |||||  ||||        || | | |    |   | ||||| || |||||
Db       107
CTCTGCCCCTTCCTACTCCTAGGACTGAACATGCCTTCCCATCCTTGCCAGGGAGCACTA 48


Qy      3277 --TGTGTATCT-CATTTAATT----TGTTCCGGTTAAGG 3308
               | | || | | |           || || ||  |||
Db        47 AGAGAGCACCTGCGTGTGCAAGGCCTGGGCCAGT--AGG 11


RESULT 3
US-10-478-914-21
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21
```

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  Query Match             34.9%;  Score 6790.5;  DB 1;  Length 3589;
  Best Local Similarity   44.7%;  Pred. No. 0;
  Matches 1717;  Conservative    0;  Mismatches 1297;  Indels  825;
Gaps  216;

Qy          1 GC------GGCGCGCCCGAGCCTAGTCCCCACGCCGCGGCGCGCC---
CGGGCTCCCTG- 50
              ||      |   |||| | | | | ||| || || || ||   | ||
|||||
Db          1 GCCTACTGGATTCGCC--
ATCATTTTGCACACTGCGAGGGGCTCCGTGTGTGCGCCCTGT 58

Qy         51 CTGATCC--
CAGAACAATCAACCATGACGACCGAATCTGGATCAGACTCGGAATCCAAGC 108
              || || | | | ||| || |  | |     ||| | | | |   ||| | |
|
Db         59 CTTGTCTGGCCGTCC--TCATCCCTTCCCCCACCCCCTG---CCGCCAC----
TCCGACC 109

Qy        109 CGGACC--AGGAGGCCGAGCCCCAGGAGGCGG-
CGGGGGCGCAGGGGCGGCGGGGGC--C 163
              || || | ||| | || || ||| |   | |  ||||| |  |||
|
Db        110 CGCTCCCAAAGTGGCT---TCACAATAGTCGGTC-----CTC---
GGCGGTGTAGGCTGC 158

Qy        164 GTGCCGGAGCCGCCCAAGGAGGAGCAGCAGCAGGCCC---------------------- 200
              |  || |  || | |       ||     || || |||
Db        159 GCACCAGGTCCACACTTAAGCGAAATCAAGGAGACCCCCTTCTACTTCTACCTTTGGGTT 218

Qy        201 TGGAG--CAGTTCGCCGCCGCTGCAGCGCACAGCACCCCGGTGCGAGGGAGGTCA--
CTG 256
              ||| |  || | || || |||||| | || | ||| ||      || | ||| |
|
Db        219 TGGTGCTCAATGCGAAGCTGCTGCAACTCAGA-CACGCC----
TAAGTCAACTCATGCAG 273

Qy        257 ACAAGGAACAGGAGTTTGCTGCCAGGGCTGCAAAACAGCTCGAATATCAGCAATTAGAAG 316
              | || | | |||| |       || | |||| |||| |    | |||
||
Db        274 AAAAAGGAGAAAAGTTT------TGGTATACAAA--TGCTCTCAGTCCAGC------
CAG 319

Qy        317 ACGATAAACTTTCTCAGAAATCATCTAGCAGTAAAC------TCT---
CTCGGTCTCCAT 367
              ||   || |  | |    |   || || || || |      ||      |||| ||
Db        320 ACACCAAGC---
CGAAAGGTTGTGCTGGCTGCAACCGAAAGATCAAGGACCGGTATCTTC 376

Qy        368 TAAAG---ATTGTCAAAAAGCCTAAAAGCATGCAG--TGC--
AAAGTGATACTTCTCGAT 420
              |||||    | | ||||     ||  |||||| || | |||     || |
Db        377 TAAAGGCACTGGACAAA-----
TACTGGCATGAAGACTGCCTGAAGTGTGCCTGC----- 426

Qy        421 GGATCAGAATATACCT--GTGATGTAGAGAAACGCTCCAGAGGACAAGTGCTGTT-
```

```
TGAT 477
                   |  ||| | || | | |  |  | |  | | || |   || | |||  | |
         ||
Db      427  ---TGTGACTGTCGCTTGGGGGAGGTGGGCTCCAC-
CCTGTACACTAAAGCTAATCTTAT 482


Qy         478
AAAGTGTGTGAACACTTGAACTTGCTAGAGAAAGACTACTTTGGGCTTACGTATCGAGAT 537
                   |||     | |    ||| ||     || || ||||||    ||| ||
         ||
Db      483  CCTTTGT-----CGCAGAGACTATCT-----GAGGCT-CTTTGG-----
TGTAACGGGAA 526


Qy      538  GCTG-AAAACCAGAAGAATTGGTTGGACCCTGCTAAGGAAATAAAAAAAC------
AGG- 589
                   |||    || || || | |  ||||||    || ||    | |
         |||
Db      527  ACTGCGCTGCCTGTAG--
TAAGCTCATCCCTGCCTTTGAGATGGTGATGCGTGCCAAGGA 584


Qy      590  -------TTCGAAGTGG--TGCTTGGCACTTTTCA----
TTTAATGTGAAATTTTATCCA 636
                   || | |  ||| |||||  ||| | |||    | ||||  || ||||| |
Db      585  CAATGTTTACCACCTGGACTGCTTTGCA--
TGTCAGCTTTGTAATCAGAGATTTTGT--- 639


Qy      637  CCAGACCCTGCCCAACTAT--
CTGAAGATATCACCAGGTACTACCTCTGCTTGCAGTTGC 694
                   |   | | || || | | ||||| | || || || | |    ||| |||   |||
         |
Db      640  ---GTTGGAGACAAATTTTTCCTAAAGA-ATAACATGAT----CCTTTGC---CAG--
AC 686


Qy      695  GAGATGACATCGTGTCCGG--------
AAGGCTGCCCTGCTCCTTTGTTACCCTGGCCTT 746
                   | |  ||| || |  || |        ||| |   ||| ||   | | | |||
         ||
Db      687  G----
GACTACGAGGAAGGTTTAATGAAAGAAGGTTATGCACCCCAGGTTCGCTGATCT- 741


Qy      747  GCTGGGCTCCTACACTGTCCAGTCAGAGCTCGGAG-
ACTATGACCCAGATGAATGTGGGA 805
                   | |  ||| ||| | |||  | ||| |||| |    | | |
Db      742  ----ATCAACATCAC--CCCATTAAGAATACAGAGCACTACATTCT--
TTTATCTTTTTT 793


Qy      806  GCGATTACATTAGTGAGTTCCGCTTTGCACCAAACCACACTAAAGAAC--------
TGGA 857
                   || | || || |    |     || ||| |   | ||| || | |
         |||
Db      794  GC---
TCCACATGTACATAAGAATTGACACAGGAACCTACTGAATAGCGTAGATATAGGA 850


Qy      858  AGACAAAGTGAT----------------
CGAGCTGCACAAGAGCCACAGAGGAATGACGC 901
                   || ||  || |             || |||||  |     || | ||| |
         |
Db      851  AGGCAGGATGGTTATATGGAATAAAAGGCGGACTGCATCTGT-
ATGTAGTGAAATTGCCC 909
```

```
Qy         902
CAGCAGAAGCAGAGATGCATTTCTTGGAAAATGCCAAAAAATTATCAATGTATGGGGTAG 961
             |||      ||||| || ||  |   | |    ||||| | ||  |  ||| || |
|
Db         910 CAGTT----CAGAGTTGAATGTTTATTATTAAAGAAAAAAGTAATGTACATAT-
GGCTGG 964

Qy         962 ATTTACAT-CATGCTA-------AGGACTCAGAAGGGGT-
AGAAATTATGTTAGGAGT-T 1011
             ||||  | | |||||         |  |||  || | ||| ||   || ||| |
|
Db         965
ATTTTTTTGCTTGCTATTCGTTTTGTGTCACTTGGCATGAGATGTTTATTTTGGACTAT 1024

Qy         1012 TGTGCAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGAT---
TTGCCTGG 1068
             |||  |    || |  | |||| |   |  | | ||    | |||| |    ||| |
Db         1025 TGTATATAATGTATTGTAATATTTGAAGCACAAATG---
TAATACAGTTTTATTGTGTTA 1081

Qy         1069 CCC--
AAGGTTCTAAAGATTTCATACAAACGGAACAACTTTTACATTAAGATCCGGCCGG 1126
             ||       |||| |    ||| |  |        || |||| || |
Db         1082 CCATTTGTGTTCCATTTGCTTCTTTGTATTG---------
TTGCATTTAGTACAATC--- 1129

Qy         1127 GAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCC-----
AAACCATC---- 1177
             || |||| |||    || |           |||| ||| |      |||| |
Db         1130 -AGTGTTTAAACTTACTGTAT----------
ATTTATGCTTTCTGTATTTACCAGCTATT 1178

Qy         1178 ------
GAGCTGCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTTTTCAGAC 1231
             ||||||  | | |  ||||| |   |||    ||   | |  | |
||
Db         1179 TTAAATGAGCTG--TAACTTTCTAGTAAAGAAT-
TGAAAAGCAAATCTCACTAATGATAC 1235

Qy         1232 TACTGTTACCAGAAGCA-------CCTCCCAAGAAATTCCTAACCTTGGGTTC---
CAAG 1281
             || | ||     ||||||        |  |  | |||| |  || |       |   ||
Db         1236 -
ACAGATAGATAAAGCAAGTCTATCAACATTAAAAATACTAAAAAATAAAGACACACACA 1294

Qy         1282 TTTCGTTATAGTGGCAGGACACAA-------GCGCAAACGAGAAGAG----
CCAGTG--C 1328
             | || ||||| ||  ||| |     ||| |       ||| |    ||||    |||||
|
Db         1295 GAGCATTTTAGTGACA-
TCCACTACTTATTGCCGCTATGAGTTAGAGTCTATCAGTGTTC 1353

Qy         1329 GTTGATAGATCGCCC-------------------AGCACCT---------
TACTTTGAAC 1360
             ||| || | | |||                      | || ||         ||| |
||
Db         1354 -
TTGTTATAACCCCCTATTTTCAGGGGGTTAAAAATCAGCTTTAAAAAAAATACATAAAAA 1412

Qy         1361 GCTCATC---
```

```
CAGCAAACGTTATACCATGTCTCGCAGCTTGGATGGAGCATCAGTGAATG 1417
         |||||    |||  || ||  || |  | || || ||  | || || |
|
Db      1413  TTTCATCTTAAAGC--ACTTT---CATTTTATACCAACGTGAAAAGTGC--
CATTTTTAG 1465

Qy      1418  AAAACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAGAGGTTG-
GTACTGGCCAG 1476
             || | | ||| | |   ||| ||| | |    | |    ||| || ||   |
Db      1466  AATAACTTTAAAGCTTAA--CAGGTTTCCTTTTAATATCCTTTTTTGTGTGCT---
CTT 1520

Qy      1477  TAC-GCCACAACAAAAGGCATCTCTCAGACCAACTTGATCA-CCACTGTGACTCC---
GG 1531
             |||   |||    || ||| | |     ||| ||| |||   || ||
|
Db      1521  TACTTACAC----AATGGCTTTGTTTTG-----CTTTTTCAGCCAC----
ACCCCTTATG 1567

Qy      1532  AGAAGAAG-GCTGAGGAGGAGCGGGACGAGGAA--
GAGGACAAACGGAGGAAGGGGGAAG 1588
             |||  || ||   | | |   |||   ||       |||| ||
||
Db      1568  TGAACTAGTGCCTTTGGGTATC---
ACGTAAAATTTTTTCCAAAGGGTTACTTTAAAAAT 1624

Qy      1589  AAGTCACGCCCATCTCGGCCATCCAGCACGAGGGAAAGACTGACAGTGAGC--
GCACGGA 1646
             || || ||  || |          || || ||||   |    | |  | |
|
Db      1625  CTGTTAC-
CACAATTATGAGATGATTTTTAAGTGATAAATTAAACTTCTTCTTGTATAAA 1683

Qy      1647  CACCGCAGCCGACGGGGAGACCACTGCCACTGAGGAGCT---
AGAAAAAACTCAAGATGA 1703
             | || ||    ||| | || |||| | ||||||     |     |     |
|||
Db      1684  TTCTGC--CC-------AGATCTCT-CCAC--
AAGAGCTGAGGGTTTCATAACTTTATGG 1731

Qy      1704  CCTGATGAAACATCAAACCAACATTAGCGAGCTGA-
AAAGAACCTTCTTAGAAACCTCAA 1762
             | | || ||| |  |   | |   ||  |||   ||| || || | |    ||
|
Db      1732  CTTAAT-AAATGTATGAC--
ACTGAAAAGATTTGAGTGTGAATCTACTGAAATCACTATA 1788

Qy      1763  CAG-
ACACTGCCGTAACGAATGAATGGGAGAAGAGGCTTTCCACCTCCCCCGTGCGACTG 1821
             | ||| || | ||  |   ||| |  ||| || ||    | |     | || ||
Db      1789  ATGCACATTGAAGCTATGATGGTATTTGAGTAGTGAGGTTACTTTTGATCGGAGCAAC-- 1846

Qy      1822
GCCGCCAGGCAGGAGGATGCCCCCATGATCGAACCACTTGTCCCTGAAGAGAAA------ 1875
                       |  |||| |    || |||     || ||| ||| |   ||||||||||
Db      1847  -------------ATAATGCTC-----ATAGAA--
TCTTCTAGAAGAAGAGAAACAAAGG 1886

Qy      1876  -ATGGAAACCAAGACGGAGTCCAGTGGATAGAGACGGAACCCACCGTGCA-
```

```
CCACCTGCC 1933
                ||  ||   |  |   |       |  ||||   ||  |   |        |        || |    |||||
|
Db     1887 GATTGATAAAATGCTGAGAACTAGTGATTATATATTTTTC------
TGTATTTACCTGAC 1940

Qy        1934
GCTTAGCACTGAGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGGCGTGTGGTGCA 1993
                  |||     |    || ||    | |  |||    ||     | |    | |||| |
|
Db     1941 ATTTA----TTTTAATGTTCAAAAAGTAAACACTTT-----
AAGTTTGATGTGTTTTACT 1991

Qy     1994 CGC-----GAGTGGGGATGCTTCTTACTCGGCGGGAGACAGCGGGGATGCTGCAGC--
AC 2046
                |  |     |    |    |   || ||   | | ||||   |  ||  ||    ||
|
Db     1992 CTCTCATTGTTTTAAGTAATTGCCAACT---CAGAATACATC----
ATTCTTAGGCTGAA 2044

Qy        2047 AGCCCGCATTCACAGGCATTAAAGGGAAAGAGGGCT--CT---------GCTT--
GACGG 2093
                |       | ||| ||     |||| | |||| || ||            || |    |
|
Db     2045 ATTTGTCTTTC-
CATTTTTTAAGGTGAAATAGTACTACCTTACGTGATAGCATACAAAGA 2103

Qy     2094 AGGGGGCTAAAGAGGAAGGAGGGGAGGAGGTCGCT-------
AAAGCTGTCCTGGAACAG 2146
                || ||  ||| ||||   || |       |||| | |         |  | |    ||||
|
Db     2104 AGAAAGCTCTAGAAAGAGAAATTATGGAGAATGATTATTTAAATTACAATTAAGGAAATG 2163

Qy        2147 GAAGAGACAGCCGCTGCTTCC-CGTGAGCGACAAG--AGGAGCAGAG----
TGCAGCC-- 2197
                |       | ||  ||||| ||   |  | ||||     | |    |   ||| ||
Db        2164 AGAATATGATCCCCT-
CTTCCGAGTTGCCCACAAACTTGCTTCTTTGCTTTTGCTCCCTG 2222

Qy     2198 ------ATCCACATTTCAGAAACTTT-----------
GGAACAAAAACCTCATTTTGAGT 2240
                | | || |||||  || |              | | |   ||||  |||||
Db        2223 TAATAGAACTACTTTTCAACAAATCTAATTTTGCACGGCACCGTTAACCATATTTT---- 2278

Qy     2241 CCTCAACGGTGAAGACGGAAACCATCAGT----TTTGGCAGTGTT----------
TCACC 2286
                | | | ||  | |   |   |  | ||   |||   |   ||||
||||
Db     2279 -CACTACAGCAAACTTAG-
TGCTATGGGTTTTCTTTTCTTTGTTTTTTTTCTTGATCACT 2336

Qy     2287 GGGAGGAGTAAAGCTAGAAATTTCCA-CAAGAAGTGCCAGTA-
GTTCACACCGAAACCAA 2344
                | |   ||  || |     | ||||||   | ||| ||  ||     ||
||||
Db        2337 TGTATAGGAAAC---AACATTTTCCAGTGTTATTTGCATATATATTTTGTCC--
TTCCAA 2391
```

```
Qy      2345 AAC---CATCACATATGAATCATCACAGGTCGATCCAGG---
CACAGATCTGGAGCC--- 2395
              |   |||  |||  |||||  || | | ||    || |    |    | | ||| |||
Db      2392 TATATGCATTACAGATGAA-AATTAAATGTTATACCTGAATTCTTGGGT-
TGGGGCCAAA 2449

Qy      2396 -----AGGC--------GTGCTGATGAG----TG--------CACAG-------
ACGATC 2423
                  | ||        ||||| || |    ||        || ||        | ||
|
Db      2450
ATATTAAGCTGAAAATAATGCTGGTGTGGATTTGTTTAAAACAAAGCTTTATTATGAAC 2509

Qy      2424 A--
CATCTGAAACCACCAGTACCACCACCACTACCCACATCACCAAAACTGTGAAAGGGG 2481
              |  ||| |||| |    ||    || |   |    | |      ||||||||| |
|
Db      2510 ATGCATGTGAATCTG--
GATATTGCCTCTTATTTTTAAGAAAATGGTTCTGTGAAAAGTG 2567

Qy      2482 --------GCATTT---CAGAGAC--AAGAATTGAGAAGCGAATAGT--CAT----
CAC- 2521
                      | ||||   || |  |    |   || || |    ||| |||    |
|
Db      2568
AATGATATGTATTTTTCCAAATGCTTCATGGTTAGGAGTCTTCAAGTTCCATGTTCCCCA 2627

Qy      2522 -----GGGGGATGC-AGACATTGACCATGACCAGGCGCT------GGCTCA-------
GG 2562
              | |  || | | | |  ||   | | ||  ||| |      ||| ||
Db      2628
GATTTGAGATATACTAAAGAAAGAAATTCAAAAGTAGCTATTTGGGGCCCACAAAAATAA 2687

Qy      2563 CAATTAAAGAGGCCAAAGAGCAGCACCC---
TGACATGTCAGTGACCAAAGTAGTGGTCC 2619
              | ||||     ||| |||||  || |   |  |||| || ||    | |
|
Db      2688 CTATTATTTTAGCCTTAGAGCCTTACACTTGTTTCATG-
AAGAGAAAGGACTTGCATAAC 2746

Qy      2620 ATAAAGAGACAGAGATCACACC------
AGAAGATGGAGAGGATTGACCAGAGGAATAAC 2673
              ||| ||| || |   | || ||| |||   || ||| || |||| | ||
Db      2747 CAAAATAAACAAAG--
CAAGACAAATTAAAAATATGTGGGGGAGAGATCAGTGAAAAG-- 2802

Qy      2674 TTAGCTTGCACATGAATGCAGTCATGC---
AAACCGTTAGGAAAACCAGAGCCTATATGG 2730
              | | || |   | ||||||| | |||     || ||     ||| | ||
||
Db      2803 -TGGTTTTC---TTAATGCAGCCCTGCTGGTCCCCATT-----AACAATTGC----
TTGA 2849

Qy      2731 AGTTCCCTC--TTCTAACCCAACTGTACTTGT----ATCT--
GTCCGTGGAAAATTTCAG 2782
              | ||| |    | |||    || | || ||||     ||||   || |  ||     |||
||
Db      2850 AATTCACATGGATGTAA---
AATTATAATTGTCAGGATCTTATTCAGATGATCTTTTAAG 2906
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```
Qy        2783  --TCCAGAAGAATTGACCTTG----ACCATTAATAAAGACACTGGCA------
GAGAGAT 2830
                   |   |   |  |||   |||     |  ||   |  || |  |||  |        ||
|
Db        2907  GTTTAACTGGTTTTGCTTTTGTTTATCTATATGTCAAAATACTTGTAAATTGGGAACAAA 2966

Qy        2831  CTTCCCATAATAAAGCAATCTGA-----TTCAGCAT-------CACT---
AAACCGATAA 2875
                |||||  |     |||   |||    ||||  |          |||| | ||| |
|
Db        2967  CTTCTC-----TCAGCTTCTTGAAGTTGTTCAACTATCCTTGCCACTGGAAGACCAAACA 3021

Qy        2876  TGCATGAAGCAAC-GATAAAATTACAAAA------GAGCAGCATTTTTAA-----
TTTTC 2923
                   |   |   |  |     |||||  |      |||  |||  |       |||
|
Db        3022  AGGTTTTCACTGCTTTTTCTTTTACATAATATGCTGAGAATTATTTCTTATGCTTTTTAC 3081

Qy        2924  -----ACAAAATGTCTCA----GTTTTCAG--------CTATACCTG--------
CTCGT 2958
                   |||||||  ||||    | ||  ||          ||  | |||             ||
|
Db        3082  TACAAACAAAATTACTCACCTGGATTAAAGATTAAGGCCTTAATCTGTTTAGATTATCTT 3141

Qy        2959  TCATAACCAACA-------ATATAAACCGTG------GTCTCA--TGTAACACA-
TAAAC 3002
                   |  ||   ||| |         |  | |     ||  |  |||          || |
||
Db        3142  TAATCTCCATGAAATCGTGAAATAAGACAAGAATAGTGTTTCAGCTGTAGGCCATTTTAC 3201

Qy        3003  AATTCA-TGCCTTTCA----TAG--TTTATTATTATTAAAGTCTAAACAAAATTGC--
AA 3053
                   |  |  |  ||||  | |      |||  ||||||   |  ||   |||| |  | |   |
Db        3202  AGCTAATTGCCCATAAATTGTAGCATTTATTGACCTGAAGTACTAAGCTAATTGTCTTGA 3261

Qy        3054  TTTCTTAGGTAACC----------TTATATTTACAATAAATGAAGATTA-
CCCTCAAATG 3102
                   |   | ||| |        ||     |  | ||| |   |   | |  || |||| |
|
Db        3262  CTACTCAAAGCCCCTGAATTGTTGTCAACTTTCCCCTTTGTGTTGTGTAGCCCTAACGT- 3320

Qy        3103  CTAGAAGC----TGTCTAGGTCCGTCCGGTGTGTCAGATTTCCTC------
AGATTAGA- 3151
                   |     |||     ||||| | | |||  ||  | ||     ||||       ||  ||
||
Db        3321  CATTTAGCTTGTTGTGTCT-GATGCCTCCAGTAGGACA-----CCTCCGATGGAGCTTTGAT 3374

Qy        3152  ---TGTGC--CAATAACCAAGTTTATTC--
AGTAAACAACTTGTACTTGTTTCATCTGGT 3204
                   ||  ||   |  |  |       |     |||   | | ||  ||  |   |  | | |  ||
|
```

```
Db      3375 TTCTGAGCAGCGAAAGC----
TCCCTTCCTAAGATGCATCTCGCATAGGCTGCCTATGAT 3430

Qy      3205 TTATTAC------TCT-CACCCATAAACAGTAATGACTCTCTGA----
CCCTCTGGAAAT 3253
                  |  ||       || ||| |  | | ||| ||| | |   |    ||| ||
|
Db      3431
GAAGGACCGTGCACCTCCACTCCAACAGAGTGCTGAGTTTAAAAGTTGACCTGTG----T 3486

Qy      3254 ATGTAAT---
GCTTCCAATCTTGCTTTGTGTATCTCATTTAATTTGTTCCGGTTAAGGA 3309
                  ||||||    ||| | |||||||| |  || ||  |   || || |     ||
|
Db      3487 TTGTAATTTCACTTTC-
ATCTTGCTTAATAAATATCTGCTGGATTCTTTCAAAAAAAAA 3544


RESULT 4
US-10-478-914-21/c
; Sequence 21, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
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;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 3589
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-21

  Query Match             34.7%;  Score 6758.5;  DB 1;  Length 3589;
  Best Local Similarity   45.0%;  Pred. No. 0;
  Matches 1745;  Conservative   0;  Mismatches 1272;  Indels  861;
Gaps  237;

Qy         2 CGGCGCGCCCGAGC-
CTAGTCCCCACGCCGCGGCGCGCC-------------------- 39
                 | || || ||||| |  ||                  |||
Db      3589 CTGC-AGCTCGAGCACATGT---------------
GGCCTTTTTTTTTTTTTTTTTTTTT 3546

Qy        40 -----------
CGGGCTCCCTGCTGATCCCAGAACAATCAACCATGACGACCGAATCTGG 88
                          |  || || |||    |  || || || || || |
||
Db      3545 TTTTTTTTTTGAAAGAATCCAGCAGAT-----ATTTATTAAGCAAGATGAAAG----
TGA 3495
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Qy          89 A---
TCAGACTCGGAATCCAAGCCGGACCAGGAGGCCGAGCCCCAGGAGGCGGCGGGGGC 145
               |    || | | |      | |  ||     |   |  ||| |    |   |   | ||
||
Db        3494 AATTACAAACACAG-------GTC-
AACTTTTAAACTCAGCACTCTGTTGGAGTGGAGGT 3443


Qy         146 GCAGGGGCGGCGGGGGCCGT--GCCGGAGCCGCCCAAG-GAGGAGCAGC--
AGCAGGCCC 200
                 |||    |||     || |    |  || | | |||  ||| |  || | |
Db        3442 GCA----CGGT-----
CCTTCATCATAGGCAGCCTATGCGAGATGCATCTTAGGAAG--- 3395


Qy         201 TGGAGCAGTTCGCCGCCGCTGCAGCGCACAGCACCC-CGGTGCGAG-------
GGAGGTC 252
               |||||  ||||| || | | |   |  || | |||| ||||| |   |
Db        3394 -GGAGCT-TTCGCTGCT-CAGAAAT-CAAAGCTCCATCGGAG-
GTGTCCTACTGGAGGCA 3340


Qy         253 ACTGACAAGGAACAGGAGTTTGCTGCCAGGGCTGCAAAACAGCTCGAA---------
TAT 303
                | ||||| | |    | ||    |  || | | ||   ||| | | ||          |
Db        3339 TCAGACAACAAGCTAAA---TGACGTTAGGGCTAC---
ACAACACAAAGGGGAAAGTTGA 3286


Qy         304 CAGCAATTAGAAGACGATAAACTTTCTCAGAAATCATCTAGCAGTAAACTCTC---
TCGG 360
               || ||||| | |     | | |   || | ||   || ||  ||||    ||| ||   ||
Db        3285 CAACAATTCAGGGGCTTTGAGTAGTC----AAGACAATTAGCTTAGTACT-
TCAGGTCAA 3231


Qy         361 T-----CTCCATTAAAGATTGTCAAAAAGCC-TAAAA--GCATGCAG-
TGCAAAGTGATA 411
               |      || || |     || | |||   |||   |||||  || | |||  || ||
Db        3230 TAAATGCTACAATTT--
ATGGGCAATTAGCTGTAAAATGGCCTACAGCTGAAACACTATT 3173


Qy         412 CTTCTCGATGGATCAGAATATACCTGTGATGTAGAGAAACGCTCCAGAGGACAAG----T 467
               ||| || |  ||| ||  |  | || | ||| |  |   || |||   |  ||||    |||
|
Db        3172 CTTGTC-TTATTTCACGATTTCATGGAGAT-
TAAAGATAATCTAAACAGATTAAGGCCTT 3115


Qy         468 GCTGTTTGATAAAGTGTGTGAACACTTG--------
AACTTGCTAGAGAAAGACTACTTT 519
                  | ||| || || ||| | |   ||| |       || ||    |||| | | ||
Db        3114 AATCTTTAATCCAG-
GTGAGTAATTTTGTTTGTGATAAAAAGCATAAGAAATAATTCTCA 3056


Qy         520 G-GGCTTACGTATC--GAGATGC--TGAAAACCAGAAGAATTGGTTGGAC--CCT---
GC 569
                |     ||| |||       | | ||  ||||||||||      ||| |||| |  ||
||
Db        3055 GCATATTATGTAAAAGAAAAAGCAGTGAAAACC-------
TTGTTTGGTCTTCCAGTGGC 3003


Qy         570 TAAGGAAATAAAAAAAC----AGGTTCGAAGTGGTGCTTGG---
CACTTTTCATTTAATG 622
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              | |   | |    || |||      ||    |  || |  |||     || ||| ||   ||
                                                                          |
Db     3002
AAGGATAGTTGAACAACTTCAAGAAGCTGAGAGAAGTTTGTTCCCAATTTACAAGTATTT 2943


Qy      623 TGAAATTTT-ATCCACCAGACCCTGCCCAACTAT--
CTGAAGATATCACCAGGTACTACC 679
            ||| || | || | ||| |       ||| ||   || || | |||| |  | |  |
Db     2942 TGACATATAGATAAACAAAAGCAAAACCAGTTAAACCTTAAAAGATCATCT-
GAATAAGA 2884


Qy      680
TCTGCTTGCAGTTGCGAGATGACATCGTGTCCGGAAGGCTGCCCTGCTCCTTTGTTACCC 739
            || ||  ||| | || | |  | |||     ||| |    |  || | |    | ||||||
Db     2883 TC--CTGACAATTATAATTTTACA-----TCCATGTGAATTTCAAG--
CAATTGTTAATG 2833


Qy      740 TGGCCTTGCTGGGCTCC--
TACACTGTCCAGTCAGAGCTCGGAGACTATGACCCAGATGA 797
            || |    || ||||| | || | |     | || ||  ||  |  |||| ||
Db     2832 GGGACCAGCAGGGCTGCATTAAGAAAACCA--CTTTTCACTGA-
TCTCTCCCCCACATAT 2776


Qy      798
ATGTGGGAGCGATTACATTAGTGAGTTCCGCTTTGCACCAAACCACACTAAAGAACTGGA 857
               | |          || | ||  |  | ||  |  | |||| |  | ||    ||
                                                                     ||
Db     2775 TTTTAATTTGTCTTGCTTTGTTTATTTTGGTTATGCA--AGTCCTTTCT------
CTTCA 2724


Qy      858 AGACA-AAGTGATCGAGCTGCACAAGAGCCACAG----AGGAAT-------
GACGCCAGC 905
            || | |||||     |    || |  | ||      || ||       | | |||
Db     2723 TGAAACAAGTGTAAG----
GCTCTAAGGCTAAAATAATAGTTATTTTTGTGGGCCCCA-- 2670


Qy      906 AGAAGC-AGAGATGCATTTCTTGGAAAATGCCAAAAAATTATC-
AATGTATGGGGTAGAT 963
            |  ||| |    || |||||     |   |  |||| |  | ||||| |
                                                                       ||
Db     2669 AATAGCTACTTTTGAATTTCTT--------
TCTTTAGTATATCTCAAATCTGGGGAACAT 2618


Qy      964 -TTACATCATG-CTAAGGACTCAGAAGGGGTAGAAATTATGTTAGGAGTT---
TGTGCAA 1018
                || | | ||    || ||   |||| | | ||  ||        || | |
                                                                       ||
Db     2617
GGAACTTGAAGACTCCTAACCATGAAGCATTTGGAAAAATACATATCATTCACTTTTCAC 2558


Qy     1019
GTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGATTTGCCTGGCCCAAGGTTC 1078
                | ||  | |   |   | |||    ||||  |||||| |  || |   ||
                                                                       ||||
Db     2557 AGAACCATTTTCTTAAAAAATAAGAGGC----AATATCCAGATTCACATG---CAT-
GTTC 2506


Qy     1079 ----TAAAGATTT-
CATACAAACGGAACAACTTTTTACATTAAGATCCGGCCGGGAGAGTT 1133
                        ||||| |||    |  |||| | | ||     |||||    |  | ||
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Db      2505 ATAATAAAGCTTTGTTTTAAAACAAATCCACACCAGCATTAT-
TTTCAGC---------- 2457

Qy      1134 TGAACAATTTGAAAGCACCATTGGGTTTAAG--CTGCCA---
AACCATCGAGCTGCCAAG 1188
             | || |||| || | |||  | || || || ||| |
|
Db      2456 TTAATATTTTGGCCCCAACCCAAGAATTCAGGTATAACATTTAATTTTC-
ATCTGTAATG 2398

Qy      1189 CGTTTATGGAAAG-------TATGTGTTGAGCATCATACATT-----------
TTTC--A 1228
             | | ||| | |||      ||| | ||| ||| | ||||
|
Db      2397 CATATATTGGAAGGACAAAATATATAT---
GCAAATAACACTGGAAAATGTTGTTTCCTA 2341

Qy      1229
GACTACTGTTACCAGAAGCACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGTTTCGTT 1288
                 || || | |||| |  | ||||||  ||||  | | |||||| |
|
Db      2340 TACAAGTGAT-CAAGAA--AAAAACAAAGAAAAAGAAAACCCATAGCACTAAGTTT-
GCT 2285

Qy      1289 ATAGTGGCA----GGACACAAGCGCAAACGAGAAGAGCCAG-TGCGTTGA----
TAGATC 1339
               ||||| |   || | |||  || | | |  || ||||   |||
||
Db      2284 GTAGTGAAAATATGGTTAACGGTGC---
CGTGCAAAATTAGATTTGTTGAAAAGTAGTTC 2228

Qy      1340 -----------------GCCCAGCACCTTACTTTGAACGCTCATC-----
CAGCAAACGT 1377
                              || || | | |||| || | ||      | | |
|
Db      2227 TATTACAGGGAGCAAAAGCAAAGAAGC-
AAGTTTGTGGGCAACTCGGAAGAGGGGATCAT 2169

Qy      1378
TATACCATGTCTCGCAGCTTGGATGGAGCATCAGTGAATGAAAACCATGAAATATACATG 1437
               | ||||| |       ||| || | | | |        |||| |  | |
|
Db      2168 ATTCTCATTTC------
CTTAATTGTAATTTAAATAATCATTCTCCATAATTTCTCTTTC 2115

Qy      1438 AAGG-----ATTCTATGTCTGCT---
GCAGAGGTTGGTACTGGCCAGTACGCCACAACAA 1489
               ||      |||| ||| ||||     |  | | | ||||   | | | ||  ||
||
Db      2114 TAGAGCTTTCTTCTTTGTATGCTATCACGTAAGGTAGTACT----
ATTTCACCTTAAAAA 2059

Qy      1490
AAGGCATCTCTCAGACCAACTTGATCACCACTGTGACTCCGGAGAAGAAGGCTGAGGAGG 1549
             | || |    |||| || |  ||| ||| || |     || | |  |||||
||
Db      2058 ATGGAA------AGACAAATT---TCAGC-CTAAGAAT-----
GATGTATTCTGAGTTGG 2014

Qy      1550 AGC------
```

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GGGACGAGGAAGAGGACAAACGGAGGAAGGGGGAAGAAGTCACGCCCATCT 1603
            ||  |  ||    |   |  |||  ||   | |      | |
|
Db     2013 CAATTACTTAAAACAATGAGAGAGTAAAACACATCAAACTTAAAGTGTTTA----
CTTTT 1958

Qy     1604 CGGCCATCCAGCACG-----AGGGAAAGACTGACA-----
GTGAGCGCACGGACACCGC- 1652
            |  |||  |         |||  ||| || || |      | |  |  |  | |
||
Db     1957 TGAACATTAAAATAAATGTCAGGTAAATACAGAAAAATATATAATCACTAGTTCTCAGCA 1898

Qy     1653 ----AGCCGACGGGGAGACCACTGCCACTGAGGAGCTAGAAAAAACTC--------
AAGA 1700
            |  |  ||  |   |   || ||   ||    |||||| |  ||           |
|
Db     1897 TTTTATCAATC-------
CCTTTGTTTCTCTTCTTCTAGAAGATTCTATGAGCATTATGT 1845

Qy     1701 TGACCTGAT-----GAAACATC---------AAACCAACATTAGC------
GAGCTGAAA 1740
            ||  | |||     |  ||| ||         |  |||| || ||||        | ||
|
Db     1844 TGCTCCGATCAAAAGTAACCTCACTACTCAAATACCATCA-
TAGCTTCAATGTGCATTAT 1786

Qy     1741 AGAACCTTCT-TAGAAAC-CTCAACAGACACTGCCGTAACG---
AATGAATGGGAGAAGA 1795
            ||   ||| ||||  | | |   |  |   | |  | ||    | | | |  |  |
|
Db     1785 AGTGATTTCAGTAGATTCACACTCAAATCTTTTCAGTGTCATACATTTATTAAGCCATAA 1726

Qy     1796 GGCTTT-----CCACCTCCCCCGT---GCGA-CT-GGCCGCC---
AGGCAGGAGGATGCC 1842
            | | |      || | || | |||    || |       |     |  || || || |
Db     1725 AGTTATGAAACCCTCAGCTCTTGTGGAGAGATCTGGGCAGAATTTATACAAGAAGAAGTT 1666

Qy     1843 CCCATGATCG--AACCACTTGTCCCTGAAGAGAAAATGGAAACCAA-----
GACGGAGTC 1895
            | |||       |   |  | |   ||| |  ||| |   ||| |      | | |
|
Db     1665 TAATTTATCACTTAAAAATCATCTCATAATTG----
TGGTAACAGATTTTTAAAGTAACC 1610

Qy     1896 CAGTGGATAGAG----AC--GGAACCCACCGTGCAC-----
CACCTGCCGCTTAGCACTG 1944
            |  ||||| | |        ||  |  ||||| | ||||      ||| |    |  |
|||
Db     1609 CTTTGGAAAAAATTTTACGTGATACCCAAAG-
GCACTAGTTCACATAAGGGGTGTGGCTG 1551

Qy     1945 AGAAGGTGGTGCAGGAGACC---
GTGTTGGTGGAGGAGC-------------------- 1980
            | ||| |   ||  |      ||   | |  | || |     || |  |||| 
Db     1550 AAAAAGCAAAACA--AAGCCATTGTGTAAGT-
AAAGAGCACACAAAAAAAGGATATTAAA 1494
```

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Qy      1981 -GG---CGTGTGGTGCACGCGAG------TGGGGAT-
GCTTCTTACTCGGCGGGAGACAG 2029
                 ||   | |||  ||     ||       |   || ||   || | ||  || | |
|
Db      1493
AGGAAACCTGTTAAGCTTTAAAGTTATTCTAAAAATGGCACTTTTCACGTTGGTATAAAA 1434

Qy      2030 CGGGGATGCT----GCAGCA------------------CAGCCCGCATT------
CACAG 2061
                 |   |||||   |  | |                  |  | | ||       | |
|
Db      1433
TGAAAGTGCTTTAAGATGAAATTTTTATGTATTTTTTTAAAGCTGATTTTTAACCCCCTG 1374

Qy      2062 GCATTAAAGGG----AAAGAGGGCTCTGCTTGACGGAGGGGGCTAA-----AGAGG-
AAG 2111
                  | ||  |||    ||  ||   ||| | |||         ||||      || ||
||
Db      1373 AAAATAGGGGGTTATAACAAGAACACTGATAGAC-------
TCTAACTCATAGCGGCAAT 1321

Qy      2112 GAGGGGAGGAGGTCGCTAAA--GC--------TGTCCT---------
GGAACAGGAA--G 2150
                 ||  | |||| ||| |||||  ||      |||| |        | |       ||
Db      1320
AAGTAGTGGATGTCACTAAAATGCTCTGTGTGTGTCTTTATTTTTTAGTATTTTTAATGT 1261

Qy      2151 AGACAGCCGCTGCTTCCCGTGAGCGACAAGAGGAGCA-
GAGTGCAGCCATCCACATTTCA 2209
                 || || |  |||||     | | |   | | ||  |||| ||  ||   |
|||||
Db      1260 TGATAGAC-TTGCTTT-----ATCTATCTGTGTATCATTAGTG-AG--
ATTTGCTTTTCA 1210

Qy      2210 GAAACTTT----GGAACAAAAACCTCATTTTGAGTC-
CTCAACGGTGAAGACGGAAACCA 2264
                 |  ||||    | | |  | |   | |   ||| || || |||
||
Db      1209 -ATTCTTTACTAGAAAGTTACAGCTCATTTAAAATAGCT----
GGTAAATACAGAAAGCA 1155

Qy      2265 TCAGTTTTGGCAGT--GTTT---CACCGGGAGGAGTAAA-GC-----
TAGAAATTTCCAC 2313
                 | | |    |||| ||||    ||| |   | | |||| ||     || |||
||
Db      1154 TAAATAT--
ACAGTAAGTTTAAACACTGATTGTACTAAATGCAACAATACAAAGAAGCAA 1097

Qy      2314 AAGAAGTGCCAGTAGT-TCACACCGAAAC--CAAAAC-------CATCACATAT---
GAA 2360
                 | | |   | | | ||  ||||    |||| |  ||        | ||| ||||
|
Db      1096
ATGGAACACAAATGGTAACACAATAAAACTGTATTACATTTGTGCTTCAAATATTACAAT 1037

Qy      2361 TCAT------CACAGGTCGATCCAGGCACAGATCTGGAGCCAGGCGT-
GCTGATGAGTGC 2413
                 |||      ||    || |||  | |  | ||||   |||| | |   | |   |
Db      1036 ACATTATATACAATAGTC---
CAAAATAAACATCTCATGCCAAGTGACACAAAAACGAAT 980
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Qy      2414 A-CAGACGATCACATCTGAAACCACCAGTACCACCAC----
CACTACCCACATCACCA-- 2466
             | || | || |||  | ||| ||| || ||    ||      || | ||
Db       979 AGCAAGCAAAAAAATC--CAGCCATATGTA-
CATTACTTTTTCTTTAATAATAAACATT 923


Qy      2467 AAACTGTGAAAGGGGGC-
ATTTCAGAGACAAGAATTGAGAAGCGAATAGTCATCACGGGG 2525
              |||| |||| ||||| ||||  || || ||| ||   |||| | |
Db       922 CAACTCTGAACTGGGGCAATTTC----ACTA-CATACAGATGC----AGTC--
CGCCTTT 874


Qy      2526 GATGCAGACAT-TGACCATGACCAGGCG--CTGGCTC-
AGGCAATTAAAGAGGCCAAAGA 2581
              || |  ||| | |||| ||  | |  ||   || | || ||| |  |||
Db       873 TATTC---CATATAACCAT--
CCTGCCTTCCTATATCTACGCTATTCAGTAGG------- 826


Qy      2582 GCAGCACCCTGACATGTCAGTGACCAAAGTA---GTGGT-
CCATAAAGAGAC-------- 2629
              ||||  |||||| |  | ||||   |||| | | ||||| |
Db       825 -----TTCCTG---TGTCAAT-
TCTTATGTACATGTGGAGCAAAAAAGATAAAAGAATGT 775


Qy      2630 AGAGATC-----ACACCAGAAGATGGAGAGGATTGACCAGAG-----
GAATAACTTAGCT 2679
              || | ||        |   |   | || | ||| || ||| |      |    | ||
Db       774
AGTGCTCTGTATTCTTAATGGGGTGATGTTGATAGATCAGCGAACCTGGGGTGCATAACC 715


Qy      2680 TGC--ACATGAATGCAGTCATGCAAACCGTTAGGAAAA----CCAG--
AGCCTATATGGA 2731
              || |  ||| || |    | | |  |||| |||   |      | |  || || |
Db       714
TTCTTTCATTAAACCTTCCTCGTAGTCCGTCTGGCAAAGGATCATGTTATTCTTTAGGAA 655


Qy      2732 ------
GTTCCCTCTTCTAACCCAACTGTACTTGTATCTGTCCGTGGAAAATTTCAGTCC 2785
              |||||
Db       654 AAATTTGTCTCCAACACAAAATC-TCTGATTACAAAGCTG-ACATGCAAAG---
CAGTCC 600


Qy      2786 AG-----AAGAATTGACCTTGAC---CATTAATAAAGACACTGGCAGAGA-
GATCTTCCC 2836
              ||      || ||||| |||| |        ||    ||  ||||| || || |||
Db       599 AGGTGGTAAACATTGTCCTTGGCACGCATCACCATC-
TCAAAGGCAGGGATGAGCTTACT 541


Qy      2837 ATAATAAAGCAATCTGATT-CAGCATCACTAAA------
CCGATAATGCATGAAGCAAC- 2888
              || |  |||  | | || |  |||  ||      | |||| |   ||   |||
Db       540 ACAG-GCAGCG--
CAGTTTCCCGTTACACCAAAGAGCCTCAGATAGTCTCTGCGACAAAG 484


Qy      2889 GATAAAAATTA-CAAAAGAG--CAGCAT---TTTTAATTTTCACAA---
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AATGTCTCAGTT 2939
           ||||| |||| |   || |  ||| |       |  |  | ||| |   |  ||| |||
Db        483
GATAAGATTAGCTTTAGTGTACAGGGTGGAGCCCACCTCCCCCAAGCGACAGTCACAGCA 424


Qy        2940 TTCAGCTATACCTGC--
TCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACACA 2997
               || |  || | || |  || ||||| |||   || |   | ||| |  | || |
|
Db        423 GGCA-CACTTCAGGCAGTC-TTCAT-GCCAG-TATTTGTCCAGTG----
CCTTTAGAAGA 372


Qy        2998 TAAACAATTCATGC-
CTTTCATAGTTTATTATTATTAAAGTCTAAACAAAATTGCAATT- 3055
               |  |  | | |||  |||||          || || |  |||| || |
|
Db        371 T-ACCGGTCCTTGATCTTTCG------------
GTTGCAGCCAGCACAACCTTTCGGCTT 325


Qy        3056 ----TCT---TAG---
GTAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCTA 3105
               |||  | |   | | |||| || |||| | | |    | || |    |||
Db        324 GGTGTCTGGCTGGACTGAGAGCATTTGTATACCAAAACT---
TTTCTCCTTTTTCTGCAT 268


Qy        3106 GAAGCTGTCTAGGTCCGTCCGGTGTGTCAGA-TTTCCTCAGATTAG--ATGTGC-
CAATA 3161
               | || || || |  |       ||||| || || |  ||| || |   || || | |
|
Db        267 G-AGTTGACTTAGGC--------
GTGTCTGAGTTGCAGCAGCTTCGCATTGAGCACCAAA 217


Qy        3162 ACCAAGTTTATTCAGTAAA-------CAACTTGTACTTGTTTC-------
ATCTGGTTTA 3207
               |||| ||  ||  |||| |      |  |||| | | ||          | ||||||
Db        216 CCCAAAGGTA-
GAAGTAGAAGGGGGTCTCCTTGATTTCGCTTAAGTGTGGACCTGGTGCG 158


Qy        3208 TTACTCTCAC---------CCATAAACAGTAATGACTCTCT--------
GAC-------C 3243
                  |  |||       || |  || | | | ||      | |
|
Db        157
CAGCCTACACCGCCGAGGACCGACTATTGTGAAGCCACTTTGGGAGCGGGTCGGAGTGGC 98


Qy        3244 CTCTGGAAAT-----ATGTAATG----CTTCCAATCTTG------------
CTTTGTGTA 3282
               | ||  |   | |  |||   |  ||| | |            |   | |
Db        97
GGCAGGGGGTGGGGGAAGGGATGAGGACGGCCAGACAAGACAGGGCGCACACACGGAGCC 38


Qy        3283 TCTC-----ATTTAATTTG-------TTCCGGTTAAGG 3308
               |||     |  || ||          ||| || |||
Db        37 CCTCGCAGTGTGCAAAATGATGGCGAATCCAGT--AGG 2


RESULT 5
US-10-478-914-61
; Sequence 61, Application US/10478914
; Patent No. 7335755
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  Query Match            30.2%;  Score 5876;  DB 1;  Length 2437;
  Best Local Similarity  42.7%;  Pred. No. 0;
  Matches 1445;  Conservative   0;  Mismatches  861;  Indels 1076;
Gaps  205;


Qy        1 GCGGCGCGCC-CGAGCCTAGTC--CCCAC-------GCCGCGGCGC---
GCCCGGGCTCC 47
              ||||    || |||||   ||   || ||       | | || |     |   |
            ||||
Db       22
GCGGAATTCCTCGAGCACTGTTGGCCTACTGGGTGTACTGTGGAGACTGTCAAAGTCTCC 81


Qy       48 CTGCTGATCCCAG-AACAATCAACCATGACGACCGAATCTGGATCAGACTCGGAA---
TC 103
              | || ||||   |    | | ||| | |||   | ||  | | |
            ||
Db       82 ---
CGGAGCCCAATTTCCGGAAGCGGTGAGTTCTGAAAGAAGTTCCTGCACCGTAGTTTC 138


Qy      104 CAAGCCGGACCAGGAGGCCGAGCC--
CCAGGAGGCGGCGGGGGCGCAGGGG--------C 153
              |   | | | |  || ||   || ||| || ||| |  ||||| | |
            |
Db      139 C---CAAGTCTGCGAATCC---CCAACCATGA-
GCGCCTCGGGCGTACTGTCCTTTACCC 191


Qy      154 GGCGGGGGC-CGTGCCGGAGCCGCCCAAGGAGGAGC-AGCAGCAG--GCCCTGGA-
GCAG 208
              || ||    | || || || | |||| | | |   || |  |  |||||| ||
            |
Db      192
AGCAAGGATGGGAGCAGGTGCTGGCCAAAGTGAAACGGGCTGTGGTTTACCTGGACGCCG 251


Qy      209 --TTCGCC----GCC---------GCTGCAG---
CGCACAGCACCCCGGTGCGAGGGAGG 250
              | |||| | | |||  |  |||||| |   | | | | | || |   |  ||| ||
            ||
Db      252
CCTGCGCCGAGAGCCTGCACTGGGGCTGCGGATCCACCCGTCTCCTGGAGGCGGTGGGGG 311
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Qy          251
TCACTGACAAGGAACAGGAGTTTGCTGCCCAGGGCTGCAAAACAGCTCGAATATCAGCAAT 310
              | |||||           ||   |||| ||| |||   ||| |||
|||||
Db          312 GCCCTGAC----------TGTCACCTGCGAGAGTT-CG----AGCCCGA-----
CGCAAT 351


Qy          311
TAGAAGACGATAAACTTTCTCAGAAATCATCTAGCAGTAAACTCTCTCGGTCTCCATTAA 370
               | |   ||                 | | |  | ||  | | |||    ||
||
Db          352 TGGTGGTGGA------------------GCCAAGCAG------CCCAAGG-
CAGTGTTTG 386


Qy          371
AGATTGTCAAAAAGCCTAAAAGCATGCAGTGCAAAGTGATACTTCTCGATGGATCAGAAT 430
               | |   |    || ||| ||  | |  |  | ||| || |    || ||
||
Db          387 TGCTGAGCTGCCTGCTGAAAGGC---CGGACCGTGGAGATCCTAC-----
GGGACATCAT 438


Qy          431
ATACCTGTGATGTAGAGAAACGCTCCAGAGGACAAGTGCTGTTTGATAAAGTGTGTGAAC 490
               | ||   | ||          | ||        | ||| ||| ||        |||
|
Db          439 CTGCC---GCAGT-------CACT-------TCCAGTATTGTGTG---------
GTGGTC 472


Qy          491
ACTTGAACTTGCTAGAGAAAGACTACTTTGGGCTTACGTATCGAGATGCTGAAAACCAGA 550
               ||  |||  |  |||      | ||          | ||         |||| |||
|
Db          473 AC---AAC---CGTGAG-----CCAC---------------------
GCTGTCCACCTCA 500


Qy          551 AGAATTGGTTGGACCCTGCTAAGGAAATAAAAAAACAG-
GTTCGAAGTGGTGCTTGGCAC 609
               |      | ||| |            ||| |  ||| ||| |
||||
Db          501 CAGCTAATCATGTCCCAGCGGCGG-----------CAGCGGCCGAGATGGAG--
GGGCA- 546


Qy          610 TTTTCATTTAATGTGAAATTTTATCCACCAGACCCT----
GCCCAACTATCTGAAGATAT 665
               ||    |||        || | |||   ||   |    | || | |||
||
Db          547 ---GCAGCCGGTGT---------TCGAGCAG---
CTGGAGGAGAAGCTGTGTGAATGGAT 591


Qy          666 ---CACCAGGTACTACCTCTGCTTGCAGTTGCGAGATGACATCGTGTCCGG--
AAGGCTG 720
               || || | |||         |||| ||   | ||||| | |
|||
Db          592 GGGCAACATGAACTA-CACGGC---------CGAGGTGT-
TCCATGTCCCGTTATTGCT- 639


Qy          721 CCCTGCTCCT-TTGTTACCCTGGCCTTG-
CTGGGCTCCTACACTGTCCAGTCAGAGCTCG 778
               ||| ||| ||| | ||  | ||||  | |  |     |   |
|
Db          640 ---TGCCCCTGTTGCTCCCC--
```

```
ACTTTGCCTTGACTCCAGCTTTTGCATCCCTTTTCCC- 693


Qy         779
GAGACTATGACCCAGATGAATGTGGGAGCGATTACATTAGTGAGTTCCGCTTTGCACCAA 838
                |||  ||||   | ||||   ||  | | | |            | || ||
Db         694 ---ACTGCTACCC--CAGGATGT----GCACCTCCTTAA------------
TAGCGCCCG 732


Qy         839 ACCACACTAAAG--AACT-GGAAGACAAAGTGAT-CGAGCTGCACAA---
GAGCCACAGA 891
                |||  || || ||  | || ||||| |   ||||| |  || ||| |   | ||
||||
Db         733
ACCGGACAAGAGGAAGCTGGGAAGCCTGGGTGATGTGGACTCCACTACGCTAACCCCAGA 792


Qy         892 GGAATGACGCCAGCAGAAGCAG---
AGATGCATTTCTTGGAAAATGCCAAAAAATTATCA 948
                |          | || | |||| |||||||   || |    | ||| |
                ||
Db         793 G---------CTGCTGCTGCAGATCAGATGC----CTAGTGTCAGGCCTCAG----
TTCT 835


Qy         949 ATGTATGGGGTAGATTTACATCATGCTAAGGACT-
CAGAAGGGGTAGAAATTATGTTAGG 1007
                |||  ||           | | ||| | |||| | | | ||| ||     || || |
Db         836 CTGTGTG-----------AACAT--TTAGGAGTACGGGAGGAGT----
GTTTTGCT--- 874


Qy         1008
AGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGATTTGCCTG 1067
                |  || |     ||| |            |  ||||||| ||
                |||
Db         875 -GTAGGTTCCTTAAGTCAGGT---------CATC--GCTGCGGAT------------
CTG 910


Qy         1068 GCCCAAGGTTCTAAAGATTTCATACAAACGGAACA--
ACTTTTACATTAAGATCCGGCCG 1125
                |||  | |  |     |  || || |||| |  ||| | ||           |||
                |
Db         911 GCCAATTATGCCCCTG----CAAAGAACAGGAAGAAGACTGCTGCA---------
GGCAG 957


Qy         1126 GGAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCCA-
AACCATCGAGCTGC 1184
                |                   ||| || | || |   | || |||| | || ||
Db         958 G--------------------GCATCAGT-
GGTTTTTGTGGACAGAACCCTGGATCTCA 995


Qy         1185
CAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTTTTCAGACTACTGTTACCAGA 1244
                || | |             |||| ||||||       |||| |||
Db         996 CAGGAGC--------------AGTTGGACATCATG-------
GAGACAACTTAGTAGAGA 1034


Qy         1245
AGCACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGTTTCGTTATAGTGGCAGGACACA 1304
                || | | | || |||| ||   ||    | |||               ||||
                ||||
Db         1035 AGATCATTTC-AGCACTTCC---CC---AGCTCC------------------
```

```
CAGGCCACA 1070

Qy         1305
AGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCACCTTACTTTGAACGCTC 1364
                |||| ||               ||    |||| | |        | | |       |
|||||
Db         1071 ----CAAATGA----------TG---TGATGGTT--------AACATGAT---
AGCGCTC 1102

Qy         1365 ATCCAGCAAACGTTATACCATGTCTCGCAGCTTGGATGGAGCATCA----
GTGAATGAAA 1420
                |  |  |||            |||    ||  |  |||  || |     ||| ||
Db         1103 A--CTGCA---------------
CTCCATACTGAGGAGGAAAATTATAATGTGGTTG--C 1143

Qy         1421 ACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAGAGGTTGGTACTGGCCAGT-
AC 1479
                |||| |                   ||||| | |         || | ||||
||
Db         1144 ACCAGG--------------------CTGTCT--TTC----------
ACAATTCAGTGAC 1171

Qy         1480 GCCACAACAAAAGGCATCTCTCAGACCAACTTGA-
TCACCACTGTGACTCCGGAGAAGAA 1538
                |||||| | |||  | || |   | || | | ||| | | ||       ||
|
Db         1172 ACCACAGCCAAAG----CCCTATGGGAAGCTTTACTGAACACTAAG-CAC-----
AAAGA 1221

Qy         1539
GGCTGAGGAGGAGCGGGACGAGGAAGAGGACAAACGGAGGAAGGGGGAAGAAGTCACGCC 1598
                |||  |  |||        ||   |  ||||     | |||||
Db         1222 GGCAGTGATGGA--------
AGTTCGGAGACATCTAGTGGAAG----------------- 1256

Qy         1599
CATCTCGGCCATCCAGCACGAGGGAAAGACTGACAGTGAGCGCACGGACACCGCAGCCGA 1658
                  |||| | |          || |||| ||| | |            || | |
|
Db         1257 -----CGGCAAGC-------AGAGAAAACCTGCCAAT-----------CA-
AGATGAGTA 1292

Qy         1659
CGGGGAGACCACTGCCACTGAGGAGCTAGAAAAAACTCAAGATGACCTGATGAAACATCA 1718
                |||||||   | ||  |   |         | ||| ||| |||     |
|||
Db         1293 TGGGGAGA-----GTCACACCGGGAC-------AGCTC---ATGTCCT-----
ATATTCA 1332

Qy         1719
AACCAACATTAGCGAGCTGAAAAGAACCTTCTTAGAAACCTCAACAGACACTGCCGTAAC 1778
                    |   |          ||||||     |||||||||          ||
|||
Db         1333 GCTCTTC--------------AAGAAC---------AACCTCAA-------
AGCTCTAAT 1362

Qy         1779
GAATGAATGGGAGAAGAGGCTTTCCACCTCCCCCGTGCGACTGGCCGCCAGGCAGGAGGA 1838
                |||| | || |         || ||||  | || |||||||| |
Db         1363 GAATCATTGTGG-----------CCTCCTCCAGCTTG-
```

```
GACTGGCCAC------------ 1398


Qy        1839
TGCCCCCATGATCGAACCACTTGTCCCTGAAGAGAAAATGGAAACCAAGACGGAGTCCAG 1898
               || |   | | | ||| |||    | | ||     || |||      |||     | |
Db        1399 AGCTCAAACGTT-GAAACAC---CCACAGACTGCCAAGTGG------- 
GACAACTTTC-- 1445


Qy        1899
TGGATAGAGACGGAACCCACCGTGCACCACCTGCCGCTTAGCACTGAGAAGGTGGTGCAG 1958
               ||| |   || |         || ||  || |   ||| || | ||
|||
Db        1446 TGGCTTTTGAAAG----------GCTCCTTCTTCAG---AGCATTGGGGAGTC--
AGCA- 1489


Qy        1959
GAGACCGTGTTGGTGGAGGAGCGGCGTGTGGTGCACGCGAGTGGGGATGCTTCTTACTCG 2018
               | |||| || |  | ||| ||     ||| ||| |  ||   | || | ||
|
Db        1490 ATGTCCGTTGTGTGTTAAATCAGCTGC------TGCCCATGATT----
AAGCCTGTAACCC- 1538


Qy        2019
GCGGGAGACAGCGGGGATGCTGCAGCACAGCCCGCATTCACAGGCATTAAAGGGAAAGAG 2078
               | ||  || ||  || ||   || |||| |
Db        1539 -AGAGAACCAACGAGGA--
CTACAGCCCTG----------------------------A 1566


Qy        2079 GGCTCTGCTTGACGGAGGGGGCTAAAGAGGAAGGAGGGGAGGAGGTCGC---
TAAAGCTG 2135
               || |||||    |        ||              || |    || |
|
Db        1567 GGAACTGCTGATC--------CT----------------------
TCTCATATATATTTA 1596


Qy        2136
TCCTGGAACAGGAAGAGACAGCCGCTGCTTCCCGTGAGCGACAAGAGGAGCAGAGTGCAG 2195
               | |||  || |||       |||      || | |  | ||   | || | ||| | |||
||
Db        1597 TTCTGTCACTGGAG-----AGC-------TCACGGTA--GACA--
AAGACCTGTGTGAAG 1640


Qy        2196 C--CATCCACATTTCAGAAA-
CTTTGGAACAAAAACCTCATTTTGAGTCCTCAACGGTGA 2252
               |   |   | | | ||||| | ||||      ||||     ||| ||
||||
Db        1641 CAGAAGAAAAAGTCAAGAAAGCATTGG---------CTCA-----GGTCTTCT---
GTGA 1683


Qy        2253
AGACGGAAACCATCAGTTTTGGCAGTGTTTCACCGGGAGGAGTAAAGCTAGAAATTTCCA 2312
               ||          ||| | | || | || ||     | |          || | | | |
||
Db        1684 GGA--------
ATCTGGATTGTCACCTTTGCTGCAAAAAATTACGGACTGGGACTCTTCA 1735


Qy        2313 CAAGAAGTGCCAGTAGTTCACACCGAAACCAAAACCATCACATATGAA-
TCATCACAGGT 2371
               | || |   | |||||| || |||||||     |   ||||| || | ||
|
```

```
Db      1736 ATTAATCTGAC---ATTTCACA---
AATCCAAAATTGCCGTGGATGAACTCTTTACT--T 1787

Qy      2372
CGATCCAGGCACAGATCTGGAGCCAGGCGTGCTGATGAGTGCACAGACGATCACATCTGA 2431
             |  |  | || | |   ||||||| || || ||  |||   ||| | | |
             ||||
Db      1788 CACTTCGGG-ATATTGCTGGAGCTCGGAGT-CTCCTGA---AACA---
GTTTAAGTCTGT 1839

Qy      2432 AAC--
CACCAGTACCACCACCACTACCCACATCACCAAAACTGTGAAAGGGGGCATTTCA 2489
             |           || | |  || |  | |  |||| ||| || |          ||||
Db      1840 ATATGTTCCTGGAAATCATACCCACCAGGCATCTTATAAGC------------
CATTGTT 1887

Qy      2490 GAGACAAGAATTGAGAAGCGAATA-GTCATCACGGGGGATGCAGA---
CATTGACCATGA 2545
             || |||| ||| | || |||| |||||| || |   |||| | ||||
             |||
Db      1888 GAAGCAAG--TTGTGGAGGAAATATTTCATCCCGAGAGGC-
CAGATTCCGTTGATATTGA 1944

Qy      2546 CCAGGCGCTGGC-
TCAGGCAATTAAAGAGGCCAAAGAGCAGCACCCTGACATGTCAGTGA 2604
             || |  | || | |||||              | | |||| ||
Db      1945 ACA--C-ATGTCTTCAGGC---------------------CTCACTGA----
TC----- 1970

Qy      2605
CCAAAGTAGTGGTCCATAAAGAGACAGAGATCACACCAGAAGATGGAGAGGATTGACCAG 2664
             ||| ||||               ||                 |||||
Db      1971 ------------TCCTTAAA--------------AC------------
TGGAT------- 1985

Qy      2665
AGGAATAACTTAGCTTGCACATGAATGCAGTCATGCAAACCGTTAGGAAAACCAGAGCCT 2724
             ||||| ||  |||||| |    || || |  || |
Db      1986 ---------TTAGCATGTTCATGAAGG------TG--AGCCG--------
GCCTCATCCT 2020

Qy      2725
ATATGGAGTTCCCTCTTCTAACCCAACTGTACTTGTATCTGTCCGTGGAAAATTTCAGTC 2784
             |   || | ||| || || || |     | |||| || |||| |
             |||||
Db      2021 AGT--GACTACCCCCTCCTGATCC-----TCTTTGTG---GTAGGTGG--
GGTCACAGTC 2068

Qy      2785 -CAGAAGAATTGACCTTGACCATTAATAAAGACACTGGCA------
GAGAGATCTTCCCA 2837
             | |||| |||  || || || |  |||||        || |
             ||||
Db      2069 TCTGAAG---TGAAAATGGTCAAAGATCTTG----
TGGCATCGTTGAAGCCAGGAACCCA 2121

Qy      2838 --
TAATAAAGCAATCTGATTCAGCATCACTAAACCGATAATGCATGAAGCAACGATAAAA 2895
             ||||    ||  ||          || ||| |  ||        |||||| ||  |||
             |
```

```
Db      2122 GGTAATCGTGCTGTC--------CA-CACGACTCC---------TGAAGCCAC-
TTAACA 2162

Qy      2896
TTACAAAAGAGCAGCATTTTTAATTTTCACAAAATGTCTCAGTTTTCAGCTATACCT--G 2953
             || |   |||| |  | |||| |  || || | | | || | |||| |
|
Db      2163 TTCC---TGAGCTG------TTATTTGC---AACTG--
ACCGACTGCATCCAGACCTTGG 2208

Qy      2954
CTCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACACATAAACAATTCATGCCT 3013
             |    ||| | |   || ||    | |   | |     || || |
|||||
Db      2209 C---TTCTGAGCATCCGCTAAGAA----GAT---
AAGACCTACTCAAGCTGGAAATGCCG 2258

Qy      3014
TTCATAGTTTATTATTATTAAAGTCTAAACAAAATTGCAATTTCTTAGGTAACCTTATAT 3073
             |  | ||| |   | |    || |  | |    | |||| | ||       |||
Db      2259 ATGCAATTTTCT----------GCCACCAC-----TCCAAATACT-------
CCTCC--- 2293

Qy      3074 TTACAATAAATGAAGATTACCCTCAAATGCTAGAA-
GCTGTCTAGGTCCGTCCGGTGTGT 3132
                 |||| |  |    |  | || || ||| |||| | ||    | || | | |  |
||
Db      2294 --ACAACCAGCGTCCCTGTCACT-AATTGCGAGAATGATG--
GAATTCTGCCTGAAGGGT 2348

Qy      3133
CAGATTTCCTCAGATTAGATGTGCCAATAACCAAGTTTATTCAGTAAACAACTTGTACTT 3192
             |              | || |       ||| ||  || ||||| |  |||| |
|||
Db      2349 C--------------TTGAT---------ACC-----TACTCAGTGAGGTACTT-
TGCTT 2379

Qy      3193
GTTTCATCTGGTTTATTACTCTCACCCATAAACAGTAATGACTCTCTGACCCTCTGGAAA 3252
             |               ||| || | | | |||| | || |      | ||   ||
Db      2380 G------------
GATTGCTGTGATTCTTAAAAAAAAAAAAAAAAAAAGGCCACATG---- 2423

Qy      3253 TATGTAATGCTTCCAATCTTGC 3274
                       |||| | | |||
Db      2424 -------TGCT--CGAGC-TGC 2435


RESULT 6
US-10-478-914-61/c
; Sequence 61, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
```

```
  Query Match              29.4%;  Score 5713;  DB 1;  Length 2437;
  Best Local Similarity   42.4%;  Pred. No. 0;
  Matches 1432;  Conservative    0;  Mismatches  863;  Indels 1080;
Gaps  220;


Qy         2 CGGCGCGCCCGAGC-CTAGTCCCCACGCCGCGGCGCGCC------------------
CGG 42
               | ||  || ||||| |  ||                  |||
               |
Db      2437 CTGC-AGCTCGAGCACATGT---------------
GGCCTTTTTTTTTTTTTTTTTTTTTAAG 2394


Qy        43 GCTCCCTGCTGATCCCAGAACAATCAACCATGACGACCGAATCTGGATC-
AGACTCGGAA 101
               || | ||  |||| ||  ||| ||| |  | || || |  | ||| |||| |
Db      2393 AATCACAGC-AATCCAAG--CAAAGTACC---TC-
ACTGAGTAGGTATCAAGACCC---- 2345


Qy       102 TCCAAGCCGGA--CCAGGAGGCCGAGCCC-CAGGAGGCGGCGGGGGCGCAGG-
GGCGGCG 157
               | || || |  ||  |||        |  | | ||    | | ||| ||| ||  | ||
               |
Db      2344 TTCAGGCAGAATTCCA-----
TCATTCTCGCAATTAGTGACAGGGACGCTGGTTGTGGAG 2290


Qy       158 GGGGCCGTGCCGGAGCCGCCCAAGGAGGAGCAGCAGCAGGCCCTG---
GAGCAGTTCGCC 214
               | |    ||  | |  || || |    ||| | |||    || |    ||| || ||
Db      2289 GAGTATTTGGAGTGGTGGCAGAA--
AATTGCATCGGCATTTCCAGCTTGAGTAGGTCTTA 2232


Qy       215 GCCGCT--GCAGC-GCACAGCACCCCGGTGC-----
GAGGGAGGTCACTGACAAGGAACA 266
               |  ||  || |  || ||| | ||  | |     |  |  ||||| |  |||
               ||||
Db      2231 TCTTCTTAGCGGATGCTCAGAAGCCAAGGTCTGGATGCAGTCGGTCAGTTGCAAATAACA 2172


Qy       267 GGAGTTTGCTGCCAGGGCTGCAAAACAGCTCGAATATCAGCAATT-
AGAAGACGATAAAC 325
               ||| |||| ||  || ||   ||| |||| | |  | ||| |
Db      2171 -------GCT--CAGGAATGTTAAGTGGCT------
TCAGGAGTCGTGTGGACAGCACGA 2127


Qy       326 TTTCTCAGAAATCATCTAGCAGTAAAC----
TCTCTCGGTCTCCATTAAAGATTGTCAAA 381
               || | | |   || || || | ||| |       | | | |||   || |  ||| |||
Db      2126 TTAC-CTGGGTTC--CTGGCT-TCAACGATGCCACAAGATCT---
```

```
TTGACCATTTTCA-- 2076


Qy        382
AAGCCTAAAAGCATGCAGTGCAAAGTGATACTTCTCGATGGATCAGAATATACCTGTGAT 441
             | | || |   | ||||    ||||  |   |||||||| |              |
Db     2075 ---CTTCAGAG---ACTGTGACCCCACCTACCACAAAGAGGATCAGGA--------
GGGG 2030


Qy        442
GTAGAGAAACGCTCCAGAGGACAAGTGCTGTTTGATAAAGTGTGTGAACACTTGAACTTG 501
            ||||     | ||    |||| || || |  | | |       | | |||||
||
Db     2029 GTAG----TCACT----AGGATGAG-GCCG---GCTCACCT--------
TCATGAACATG 1990


Qy        502 CTAGAGAAAGACTACTTTGGGCTTACGTATCGAGATGCTG-
AAAACCAGAAGAATTGGTT 560
            ||    ||| | |||  |          ||||| | |  | || ||||| ||
Db     1989 CT----AAATCCAGTTTTAAG----------GAGAT-
CAGTGAGGCCTGAAGACATG--- 1948


Qy        561
GGACCCTGCTAAGGAAATAAAAAAACAGGTTCGAAGTGGTGCTTGGCACTTTTCATTTAA 620
            || | |  | | || |  | | |||| | || |        |||| | |
Db     1947 ------TGTTCA------ATATCAACGGAATC-----------TGGC------
CTCTCGG 1917


Qy        621 TGTGAAATTTTATCCACCAGACCCTGC-CCAACTAT--CTGAAGATATCACC----
AGGT 673
                |||||| || ||| ||| | | ||| |||| || || |  | ||  ||
Db     1916 GATGAAATATT-TCCTCCACAACTTGCTTCAACAATGGCTTATAAGAT-
GCCTGGTGGGT 1859


Qy        674
ACTACCTCTGCTTGCAGTTGCGAGATGACATCGTGTCCGGAAGGCTGCCCTGCTCCTTTG 733
            | | ||  || ||     || | | || |   ||   |  || |  || |  |  ||  |||||
Db     1858 ATGATTTCCAGGAACATATACAGACTTAAACTGTTTCAGG-AGACT-
CCGAGCTCCAGCA 1801


Qy        734 TTACCCTG----
GCCTTGCTGGGCTCCTACACTGTCCAGTCAGAGCTCGGAGACTATGAC 789
             || ||| |    |   | | || ||  |  | |  | | | || | |  ||| |  | || |||
Db     1800 ATATCCCGAAGTGAAGTAAAGAGTTCATCCACGG--CAATTTTGGATTTGTGA-
AATGT- 1745


Qy        790 CCAGATGAATGTGGGAG--CGATTACATTAGTGAGTTCCGCTTTG----CA--
CCAAA-- 839
             ||||| |||    |||  | | | | || |  |    | |  || |  | || |
Db     1744 -
CAGATTAATTGAAGAGTCCCAGTCCGTAATTTTTTGCAGCAAAGGTGACAATCCAGATT 1686


Qy        840 CCACACTAAAGAACTGGAAGACAAAGTGATC--GAGCTGCACAAGAGC--
CACAGAGGAA 895
             || ||| |||| ||  || ||||  || || |  | | ||  | | |    || |||| |||
Db     1685 CCTCACAGAAGACCTG--
AGCCAATGCTTTCTTGACTTTTTCTTCTGCTTCACACAGGTC 1628


Qy        896 TGACGCCAGCAGAAGCAGAGATGCATTTCTTGGAAAATGCCA-
AAAAATTATCAATGTAT 954
```

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                   |     |  |   |||              |||     |  ||  ||  ||  ||  |||   |||
Db       1627 TTTGTCTACCGTGAGC-----------TCT---
CCAGTGACAGAATAAATATATATGAGA 1582

Qy        955 GGGGT-AGATTTACATCA-TGCT-AAGGACTCAGAAGGGGTAGAAATTAT--
GTTAGGAG 1009
                   ||  ||     |  |  |||  |||   ||  |||       ||  |     |  |  ||||
|
Db       1581 AGGATCAGCAGTTCCTCAGGGCTGTAGTCCTC-------
GTTGGTTCTCTGGGTTACAGG 1529

Qy       1010 TTTGTGCAAGTG-GTCTGTTGATATATCGCGACCGGC--
TGCGAATAAACAGATTTGCCT 1066
                   ||    ||  |  |    |  |  ||||  ||  |  |  ||  |    |||                     ||
                                                                                      ||
Db       1528 CTTAATCATGGGCAGCAGCTGATTTAACACAACGGACATTGC-------------
TGACT 1482

Qy       1067 GGCCCAAGGTTCTAAAGA-------
TTTCATACAAACGGAACAACTTTTACATTAAGATC 1119
                   |||||  |  |||  ||||         |||||  |   |  |||  |    |  |    ||  |    |
|
Db       1481 -CCCCAATGCTCTGAAGAAGGAGCCTTTCA-AAAGCCAGAA-
AGTTGTCCCACTTGG--C 1427

Qy       1120 CGGCCGGGAGAGTTTGAACAATTTGAAAGC----ACCATTGGGTTTAAGCTGCC--
AAAC 1173
                   |  |  |  |  |  ||||  |||   ||||   |||      |||        |||      ||  ||||||     |
Db       1426 AGTCTGTGGGTGTTTCAAC-GTTTG--AGCTGTGGCCA----
GTCCAAGCTGGAGGAGGC 1374

Qy       1174 CATCGGAGCTGCC-
AAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTTTTCAGAC- 1231
                   ||     |  |  |    |  |  |    ||    ||  |||   |    |  ||                    |
|||
Db       1373 CACAATGATTCATTAGAGCTTTGAGGTTGTTCTTGAAGAGCTGAATA------
TAGGACA 1320

Qy       1232 --TACTGTTACCAGAAGCAC-
CTCCCAAGAAATTCCTAACCTTGGGTTCCAAGTTTCGTT 1288
                   |||  ||  ||  |          ||  |||||  |            |  |||  |  ||||       |    ||  ||||
Db       1319 TGAGCTG-TCCCGGTGTGACTCTCCCCA-----
TACTCATCTTGATTGGCAGGTTT---- 1270

Qy       1289
ATAGTGGCAGGACACAAGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCAC 1348
                   |     ||  |  |  |      |     ||  |||  |  |  |  |                          |||
|||
Db       1269 -TCTCTGCTTGCCGCTTCC----ACTAGATGTCTCCGAACTT------------
CCATCAC 1226

Qy       1349 --CTTACTTTGAACGCTCA---TCCAGCAAACGTTATACCAT--
GTCTCGCAGCTTGGAT 1401
                   |  |  |||||     |||  |    |  |||  ||||     |  ||  |  |  ||              ||||
|
Db       1225 TGCCT-CTTTGT--GCTTAGTGTTCAGTAAA-GCT-TCCCATAGGGCT------
TTGGCT 1177

Qy       1402 GGAGCATCA-------
```

```
GTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCTGC 1454
          |  |   |||     |||||  ||| |  ||     ||| ||  | |
                                                                  |
Db     1176 GTGGTGTCACTGAATTGTGAAAGACAGCC-TGGTGCAACCAC-----
ATTATAATTTTCC 1123


Qy      1455
TGCAGAGGTTGGTACTGGCCAGTACGCCACAACAAAAGGCATCTCTCAGACCAACTTGAT 1514
          | | || ||| ||  |||| ||                   || |||    |||
||
Db     1122 TCCTCAGTATGG-AGTG--CAGTGAGC--------------GCTATCATGTTAACC--
AT 1082


Qy      1515 CACCAC---
TGTGACTCCGGAGAAGAAGGCTGAGGAGGAGCGGGACGAGGAAGAGGAC-- 1569
          ||| |   |||| |    |||| ||| ||  ||
Db     1081 CACATCATTTGTGTGGCCTGGGA-----GCTGGGGAAGTGC-------
TGAAATGATCTT 1034


Qy      1570 --
AAACGGAGGAAGGGGGGAAGAAGTCACGCCCATCTCGGCCATCCAGCACGAGGGAAAGA 1627
          ||         |||   |||| || | ||| | ||| | ||| | ||
Db     1033 CTCTAC-----------TAAGTTGTCT---CCATGATGTCCA-
ACTGCTC---------- 999


Qy      1628 CTGACAGTGAGCGCACGGACACCGCAGCCGACGGGGAGACCACTG-
CCACTGAGGAGCTA 1686
          | |||||  |                   |  ||       ||| ||||
Db      998 ----CTGTGAGATC----------------CAGGGT----
TCTGTCCAC---------- 974


Qy      1687
GAAAAAACTCAAGATGACCTGATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAACC 1746
            |||||     |||| ||||             ||  |      ||| |
                                                                |
Db      973 --AAAAACCACTGATGCCCTG-------------CCTGC-------
AGCAGT-------C 943


Qy      1747
TTCTTAGAAACCTCAACAGACACTGCCGTAACGAATGAATGGGAGAAGAGGCTTTCCACC 1806
            |||||     |||      |  ||| |  | |         ||        |||
Db      942 TTCTT-----CCT----GTTCTTTGCAGGGGC--ATAATTGG-------------
CCAGA 907


Qy      1807
TCCCCCGTGCGACTGGCCGCCAGGCAGGAGGATGCCCCCATGATCGAACCACTTGTCCCT 1866
          ||| |   |||| || |    |  | || |     | | | ||||
||||
Db      906 TCCGC--AGCGA-TG---ACCTGACTTAAGGA-ACCTAC---
AGCAAAACACTCCTCCCG 857


Qy      1867
GAAGAGAAAATGGAAACCAAGACGGAGTCCAGTGGATAGAGACGGAACCCACCGTGCACC 1926
          |     |||||   ||   || ||| | ||
Db      856 TACTCCTAAATGTTCAC----
ACAGAGAACTGAGG-------------------------- 826


Qy      1927 ACCTGCCGCTTAGCA-
CTGAGGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGGCGT 1985
              |||| | || ||| ||||         |||||     |           ||| ||
```

```
|
Db        825 -CCTGACACTAGGCATCTGATC------TGCAG-----C-------------
AGCAGC-T 792

Qy       1986 GTGGTGCACGCG-
AGTGGGGATGCTTCTTACTCGGCGGGAGACAGCGGGGATGCTGCAGC 2044
              ||| |   ||| |||||  |      ||    ||  |     |||         ||
|
Db        791 CTGGGGTTAGCGTAGTGGAG-----TCCACATCACC------CAG----------
GCTTC 753

Qy       2045 ACAGC--CCGCAT-TC---ACAGGCATTAAAGGGAAAGAGG-
GCTCTGCTTGACGGAGGG 2097
              ||||  || | ||    | ||| ||     || |||| || |   |    | |
||
Db        752 CCAGCTTCCTCTTGTCCGGTCGGGCGCTATT---AAGGAGGTGCACATC----
CTGGGGT 700

Qy       2098 GGCTAAAGAGGAAGGAGGGGAGGAGGTCGCTAAAGCT---
GTCCTGGAACAGGAAGAGAC 2154
              ||         | ||| |   ||  || ||||||   ||| || | ||
Db        699 AGC----------
AGTGGGAAAAGGGATGCAAAAGCTGGAGTCAAGGCAAAG-------- 658

Qy       2155
AGCCGCTGCTTCCCGTGAGCGACAAGAGGAGCAGAGTGCAGCCATCCACATTTCAGAAAC 2214
              ||       | |||| |  ||| |||     ||| ||| ||        |
||
Db        657 ------TG------GGGAGCAAC---AGGGGCA------AGCAAT-AAC------
GGGAC 626

Qy       2215 TTTGGAACAAAAACCTCATTTTGAGTCCTCAACGGTGAAG---
ACGGAAACCATCAGTTT 2271
              ||||||||           |||| | ||| ||   | |    |||||
Db        625 -ATGGAACA-----------------
CCTCGGCCGTGTAGTTCATGTTGCCCATC----- 589

Qy       2272
TGGCAGTGTTTCACCGGGAGGAGTAAAGCTAGAAATTTCCACAAGAAGTGCCAGTAGTTC 2331
                     ||  |||||         | |||| |  | || || |     ||| |
Db        588 ---CA----TTCAC----------ACAGCT-----TCTCCTCCAGC--
TGCTCG-----A 558

Qy       2332
ACACCGAAACCAAAACCATCACATATGAATCATCACAGGTCGATCCAGGCACAGATCTGG 2391
              ||||||      |   || ||    |||| | | |  |     | |||| |
||||
Db        557 ACACCGGCTGC-TGCCCCTC----------CATCTC-GGCCG---CTGCCGCCG--
CTGG 515

Qy       2392 AGCCAGGCGTGCTGATGAGTGCACAGAC---
GATCACATCTGAAACCACCAGTACCACCA 2448
              |  |   |||  || |||| |    || | |||||||
Db        514 GACATGATTAGCTGTGAGGTGGACAG-
CGTGGCTCACGGTTGTGACCACCA--------- 465

Qy       2449
CCACTACCCACATCACCAAAACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGC 2508
              ||||  ||         || ||| |     | | | ||    ||    |
|
```

```
Db        464 --------CACAATAC--------TGGAAGTG------ACTGCGGCA--
GATGATGTCCC 429

Qy       2509 GAATAGTCATCACGGGGGATGCAGACATTGACCATGACCAGGC-GCT-
GGCTCAGGCAAT 2566
                  || |  ||  | ||||   |  |  || |||  || ||  ||||| |||  || ||  ||
|
Db        428 GTAGGATCTCCACGG----TCCGGCCTTT---CAG---
CAGGCAGCTCAGCACAAACACT 379

Qy       2567 TAAAGAGGCCAAAGAGCAGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGA 2626
                             |||  | || || |        |  |  || |         |||||
Db        378 -------GCC-TTGGGCTGCT--------------TGGC-----------
TCCA------ 358

Qy       2627 GACAGAGATCACACCAGAAGATGGAGAGGATTGACCAGAGGAATAACTTAGCTTGCACAT 2686
                             |||||         ||||  |  ||           ||| | ||
Db        357 ----------CCACCA-------------ATTG--CGTCGG---------
GCTCGAAC-- 334

Qy       2687 GAATGCAGTCATGCAAACCGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCTTCTAAC 2746
                         || |||      ||   || |||  |
Db        333 --------TCTCGCAG---GT---
GACAGTCAGGGCC----------------------C 310

Qy       2747 CCAACTGTACTTGTATCTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCAT 2806
                     || || |                ||            ||||| |||  |    | || |
Db        309 CCCACCG-------------CC--------------TCCAGGAGACGGG---
TGGATCC- 281

Qy       2807 TAATAAAGACACTGGCAGAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTA 2866
                             ||||          |||     |  ||| ||      || ||
Db        280 --------------GCAG---------CCCC----AGTGCAGGCT--
CTCGGC------- 257

Qy       2867 AACCGATAATGCATGAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACA 2926
                             ||| |||  | |             ||    | |
||||
Db        256 ----------GCAGGCGGCGTC----------CAGGTAAAC---------------
CACA 232

Qy       2927 AAATGTCTCAGTTT--
TCAGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGT 2984
                             || |||| |||  |||| |||||||||      ||| | |         |
|||
Db        231 GCCCGTTTCACTTTGGCCAGC---ACCTGCTC--------CCATCCTTG-----
CTGGGT 188

Qy       2985 CTCATGTAACACATAAACAATTCATGCCTTTCATAGTTTATTATTATTAAAGTCTAAACA 3044
                       |   ||| ||  |   | | |    |||| | |   |||
Db        187 ---AAAGGACA-GTACGCC---
CGAGGCGCTCATGGTTGGGGATTC-------------- 149
```

```
Qy      3045
AAATTGCAATTTCTTAGGTAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCT 3104
                 |||   ||| || |||       ||| | | ||  | | | ||| |
 ||
Db       148 -----GCAG--ACTTGGGAAAC--------TACGGTGCAGGA--ACTTCTTTCAGA-
ACT 107

Qy      3105
AGAAGCTGTCTAGGTCCGTCCGGTGTGTCAGATTTCCTCAGATTAGATGTGCCAATAACC 3164
                 |||        ||||| | |     ||| |    | || || |
 ||
Db       106 CACCGCT-----------TCCGGAAATTGGG-----
CTCCGGGAGACTTTGACAGTCTCC 63

Qy      3165 A-AGTTTATTCAGTAAACAACTTGTACTTG----
TTTCATCTGGTTTATTACTCTCACCC 3219
                 | ||| |  ||||| | |   || || |     ||| | | |||
Db        62
ACAGTACACCCAGTAGGCCAACAGTGCTCGAGGAATTCCGCAGCTTT------------- 16

Qy      3220 ATAAACAGTAATGAC 3234
                 | ||| | | ||
Db        15 TAGAGCAGAAGTAAC 1


RESULT 7
US-10-478-914-20/c
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match            28.4%;  Score 5535.5;  DB 1;  Length 2495;
  Best Local Similarity   42.5%;  Pred. No. 0;
  Matches 1399;  Conservative   0;  Mismatches  988;  Indels  905;
Gaps  191;

Qy         1
GCGGCGCGCCCGAGCCTAGTCCCCACGCCGCGGCGCGCGCCCGGGCTCCCTGCTGATCCCAG 60
           |||||   | ||| |||       || ||  || || |  |   ||| |  |
Db      2492 GCGGC---CGCGA-CCT---------GCAGC-
TCGAGCACATGTGGCCTTTTTTTT---- 2451
```

```
Qy          61 AACAATCAACCATG--
ACGACCGAATCTGGATCAGACTCGGAATCCAAGCCGGACCAGGA 118
               |    ||||   ||| |||||  |    |    | ||||
|
Db        2450 TTTTTTTTTTACATGTTTAAATATATTTTATTTCAAGTTAATATAAC-
AGCC--------A 2400

Qy         119 GGCCGAGCCCCAGGAGGCGGCGGGGGCGCAGGGGCGGCGGGGGCCGTGCCGGAGCCGCCC 178
                  |    |   |    |  |    ||   ||   ||    || ||||  |    |
|
Db        2399 TGATTTGTTCATTTAAGT----GAAATGCT---TCGATAAAAACC---CCGGTGT--
CAC 2352

Qy         179 AAGGAGGAGCAGCAGCAGGCCCTGGAGCAGTT-
CGCCGCCGCTGCAGCGCACAGCACCCC 237
                  ||    |    | ||  |    ||| |||  |  | ||        ||
|
Db        2351 TTGGTTAAAATATTGGAGACAGATTAAATGTTAAGCCACTATAGTAGTG------
ACTCT 2298

Qy         238 GGTGCGAGGGAGGTCACTGACAAGGAACAGGAGTTTG--
CTGCCAGGGCTGCAAAACAGC 295
                 |||   ||   || | |  || | | |  || ||  |||| | ||||
Db        2297 GGTTCTTTAGA---CTATTGCATGTACCTTGTTAATGAACT-
ACAGGAATGCACA----- 2247

Qy         296 TCGAATATCAGCAATTAGAAGACGATAAACTTTCTCAGAAATCATCTAGCAGTAAACTCT 355
                | ||    ||| |  |  | | | |  ||||  |    |
||
Db        2246 TTGATATAATGCA---CAATGTC-TTCACATGTCTC---AATCCTCATTC--------
CT 2202

Qy         356 CTCGGTCTCCATTAAAGATTGTCAAAAAGCCTAAAAGCATGCAGTG--
CAAAGTGATACT 413
                ||   ||| || | |   || || || | ||||    ||| | |
|||
Db        2201 CT-----TCCTTTCATGCCT---------CCCTAATGCCT-
CAGTATCCAATATAAAACT 2157

Qy         414 TCTCGATGGATCAGAATATACCTGTGATGTAGAGAAACGCTCCAGAGGACAAGTGCTGTT 473
                |                    |||  ||  | |            || ||
||
Db        2156 AC------------------------------AAAAACTAC--------
TGTTCTTTT 2137

Qy         474 TGATAAAGTGTGTGAACACTTGAACTTGCTAGAGAAAGACTACTTTGGGCTTACGTATCG 533
                | |  |||| ||    | || || | |     | | || ||    || |
Db        2136 CGTTTGAGTG-GTATTTAATTAAAACTTC---------
AATTCTATGTTATTTC------ 2093

Qy         534 AGATAGCTGAAAACCAGAAGAAGAATTGGTTGGACCCTGCTAAGGAAATAAAAAAAACAGGTTCG 593
                | |    |||| ||| || |    | | || | | |||    ||
|
Db        2092 ---CACAG---TCCAGTA-ATTTATTTTAAATTTG--
```

```
AGTAATTTCAAATTCCACAAACA 2042


Qy          594 AAG-
TGGTGCTTGGCACTTTTCATTTAATGTGAAATTTTATCCACCAGACCCTGCCCAAC 652
                || || |   ||| |    |||| | |||| ||| | ||  |    || ||    ||
Db         2041 AAACTGAAGAACAGCAAT----ATTTTGTTTGAATTTCTCTCTTCTGTACACT---
CAGT 1989


Qy          653
TATCTGAAGATATCACCAGGTACTACCTCTGCTTGCAGTTGCGAGATGACATCGTGTCCG 712
                 |||| || | ||| |  | | | | |    |    |   | |||| | |  | ||
|
Db         1988 GATCT-AAAACACCACAATATCCAACATACACAAACC--
TCAGGGAAGGGTTAGTAAAC- 1933


Qy          713 GAAGGCTGCCCTGCTCCTTTGTTACCCTGGC-CTTGCTGGGCTCCT-----
ACACTGTC- 765
                | | |  ||| | ||| || ||  || ||| |||||   |
|||
Db         1932 --------ACACACAAGATTGGAATCATGGTGCT--
CTTTGCTCCTGAATGGAATGGTCC 1883


Qy          766 --CAGTCAGAGCTCGGAGACTATGACCCAGATGAATGTGGG-AGCGATTACAT---
TAGT 819
                |||  | ||| |  || |   |  ||      || ||| | | ||||||
|||
Db         1882 CACAGAAAAAGCAC--AGGATACAGCACA---
ACATAAGGGCACCTGTTACATATGAAGT 1828


Qy          820 GAGTTCCGCTTTGCACCAAACCACACTA--
AAGAACTGGAAGACAAAGTGATCGAGCTGC 877
                |||            |||| || ||||  |    || | | || | ||    | |
|
Db         1827 GAG-------------CAAAACATACTAGCATTTTCTATATG-CATAATG---
GGGAAAC 1785


Qy          878
ACAAGAGCCACAGAGGAATGACGCCAGCAGAAGCAGAGATGCATTTCTTGGAAAATGCC- 936
                |  || ||| || |          || | | |        || | | | | || | || ||
|
Db         1784 -------
CTGCATAGGTTAGAGGGCCTTTTACGCTCATTTAAAAATCAGGCAAGTTGTCT 1732


Qy          937 -
AAAAAATTATCAATGTATGGGGTAGATTTACATCATGCTAAGGACTCAGAAGGGGTAGA 995
                || | || |||||    ||| ||    | || ||    | | |||
||
Db         1731 GTAACATTTTTCAATAATCTGGGAAGCACTGCA--ATCCAGTGTAC------------
GA 1686


Qy          996
AATTATGTTAGGAGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAA 1055
                | | || | ||||          ||| ||| |   |    | |  |||
|
Db         1685 TGTGCTGATTAGTGTT----------GTCT-TTGTT-------GGC--
ACTG-------A 1653


Qy         1056 CAGATTTGCCTGG-C-----CCAAGGTT----
CTAAAGATTTCATACAAACGGAACAACT 1105
                ||| |||| ||| |    ||| |||   || | ||| |  |   |    |||
```

```
               |
Db        1652
CAGTCTTGCATGGTCATATGCCAGTGTTTTTGCTTTAGCTTTTCTTTGAATAAAACAGAT 1593


Qy        1106 TT---
TACATTAAGATCCGGCCGGGAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTA 1162
               ||    |  |||| ||| |    ||           ||||| ||||
|||||
Db        1592 TTAAATGCATTTAGA-CAATACG------------TATTTGTAAGCT------- 
GTTTA 1554


Qy        1163
AGCTGCCAAACCATCGAGCTGCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACAT 1222
               || ||  |  | |     ||| | |      |  ||| | ||| || |
|
Db        1553 ------CATACACTAAATTT---AAGAGATT-----CAATAT---
TAGAGTTTCTTTGTT 1511


Qy        1223
TTTTCAGACTACTGTTACCAGAAGCACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGT 1282
               | || | ||| ||   |||   |||  |  | |   ||| |||
||
Db        1510 TCTTTAAAC-AC---TACAGAGTGCAAAT--CAGGTTCTTCACAAC-----------
AGA 1468


Qy        1283
TTCGTTATAGTGGCAGGACACAAGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCC 1342
               ||   ||| |  |||| |   |           ||||   || | | || | |
|||
Db        1467 TTGAATATTG-AGCAGTTCTTTA-----------
AAGAAAGAGGGGGAAGAAAAAAGCC 1420


Qy        1343 CA---
GCACCTTACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCGCAGCTTGG 1399
               || | |   || ||||| |    |  |||   || | |
||
Db        1419 CAAGTGAATAAAACATTGAA-ACTATTCC--CCTTCGAAAATAAAT--------
TCTAAA 1371


Qy        1400
ATGGAGCATCAGTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAG 1459
               |||  |    ||||| |  | |    | |||| | | | |  || | |
|
Db        1370 ATGATGTG-----GAATGTGAAATAAGGTTTTAACAT-AGGTGATCCAAGTTT-----
AT 1322


Qy        1460 AGGTTGGTACTGGC--CAGTACGCCAC-
AACAAAAGGCATCTCTCAGACCAACTTG---- 1512
               || | |  ||   ||    ||| |  || ||||| |   ||| ||  |||
Db        1321 AGTTAGAAACAAAAAGAAGTCCTTCATGAAATAAAGGTTAC---
AAGAACACGTTGCCTG 1265


Qy        1513 -ATCACCACTGTGACTCCGGAGAAGAAGGCTGAGGAGGAG---CGGGACGAGGA-
AGAGG 1567
                |  || |  |     | |||||| || ||   || |   | | |||| | ||
                |
Db        1264
TTTTCCCCCATTATAAACTGAGAAGTGGGTAAAGACGATGTTTCAGTACGAAAATAGGTG 1205


Qy        1568 ACAAACGGAGGAAGGGGGAAGAAGTCA-CGC-
CCATCTCGGCCATCCAGCACGAGGGAAA 1625
```

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                    || |  |||                   ||| |||  ||||||  ||| | | ||
|||
Db      1204 ACTACAGGA---------------TCAGCGCTTCATCTC--ACATGCTGTACCC---
AAA 1165

Qy      1626 GACTGACAGTGAGCGCACGGACACCGCAGCCG-
ACGGGGAGACCACTGCCACTGAGGAGC 1684
             | | | | |||     | | |   | |  ||| |  |||| |   ||| |  |||
||
Db      1164 GCCAGGCTGTG-----GCTGTCCATACGGTGGTGCGGTATAACCATAACCA-
AAAGGTGC 1111

Qy      1685
TAGAAAAAACTCAAGATGACCTGATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAA 1744
                        ||  || | | |              ||||| |     ||| |
Db      1110 ---------CTGGGGAGGGACGG--------------CAACA--------CTG----
GGT 1086

Qy      1745 CCTTCTTAGAAACCTCAACAGACACTG-CCGTAACGAATGAAT--
GGGAGAAGAGGCT-- 1799
             ||| || |   | | |||||  ||| ||| ||||  |   |     |  |||
Db      1085 CCTGC-
TGTCAGCATCAACTGGGGCTGACCATAAACAATGGGTTGTGTCTCTGTAGCTTG 1027

Qy      1800 TTCCACCTC----CCCCGTGCGACTG--
GCCGCCAGGCAGGAGGATGCCCCCATGATC-- 1851
             ||| | ||   | | ||| ||| || ||| |||| |   |      || || |  ||
Db      1026 TTCTTCTTCTTTTCTCAGTGATTCTGAAGCATCTA------
ATTTATCCACCTTTGTCAA 973

Qy      1852 GAACCACT---
TGTCCCTGAAGAGAAAATGGAAACCAAGACGGAGTCCAGTGGATAGAGA 1908
             | || ||  || || ||| | | |||| |  | | | |||| | ||
|
Db       972 GTACTCCTTCATGACCTGGATGA-AATAGGG----
CATGGCAAAATCCATGATATTGTG- 919

Qy      1909 CGGAACCCACCGTGCACCACCT-----GCCGCTTAGCACTGAGAAGGTGGT-
GCAGGAGA 1962
                     || || ||||      ||       | |    | || || | ||| | ||  ||||
|
Db       918 ------CCTCCATGCAGTTTCTAGGACGACATCTGGC-
CTTAAAAGATCGTAACAGGTAA 866

Qy      1963 CCGTGTTGGTGGAGGAGCGGCGTGTGGTGCACGCGAGTGGGGATGCTTCTTACT--
CGGC 2020
             |        ||   || ||| |       |||| |      ||| || ||  |
||
Db       865 AC--------AGACAAGCTCC----AAAGCACTC----------
TCTTTTTTCTTCCTGC 828

Qy      2021 GGGAG--
ACAGCGGGGATGCTGCAGCACAGCCCGCATTCACAGGCATTAAAGGGAAAGAG 2078
             |   ||  || || ||  | |  ||||   |   |||||   | ||  ||
|||
Db       827 AAAAACCACTGCAGGAGTTCTTCAGC-CA------ATTCAGTATCTTT--
AGATTCAGAA 777

Qy      2079 GGCT-
CTGCTTGACGGAGGGGGCTAAAGAGGAAGGAGGGGAGGAGGTCGCTAAAGCTGTC 2137
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                   |   |  | | | |  |    |          | |                            |  | |
                   | | | | | |
Db        776 GCATACTGCATTGCATC-----CTT-----------------------
GTAAAGGCTGTC 745

Qy      2138 ---CTGGAACAGGAAGAGACAGC-CGCTGCTTCCCGTGA--
GCGACAAGAGGAGCAGAGT 2191
                   | | | | | | |        |   |  | | | | | | | | |  | | |   |    |      |  | |
Db        744 TTTCTTGCACAG-----
CTCTACACTCTGTTTCCAGCGATTGTTGCCTTTGAAGAGATAA 690

Qy      2192
GCAGCCATCCACATTTCAGAAACTTTGGAACAAAAACCTCATTTTGAGTCCTCAACGGTG 2251
                   | | | | | | | |  | | | |     | | | |         | | |   |   | | | |  | |    | | |    | | | |
                   | |
Db        689 GCAGCAATTCTCCT-----GAACT------CAATGAGTTCATGTT-TTTCC-
AAACGCTG 643

Qy      2252 AAGACGGAAACCATCAGTTTTGGCAGTGTT-
TCACCGGGAGGAGTAAAGCTAGAAATTTC 2310
                   |   | | | |   | | | | | |  | | |  | | |   |          |    | | | |   | |
                   |
Db        642 A----GCAAGCGA--GATATTGTCAAAGTTGTCATAAG--------
CATCTATTGATGTT 597

Qy      2311 CACAAGAAGTGCCAGTAGTTC--
ACACCGAAACCAAAACCATCACATATGAATCATCACA 2368
                   |  |    | |  | | |  |       | |     |  | | |  | | | |           | | |   | | |
Db        596 CGC----AGAGCCTGATAATCTTCTTCGTGTAATAAAAA-----------
GATTGTTCAAT 552

Qy      2369 GGTCGATCCAGGCACAGATCTGGAGCCAGGCGTGCTGA--
TGAGTGCACAGACGATCACA 2426
                   | | |  | |  | | | | | | |  | |   |   | | | | | | |   | | |   | | | | | | |  |
Db        551 ----GATTCATTCACAGATTTGTTGTTATG-
GTTCTGAACTGAACGCAAATACGGT---- 501

Qy      2427
TCTGAAACCACCAGTACCACCACCACTACCCACATCACCAAAACTGTGAAAGGGGGCATT 2486
                   | | | | | | |                           |  | | | |   | |      |
                   | |
Db        500 ------TTCACCAGTG-----------------------GTAGCTGTTTAA-----
CCTT 475

Qy      2487
TCAGAGACAAGAATTGAGAAGCGAATAGTCATCACGGGGGATGCAGACATTGACCATGAC 2546
                   |  | |   | |  | | | | | |          |    | | | |  |
                   | | |
Db        474 GCTGA---AATAATTGA------------CTGCACGAGTG----------------
TGAT 446

Qy      2547 CAGGCGCTGGCTCAGGCAATTAAAGAGGCCAAAGAG-CAGCACCCTGA-
CATGTCAGTGA 2604
                   |                 | | |           | |    | | | | | | | | |  | | | |   | | |  |
                   |
Db        445 C--------------CAA---------
CCGTGGAGACAGCACCATCAGCAATCATTTA 410

Qy      2605 CCAAAGTAGTGGTCCATAAAGAGAC-
AGAGATCACACCAGAAGATGGAGAGGATTGACCA 2663
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                  ||                | | | | |  |  | |  | |         | | |  | |  |  | | | |
                                                                                        |
Db        409 ACA--------------ACAGAGGCTTGAATTCT------
AAGTAGAACTGTATTGCTCT 370


Qy       2664
GAGGAATAACTTAGCTTGCACATGAATGCAGTCATGCAAACCGTTAGGAAAACCAGAGCC 2723
                   |  | |||      || |||   | ||  |        || | | | | |
Db        369 GTAGTATAG------TTCCACAT--TGGCAACCTTG------
GTAATGATATC------- 331


Qy       2724 TATATGGAGTTCCCTCTTCTAACCCAACTGTACTTGTATCTGTC--
CGTGGAAAATTT-- 2779
              | || ||| ||| |      |||| ||  |     |  | | ||  | | || | || |  |
Db        330 --TTTGAATTGCC--
CTTCTTTCCAGGCATCAGTTGGATGATTCATCATGGTAATTATGG 275


Qy       2780 CAGTC-
CAGAAGAATTGACCTTGACCATTAATAAAGACACTGGCAGAGAGATCTTCCCAT 2838
              || |  || |     |      |||| |      | |||  ||||      |      || |||
                                                                           ||||
Db        274 CATTATCATATTCTTCATACTTGTC---ATACAAAAACAC---C----
AGTTCTGCCCAA 225


Qy       2839
AATAAAGCAATCTGATTCAGCATCACTAAACCGATAATGCATGAAGCAACGATAAAATTA 2898
                 |    ||    ||  ||| ||| |  || | |
Db        224 AGATGAG----
CTTGTTCTGCAGCTCTTAGC----------------------------- 198


Qy       2899
CAAAAGAGCAGCATTTTTAATTTTCACAAAATGTCTCAGTTTTCAGCTATACCTGCTCGT 2958
                                 | ||  ||| ||||||            ||| ||| |
Db        197 ----------ACCTTGGGAATATTCACT-------------------
CTAGACCAG----- 171


Qy       2959
TCATAACCAACAATATAAACCGTGGTCTCATGTAACACATAAACAATTCATGCCTTTCAT 3018
              | ||| |      ||| |    |       ||  |            ||||
Db        170 -----AACAGC-------TCCAGGTGCTC-----CCTCAT--------------
TTTCTG 142


Qy       3019
AGTTTATTATTATTAAAGTCTAAACAAAATTGCAATTTCTTAGGTAACCTTATATTTACA 3078
              ||    |||   ||| |||  |        | ||| ||| |   |||| |      ||
                                                                           |
Db        141 AG--GCTTAAATTTAGAGTAT----AGAATAGCTAATTC---AGTAAAC-----
ATTCCC 96


Qy       3079 ATAAATGAAGATTACCCTCAAATGCTAGAAGCTGTCTAGGTCCGTCC-
GGTGTGTCAGAT 3137
              ||         ||    | ||||| |   | ||   ||| |   |||| ||||
Db        95 AT-----GTGAGCTCGCTCAAGTCCCAG-TGCTG-CT---TCCAACATGGTG-
ATCAGC- 48


Qy       3138 TTCCTCAGATTAGATGTGCCAATAACCAAGTT-TATTCAGTAAACAACTTGT 3188
              || |||| |||  |    |||| ||  |  || |  |   ||||| | |   || 
Db        47 -TCTTCAAAATA-----GCCACGATCCTGATAGTAGCCAGTAGGCCAACAGT 2
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RESULT 8
US-10-478-914-64
; Sequence 64, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 2120
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-64

  Query Match             28.1%;  Score 5468.5;  DB 1;  Length 2120;
  Best Local Similarity   41.6%;  Pred. No. 0;
  Matches 1334;  Conservative   0;  Mismatches  710;  Indels 1161;
Gaps  198;

Qy         3 GGCGCGCCCGAGCCTAGTCCCCACGCCGCGGCGCGCC-
CGGGCTCCCTGCTGATCCCAGA 61
             |||  |  || |    ||  |  |  |  |     ||  |||  | |||        |
||
Db         3 GGCCTGTACG-GAAGTGTTACTTCTGCTCTAAAAGCTGCGGAATTCCT-------
CGAGC 54

Qy        62 ACAATCAACCATGACGACCGAA--
TCTGGATCAGACTCGGAATCCAAGCCGGACCAGGAG 119
             || |  ||     || | |  ||| |  || | |||    |  |||
Db        55 ACTGTTGGCCT-----ACTGGAGTGCTGAAGTAGGCGCGGA---
CGTGCC---------- 96

Qy       120
GCCGAGCCCCAGGAGGCGGCGGGGGCGCAGGGGCGGCGGGGGCCGTGCCGGAGCCGCCCA 179
               |  |  |||     ||| ||| || ||||| ||  ||| | ||  ||||| |  |
|||
Db        97 -CGGTGCC-----TGGC-GCGTGGTAGCAGGCGC-
CCGGTGCCCCGGCCGGCGAAGACCA 148

Qy       180 AGGAGGAGCAGCAGCAGGCCCTGGAGCAGTTCGCCGCC-
GCTGCAGCGCACAGCACCCC- 237
               || |      |  |  || || ||| |       ||  ||| |||| ||  |     | | |
Db       149 TGGCGTTCATGGTGAAGACCATGGTG-----GGCGGCCAGCTGAAGAAC----
CTCACTG 199

Qy       238
GGTGCGAGGGAGGTCACTGACAAGGAACAGGAGTTTGCTGCCAGGGCTGCAAAACAGCTC 297
             || ||  |||||||    | | |||| |||   ||  |  || | | | |     ||||
|
Db       200 GGAGCCTGGGAGG----CGGCGAGGATAAGGGAGATGGGGACAAGTCGG-----
```

```
CAGC-C 249


Qy        298
GAATATCAGCAATTAGAAGACGATAAACTTTCTCAGAAATCATCTAGCAGTAAACTCTCT 357
              ||| ||||        | | |||  |    | |        || ||||
Db        250 GAAGCTCAG---------GGC-ATGAGC-----CGGG--------
AGGAGTA-------- 278


Qy        358
CGGTCTCCATTAAAGATTGTCAAAAAGCCTAAAAGCATGCAGTGCAAAGTGATACTTCTC 417
              ||          | ||| ||          | |||||   ||| ||| ||
Db        279 CG----------AGGAGTATC---------AGAAGCAACTCGTG-
GAAGAGA-------A 311


Qy        418
GATGGATCAGAATATACCTGTGATGTAGAGAAACGCTCCAGAGGACAAGTGCTGTTTGAT 477
              |||||| | || ||    | |  |||| ||           || || |    |
Db        312 GATGGAGCGGGATGCACAGTTCACACAGAGGAAGGC-----------AGAGCGG---
GCC 357


Qy           478 AAAGTGTGTGAACACTTGAACTTGCTAGAGAAAGACTACTTTGGGCTTAC--
GTATCGAG 535
               | | || || |       |||| | ||| ||| ||  |    |||| |     |
||||
Db           358 ACACTGCG-GAGC-----CACTTCCGAGACAAATAC--C----
GGCTACCCAAGAACGAG 405


Qy           536 A-TGCTGAAAACCAGAAGAATTGGTTGGACCCTGCTAAGGAAATAAAAAAACAGGT-
TCG 593
               |   |  ||| |  |||||        || |   ||             |||||
|
Db           406 ACAGATGAGAGCCAGAT-------------CCAGAT--GG-----------
CAGGTGGAG 439


Qy           594
AAGTGGTGCTTGGCACTTTTCATTTAATGTGAAATTTTATCCACCAGACCCTGCCCAACT 653
               | |||| |||                               || | || |  ||| |
|
Db           440 ACGTGGAGCT------------------------------
GCCCCGGGAGCTGGCCAAGAT 470


Qy           654
ATCTGAAGATATCACCAGGTACTACCTCTGCTTGCAGTTGCGAGATGACATCGTGTCC-- 711
               ||| || ||| | |         | || |||| | | |||| | || | ||  ||||
Db           471 GATCGAGGAGGACACAGAGGA------------GGAGGAG-GAGAAGGCCTC-
AGTCCTT 516


Qy           712 GGAAGGCTGCCCTGCTCCTTTGTTACCCTGGCCTTG---CTGGGCTC-CT-----
ACACT 762
               || |||| || |  |||       ||||| ||||  ||||||||| ||     |||
Db           517 GGGCAGCTGGCCAG--CCTT------CCTGG-
CTTGAACCTGGGCTCACTCAAGGACAAG 567


Qy           763 GTCCAGTCAGAGCTCGGAGA-CTATGACC--
CAGATGAATGTGGGAGCGATTACATTA-G 818
               | ||||  || ||| |||    |   ||| |||   | | | | | ||
|
Db           568 GCCCAGGCCACACTGGGGGATCTCAAGCAATCAGCTGA-----GAAGTG-
TCACGTCATG 621
```

```
Qy        819 TGAGTTCCGCTTTGCACC----
AAACCACACTAAAGAACTGGAAGACAAAGTGATCGAGC 874
              |||  || ||| | ||     ||| |||||   |  |||| | |    ||| |
              ||
Db        622 TGA---CCACTT--CCCCGGGGTTACC-CACT---GGGCTGG--GCCCCCATGA--
GGGC 668


Qy        875
TGCACAAGAGCCACAGAGGAATGACGCCAGCAGAAGCAGAGATGCATTTCTTGGAAAATG 934
              |   |||||        | || ||        |  ||| || |   ||| || | | |
Db        669 T----AAGA---------GTGTGTCAACTTC-----CAGGGACCCA-
TACT--------- 700


Qy        935 CCAAAAAATTATCAATGTATGGGG-
TAGATTTACATCATGCTAAGGACTCAGAAGGGGTA 993
              |||           |  ||||| |  ||| | | |||      | ||
Db        701 CCA--------------TTTGGGGCTTTGTTTCC--CTTGC------
CCCA--------- 729


Qy        994
GAAATTATGTTAGGAGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATA 1053
                                   ||||| ||    ||| | |   |     | ||     |||
Db        730 --------------------TCCTAGT--TCC-AAGACCTTTCCCATCC--
ATGC----- 759


Qy        1054
AACAGATTTGCCTGGCCCAAGGTTCTAAAGATTTCATACAAACGGAACAACTTTTACATT 1113
                |        ||  ||| |   |||   |  | |||| | |
Db        760 --C-------CCAAGCCTA----
TCTTCTGGTTTCTTCCT-------------------- 786


Qy        1114
AAGATCCGGCCGGGAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCCAAAC 1173
              ||| || |||||            | || ||||     || | ||  |
              |
Db        787 ---CTCC-GCTGGGAG-------------TAAAGTCCCCATC---
TTCACTCTAC----C 822


Qy        1174 CATCGGAG---
CTGCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTTTTCAGA 1230
              | | |  |      | ||        |  | |||| | || ||    || |
              ||
Db        823 CTTCAGGACCCTCCCCACC-----AGCTCAGCCTGTGGAG-
GCCTCCCAAGATTGTAGGA 876


Qy        1231
CTACTGTTACCAGAAGCACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGTTTCGTTAT 1290
              |              | || |||| |  ||| || || ||  |||||| |||
Db        877 AT-----------AGGCCCATCCC------TCTCTGGCCAT-GGCCCCAAG-
TTC----- 912


Qy        1291
AGTGGCAGGACACAAGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCACCT 1350
              | | ||||| | ||| |    |||| ||              | | ||
Db        913 -----CTGCACACAGGAGCACCCACAGAGAGACA--------------
CACACA------ 947


Qy        1351
TACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCGCAGCTTGGATGGAGCATCA 1410
              | || | | |                || || | ||
```

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|||
Db        948 ------GGACACAAAAC--------------CCCTGGCACG---------------
TTCA 972


Qy       1411
GTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAGAGGTTGGTACT 1470
              | || ||| |  || ||| |                   | |||
Db        973 GAGACAGAAGCCACAGACACATCC-------------------
CGGCA------------ 1001


Qy       1471
GGCCAGTACGCCACAACAAAAGGCATCTCTCAGACCAACTTGATCACCACTGTGACTCCG 1530
               |||   | ||| |||  ||||       |||
||||
Db       1002 ---CAGACAGACAC-ACACGAGGC------CAG----------------------
CTCC- 1028


Qy       1531
GAGAAGAAGGCTGAGGAGGAGCGGGACGAGGAAGAGGACAAACGGAGGAAGGGGGAAGAA 1590
                           ||       |||
Db       1029 ----------CT-------
TGCG----------------------------------T 1035


Qy       1591 GTCACGCCCATCTCGGCCATCCAGCACGAGGGAAAGACTGACAGTGAGC--
GCACGGACA 1648
               |||  |||| || | | || ||| |||    ||||  |||| || |||| | |
||||
Db       1036 GTCCAGCCCCTC-CAGACA-CCACCACTC-
AGAAACTCTGAGAGAGAGCATGGGCAGACA 1092


Qy       1649 -
CCGCAGCCGACGGGGAGACCACTGCCACTGAGGAGCTAGAAAAAACTCAAGATGACCTG 1707
              || |||| ||| |||| ||          ||| |                        ||
|
Db       1093 CCCTCAGCAGAC-AGGAGGCCT-----------GAGTT------------------
CCAG 1122


Qy       1708
ATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAACCTTCTTAGAAACCTCAACAGAC 1767
                            || ||| ||| || |||| ||| | ||||  ||| |       ||| |
||
Db       1123 --------TC--TCCACCTTTATTGTTCTTGAAAGCCCCTGCT-------CTC-
TCTGA- 1163


Qy       1768
ACTGCCGTAACGAATGAATGGGAGAAGAGGCTTTCCACCTCCCCCGTGCGACTGGCCGCC 1827
               ||| ||                        |||| | ||       || |
Db       1164 ---GCCTTA----------------------TTTCATCATC-----
TGTAA--------- 1184


Qy       1828
AGGCAGGAGGATGCCCCCATGATCGAACCACTTGTCCCTGAAGAGAAAATGGAAACCAAG 1887
               | | ||| ||   ||| |    ||||                               |
|||
Db       1185 ---AATGGGAATGTCC---TGAATG----ACTT----------------------
CTAAG 1212


Qy       1888 ACGGAGTCCAGTGGATAGA---
GACGGAACCCACCGTGCACCACCTGCCGCTTAGCACTG 1944
                 |     ||  ||| ||| | ||   | | || ||| |     |||| | || |
```

```
   ||
Db       1213 GCTCTTTC---TGGCTTGAACTGTCAGAGCCAAGC-----CCACATCCCTC------
CT- 1257


Qy       1945
AGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGGCGTGTGGTGCACGCGAGTGGGG 2004
                  ||| |||||                    | ||| ||     |||
Db       1258 ------TGG-GCAGG----------------GCAGCAGC------
TGC----------- 1276


Qy       2005
ATGCTTCTTACTCGGCGGGAGACAGCGGGGATGCTGCAGCACAGCCCGCATTCACAGGCA 2064
                  ||| |  ||| ||       ||||| |||||          |||
Db       1277 -TGCCACAGCCTC---------CAGCG-----GCTGC---------------
CAC----- 1301


Qy       2065 TTAAAGGGAAAGAGGGCTCTGCTTGACGGAG-
GGGGCTAAAGAGGAAGGAGGGGAGGAGG 2123
                          | |||||||| | ||||| | |||     |  ||| ||
 |||
Db       1302 ----------TGTGGGCTCTGGGAGCCGGAGCGATGCT------
GTGTGAGAGGCAGAGT 1345


Qy       2124 TC----
GCTAAAGCTGTCCTGGAACAGGAAGAGACAGCCGCTGCTTCCCGTGAGCGACAA 2179
                  |   | | |||||| |  ||||| ||| | | | ||  || || | |
Db       1346 GCCAAGGATGAAGCTGGCACTGAACAGTAAGCGGCTCCAG--GCCTCCTCTGGGC--
C-- 1399


Qy       2180
GAGGAGCAGAGTGCAGCCATCCACATTTCAGAAACTTTGGAACAAAAACCTCATTTTGAG 2239
                  ||| |  |||||  |   | ||| | || || ||    ||| | |
 ||
Db       1400 ------CAGGGCCCAGCCAATTTCTGTTCTGTTCCTGTAGAACG-----CTC-
TCTGGAT 1447


Qy       2240 TCCTCAACGGTGAAGACGGAAAC-
CATCAGTTTTGGCAGTGTTTCACCGGGAGGAGTAAA 2298
                  ||| | |         |||| | ||  | || | ||       ||      |||
 ||
Db       1448 TCCATAGC--------TGGAATCTCCTC--TCTTAGC------TC---------
AGTGAA 1482


Qy       2299
GCTAGAAATTTCCACAAGAAGTGCCAGTAGTTCACACCGAAACCAAAACCATCACATATG 2358
                  ||| ||| | || || |  |||||                    ||| || ||
Db       1483 AAATAAAAATCCCAAATGGTGTGCC--------------------
TACCTTCCCA---- 1517


Qy       2359
AATCATCACAGGTCGATCCAGGCACAGATCTGGAGCCAGGCGTGCTGATGAGTGCACAGA 2418
                  | ||         | | |||     ||||| || || |||| ||
 ||
Db       1518 ---CTTC--------TTACTGGCTT----------CCAGGAGTCTTG--
GAGTTCATAGC 1554


Qy       2419 CGATCACATCTGAAACC--ACCAGTACCACCACCACTACCCACAT-
CACCAAAACTG--T 2473
                  |   |   ||| ||  || | |    || |||| ||||| | || |   || |
Db       1555 CCCCCGAGCCTG---
```

```
CCTTAAAGGGGTGTCCTCCACCCCCCACCTACAGCTTCACAGGAG 1611


Qy      2474 GAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAAT-------
AGTCATCACGGG-- 2524
             |  || |||||| | ||| |  | || |  ||||| |  |        || || |||
Db      1612 GGGAGAGGGCA-TCCAGTGCTAGGAGT--
AGAAGTGTCTCCAGCTCTGTTCTCTTGGGGC 1668


Qy      2525 ---GGATGCAGACATTGACCATGAC-
CAGGCGCTGGCTCAGGCAATTAAAGAGGCCAAAG 2580
               || || ||   |  | ||| | |  | | || || |   || | |||| |
|
Db      1669 CCTGGGTGAAGGTGGGGTCTGGGGCTTATGAAATAGGTCTGGGCTTTGAGGAGG--
ATGG 1726


Qy      2581 AGCAGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAG--
ACAGAGATCAC 2638
             ||||||| | |   |||| |       ||| | ||| |   | | || ||||
|||
Db      1727 AGCAGCCTCAT--TATGTGGG-----
GAAGATGGGGCCTCTGGGGCGTCACTGAGACCAC 1779


Qy      2639
ACCAGAAGATGGAGAGGATTGACCAGAGGAATAACTTAGCTTGCACATGAATGCAGTCAT 2698
             |         | ||  || | ||  || |   || |   || | |||    || |||
|
Db      1780 A---------GGTGGGG-----CCGGGG------CTGGAC---CGCA-----
GCTGTCTT 1811


Qy      2699
GCAAACCGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCTTCTAACCCAACTGTACTT 2758
             |          || |  || | |||||     |  ||| || || ||||
Db      1812 G----------GG--TGCCTGTGCCT-------GCACCC-
CTCCTCACCC---------- 1841


Qy      2759
GTATCTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCATTAATAAAGACAC 2818
             | ||| |          | ||||| ||         || || |||||
Db      1842 G-----------TAGAGA---------CGGAAGATGTG--------
CAAAAAGAAAGA--- 1870


Qy      2819
TGGCAGAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTAAACCGATAATGC 2878
             || || | |            ||| ||      |||| |||
Db      1871 ----AGGAAGGGCAAC---------TGCATTC-----
CAGCCCCAC-------------- 1898


Qy      2879
ATGAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACAAAATGTCTCAGT 2938
             |  ||| | ||     |||| || |  | | ||| |                |||
Db      1899 -----ACTGTGATGACTTT------GAGCC-----TGTCCTTTCC---------
CTCC-- 1931


Qy      2939
TTTCAGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACACAT 2998
             || |||   | |||| || |   || | | ||| | | |
||
Db      1932 -TTGAGCCTGTCTTGCTTGTCC----CCTGTAAAATGAACAGT--
CCCCCTCTCCCCCAA 1984
```

```
Qy      2999 A----AACAATTCATGCCTTTCATA-GTTTATTATTATTAAAGTCTA-AACAAA--
ATTG 3050
             |   || ||| ||||  ||||| | | |  |||  ||||| || ||||| ||
Db      1985 ATAGTAATAATACATG--
TTTCAAAGGGTGACCATTTATAAAGCATATGACAAACCATAT 2042


Qy      3051 CAATTTCTTAGGTAAC-
CTTATATTTACAATAAATGAAGATTACCCTCAAATGCTAGAAG 3109
              ||||    |   ||||| | |  |||| || ||| || |    || || |||| |
||
Db      2043 CAATAAAT---GTAACTCATTCTTTTAAAAAAAAAAAAAAAAAGGCCACATGTGCTCG-
AG 2098


Qy      3110 CTGTCTAGGTC-CGTCCGGTGTGTC 3133
             |||  ||||| || ||| |  | |
Db      2099 CTG--CAGGTCGCGGCCGCT-AGAC 2120



RESULT 9
US-10-478-914-20
; Sequence 20, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
;   CURRENT FILING DATE:  2003-11-26
;   PRIOR APPLICATION NUMBER: PCT/JP02/05294
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-162775
;   PRIOR FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: JP 2001-255226
;   PRIOR FILING DATE: 2001-08-24
;   NUMBER OF SEQ ID NOS: 417
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 2495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-20

  Query Match             28.0%;  Score 5459;  DB 1;  Length 2495;
  Best Local Similarity   41.8%;  Pred. No. 0;
  Matches 1389;  Conservative   0;  Mismatches 1004;  Indels  930;
Gaps  170;

Qy        29 CGCGGCGCGCC--
CGGGCTCCCTGCTGATCCCAGAACAATCAACCATGACGACCGAATCT 86
               | |   |||  | |||| |  | |   | |   | |      | |   ||| || |
|||
Db         1 CACTGTTGGCCTACTGGCTACTATCAGGATCGTGG-----
CTATTTTGAAGAGCTGATC- 54

Qy        87
GGATCAGACTCGGAATCCAAGCCGGACCAGGAGGCCGAGCCCCAGGAGGCGGCGGGGGCG 146
               |    | ||||| |  | || | |||  ||||| |            |  |||
Db        55 ---ACCATGTTGGAAGCAGCACTGGGACTTGAG--CGAGCTC---------
ACATGGGAA 100
```

```
Qy        147 CAGGGGCGGCGGGGGCCGTGCCGGAGCC---------
GCCCAAGGAGGAGCAGCAGCAGG 197
                 | |      || | |   | |            ||| || |   |  | |||
Db        101
TGTTTACTGAATTAGCTATTCTATACTCTAAATTTAAGCCTCAGAAAATGAGGGAGCA-- 158


Qy        198 CCCTGGAGCAGTTCGCCGCCGCTGCAGCGCACAGCACCCCGGTGCGAGGGAGGTCACTGA 257
                 |||||||| |||                            | ||| | || |   | |
Db        159 -CCTGGAGCTGTT-------------------------CTGGT-
CTAGAGTGAATATTCC 191


Qy        258 CAAGGAACAGGAGTTTGCTGCCAGGGCTGCAAAAC-
AGCTCGAATATCAGCAATTAGAAG 316
                 |||||        ||||    || ||||| ||| |||||   | |  |||   |
Db        192 CAAGG----------TGCT--AAGAGCTGCAGAACAAGCTCATCTTTGGGCAG--
AACTG 237


Qy        317 ACGATAAACTTTCTCAGAAATCATCTAGCAGTAAACTCTCTCGGTCTCCATTAAAGATTG 376
                 | |    || |    | |||| ||| |||| | |  |       | |||| |    ||
Db        238 GTGTTTTTGTATGACAAGTATGAAGAATATGATAATGC-
CATAATTACCATGATGAATCA 296


Qy        377 TCAAA---AAGCCT--
AAAAGCATGCAGTGCAAAGTGATACTTCTCGATGGATCAGAATA 431
                 || ||   | |||| |||       ||| | ||||| || || | | |
Db        297 TCCAACTGATGCCTGGAAAGAAGGGCAATTCAAAGATATCATTACCAAGG---------T 347


Qy        432 TACCTGTGATGTAGAGAAACGCTCCAGAGGACAAGTGCTGTTTGATAAAGTGTGTGAACA 491
                 | ||     |||| || || ||| ||| ||||| | |   || |    | |
Db        348 TGCC---AATGTGGAACTATACTACAGAG--CAA-
TACAGTTCTACTTAGAATTCAAGCC 401


Qy        492 CTTGAACTTGCTAGAGAAAGACTACTTTGGGCTTACGTATCGAGATGCTGAAAACCAGAA 551
                 || | |||| ||    || || ||      | |    || |  | | | ||||||   |||
Db        402 TCTG---TTGTTA-------AATGATTT--GCTGA-------TGGTGCTG-
TCTCCA--- 438


Qy        552 GAATTGGTTGGACCCTGCTAAGGAAATAAAAAAACAGGTTCGAAGTGGTGCTTGGCACTT 611
                 |||||||| | || | |     | |||| |  |  || | |   ||| |   ||
Db        439 ----CGGTTGGATCACACTCGTGCAGTCAATTAT----TTCAGCAAGGT--
TAAACAGCT 488


Qy        612 TTCATTTAATGTGAAATTTTATCCAC--------CAGACCCTGCCCAAC-
TATCTGAAGA 662
                 || |  ||||||  ||| |         |||| ||   |||| |||||!
Db        489 ACCACT---
GGTGAAACCGTATTTGCGTTCAGTTCAGAACCATAACAACAAATCTGTGAA 545


Qy        663 TATCACCAGGTACTA-
CCTCTGCTTGCAGTTGCGAGATGACATCGTGTCCGGAAGGCTGC 721
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                    |      |     |  | || | | |   ||  | ||    |    | | | |          |   | |  ||
    Db        546  TGAATCATTGAACAATCTTTTTATTACAGAAG-AAGAT-------TATCAGGCT--
||||
CTGC 595

Qy        722  CCTGCTCCTTTGTTACCCTGGCCTTGCTGGGCTCCTACACTGTCCAG-----
TCAGAGCT 776
                      || | | | |    |  | |          ||   ||| | || |      |||| |
|
    Db        596  GAACATCAATAGATGCTTATGAC------
AACTTTGACAATATCTCGCTTGCTCAGCGTT 649


Qy        777  CGGAGACT-
ATGACCCAGATGAATGTGGGAGCGATTACATTAGTGAGTTCCGCTTTGCAC 835
                      ||| |   |||| |     ||| |    ||||          |  | ||||   |
|
    Db        650  TGGAAAAACATGAACTCATTGAGTTCAGGAG-------------
AATTGCTGCTTATCTC 696


Qy        836  --CAAA--
CCACACTAAAGAACTGGAAGACAAAGTGATCGAGCTGCACAAGAGCCACAGA 891
                       |||| | ||| |    ||||| | | ||||| | ||||||  |||||
    Db        697  TTCAAAGGCAACAAT----CGCTGGAA-ACAGAGTG-
TAGAGCTGTGCAAGA-------- 742


Qy        892  GGAATGACGCCAGCAGAAGCAGAGATGCATTTCTTGGAAAATGC--------
CAAAAAAT 943
                      |  | |||| |    ||  |||||| | |    |  ||||         |  |||
    Db        743  ------AAGACAGCCTTTACAAGGATGCAATGC----
AGTATGCTTCTGAATCTAAAGAT 792


Qy        944
TATCAATGTATGGGGTAGATTTACATCATGCTAAGGACTCAGAAGGGGTAGAAATTATGT 1003
                       |  || ||| ||| ||| |   | ||     || | | | |  || | | |||||   |
    Db        793  ----ACTGAATTGGCT-GAAGAAC-TCCTGCAGTGGTTTTTGCA--
GGAAGAAAAAAGAG 844


Qy        1004
TAGGAGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGATTTG 1063
                      |   || | ||   | |||||||| |    | |     |  |
||
    Db        845  AGTGCTTTGGAGC---TTGTCTGTTTACCTGTTACGATC-------------------
TTT 883


Qy        1064
CCTGGCCCAAGGTTCTAAAGATTTCATACAAACGGAACAACTTTTACATTAAGATCCGGC 1123
                      ||||         |||| || |                     |||   |
||
    Db        884  TAAGGCC-----------AGATGTCGTCC----------------------
TAGAAACTGC 911


Qy        1124
CGGGGAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCCAAACCATCGAGCTG 1183
                      ||||       | |||||  |       || |||  ||  |||||||  || |       |
    Db        912  ATGGAG-----GCACAATAT--------CA-TGGATTT----
TGCCATGCCCTATTTCAT 953


Qy        1184  CCAAGCGTTTATGGAAAGTATG----TGTTGAGCATCATACATTTTTCAGACT-
ACTGTT 1238
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                    | | |   |   |  | | | |        | |          |  | |      |       | |  | |   | | | | | | |  |  | | | |
Db        954
CCAGGTCATGAAGGAGTACTTGACAAAGGTGGATAAATTAGATGCTTCAGAATCACTGAG 1013

Qy       1239 ACCAGAAGC--
ACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGTTTCGTTATAGTGGC 1296
                 |  | | | | |   | |     | |     | | |   | | | |         |    |  | |      | | | | | |
|
Db       1014 AAAAGAAGAAGAACAAGCTACAGAGACACAACC-------CATTGT----
TTATGGT--C 1060

Qy       1297 AGGACACAAG----CGCAAACGAGAAGAGCCAGTGCGTTG--
ATAGATCGCCCAGCACCT 1350
                 | |  | | |         | |   | |    | | |  | | | | |   | | | |      |    | |  | |
| | | | | |
Db       1061 AG--CCCCAGTTGATGCTGACAGCAGGACCCAGT--
GTTGCCGTCCCTCCCCAGGCACCT 1116

Qy       1351
TACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCGCAGCTTGGATGGAGCATCA 1410
                     | | | |              |   |  | | | | | | |     | | | |    |      | | | |       | | |
| |
Db       1117 ---TTTG------------GTTATGGTTATACC--GCACCACCGTATGGAC--
AGCCACA 1157

Qy       1411
GTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAGAGGTTGGTACT 1470
                       |             | |   |                       | |  | |
| | | | |
Db       1158 G----------CCTGG------------------CTTTG---------------
GGTAC- 1173

Qy       1471
GGCCAGTACGCCACAACAAAAGGCATCTCTCAGACCAACTTGATCACCACTGTGACTCCG 1530
                     | |  | |   |  |     | | | | |                     |   | | | | |   | |   |
|
Db       1174 AGCATGTGAGATGAAGC-----GCTGATC-CTG-------
TAGTCACCTATTTTCGTACT 1220

Qy       1531
GAGAAGAAGGCTGAGGAGGAGCGGGACGAGGAAGAGGACAAACGGAGGAAGGGGGAAGAA 1590
                       | |  |        |  | |
Db       1221
GAAACATCGTCT------------------------------------------------ 1232

Qy       1591
GTCTCACGCCCATCTCGGCCATCCAGCACGAGGGAAAGACTGACAGTGAGCGCACGGACACC 1650
                       |  | | | |  | | | |     |   | |  | | | | | | | |  | | | | |    | |  |   | |
Db       1233 -TTACCCACTTCTCAG---TTTATAATGGGGGAAA--ACAGGCAACGTGTTCTTGTA-
ACC 1286

Qy       1651
GCAGCCGACGGGGAGACCACTGCCACTGAGGAGCTAGAAAAAACTCAAGATGACCTGATG 1710
                       |   | | |  | |        |    | |   | |        | | | |      | | | | |
| |
Db       1287 TTTATTTCATGAAGGACTTCT----TTTTGTTTCT------AACT----ATAAACT--
TG 1330

Qy       1711
```

```
AAACATCAAACCAACATTAGCGAGCTGAAAAGAACCTTCTTAGAAACCTCAACAGACACT 1770
            | |     ||| | |           | ||||||| ||        |||
|||
Db     1331 GATC-----ACCTATGTT------------AAAACCTTATT------
TCACATTCCACA 1366


Qy     1771 GCCGTAACGAATGAATGGGAGAAGAGGC----TTTCCA------
CCTCCCCCGTGCGACT 1820
            | |  |||| ||    |||| ||    |||| |      || | | ||
|
Db     1367
TCATTTTAGAATTTATTTTCGAAGGGGAATAGTTTCAATGTTTTATTCACTTGGGCTTTT 1426


Qy     1821 GGCCGCCAGGCAGGAGGATGCCCC-----CATGATCGAACCACT---TGTCC---
CTGAA 1869
            | |        |||    |||| |   | |  ||||  ||   | | |   |||
Db     1427 TTTCTTC-------------
CCCCTCTTTCTTTAAAGAACTGCTCAATATTCAATCTGTT 1473


Qy     1870 GAGAAAATGGAAACCAAGACGGAGTC--
CAGTGGATAGAGACGGAACCCACCGTGCACCA 1927
            | |||    ||| |   | | ||   |||| || |||        ||   | |
|
Db     1474 GTGAA----GAACCTGATTTGCACTCTGTAGTGTTTAAAGA-------
AACAAAGAAACT 1522


Qy     1928
CCTGCCGCTTAGCACTGAGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGGCGTGT 1987
            |      | | || || | |||| | | |       |     | |||
|
Db     1523 CTAATATTGAATCTCTTA-AATTTAGTGTATGTAAACAGCTT------
ACAAATACGTAT 1575


Qy     1988
GGTGCACGCGAGTGGGGATGCTTCTTACTCGGCGGGAGACAGCGGGGATGCTGCAGCACA 2047
            ||     | |     |||| | | || |    | | ||    | | ||| ||||
Db     1576 TGT-----CTA-----AATGCATTTAAATCTGTTTTATTCA-
AAGAAAAGCTAAAGCA-- 1622


Qy     2048
GCCCGCATTCACAGGCATTAAAGGGAAAGAGGGCTCTGCTTGACGGAGGGGGCTAAAGAG 2107
                 |  ||| |||||    | | |   ||| |||| | |   | | || ||
|
Db     1623 -----AAAACACTGGCAT-----------
ATGACCATGCAAGACTGTCAGTGCCAACAAA 1666


Qy     2108 GAAGGAGGGGAGGAGGTCGCTAA--
AGCTGTCCTGGAACAGGAAGAGACAGCCGCTGCTT 2165
                 ||            | |||| |||  | | | || |   || || |
|||||
Db     1667 GAC-----------AACACTAATCAGC--ACATCGTAC---ACTGGATTGCAG-
TGCTT 1708


Qy     2166 CCC--
GTGAGCGACAAGAGGAGCAGAGTGCAGCCATCCACATTTCAGAAACTTTGGAACA 2223
            |||  | | || || |    | |||| | ||  |||| ||       ||
|
Db     1709 CCCAGATTATTGAAAAATGTTACAGA---CAACTTGCCTGATTTTTAAAT-----
GAGCG 1760
```

```
Qy        2224
AAAACCTCATTTTGAGTCCTCAACGGTGAAGACGGAAACCATCAGTTTTGGCAGTGTTTC 2283
                  |||          |  ||||             ||||      |  ||||
|||||
Db        1761 TAAA---------AGGCCCTC--------------TAACC-------TATGCAG-
GTTTC 1789

Qy        2284
ACCGGGAGGAGTAAAGCTAGAAATTTCCACAAGAAGTGCCAGTAGTTCACACCGAAACCA 2343
                  ||   |  |  ||  |||||| |  |  |        |   ||  | | |||
Db        1790 CCCATTATGCATA----TAGAAAATGCTA--------
GTATGTTTTGCTCAC------- 1829

Qy        2344
AAACCATCACATATGAATCATCACAGGTCGATCCAGGCACAGATCTGGAGCCAGGCGTGC 2403
                    ||||||      |  ||||||     || |  ||             |
|||||
Db        1830 -------TTCATATG-----TAACAGGT--------GCCCTTAT---------
GTTGTGC 1860

Qy        2404
TGATGAGTGCACAGACGATCACATCTGAAACCACCAGTACCACCACCACTACCCACATCA 2463
                    ||                              ||  ||
Db        1861 TGT----------------------------
ATCCTGT---------------------G 1871

Qy        2464
CCAAAACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAATAGTCATCACGG 2523
                  |  | ||||        ||| |  |||       ||| || |||| || || || ||
Db        1872 CTTTTTCTGT-----GGGACCATTC---------CATTCAGGAGCAAAGAG-
CACCAT-- 1914

Qy        2524
GGGATGCAGACATTGACCATGACCAGGCGCTGGCTCAGGCAATTAAAGAGGCCAAAGAGC 2583
                  ||| |  ||| |  | | ||| |     ||     | | |||| | |  ||
Db        1915 --GATTCCAATCTTG----TGT----GTGTTTACTAA--
CCCTT--------------- 1946

Qy        2584
AGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAGACAGAGATCACACCAG 2643
                  |||||  | ||  |  || ||  ||| |||     |  | |      |||||||
Db        1947 ----CCCTG--AGGTTTGTG---TATGT--
TGGATATTGTGGTGTTTTAGATCACT---- 1991

Qy        2644
AAGATGGAGAGGATTGACCAGAGGAATAACTTAGCTTGCACATGAATGCAGTCATGCAAA 2703
                  ||| | | ||  ||||  ||| |   || | | ||| ||  | ||
Db        1992 ------GAGTGTACAGAAGAGAGAAATT------
CAAACAAAATATTGCTGTTCTTCA-- 2037

Qy        2704 CCGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCTTCTAACCCAACTGTAC---
TTGT 2760
                  |||   |         | | |||| |  |     | || ||| ||  |
|
Db        2038 --GTTTTG------------TTTGTGGAATT---
TGAAATTACTCAAATTTAAAATAAAT 2080

Qy        2761 ATCT-
GTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCATTAATAAAGACACT 2819
                  || | |||| |||| || |||||||| ||     ||||| | ||
```

```
           |
Db       2081 TACTGGACTGTGG-AAATAACA------TAGAATTGAAGTT-
TTAATTAAATACCACTCA 2132

Qy       2820 GGCAGAGAGATCTTCCCATAATAAAGCAATCT----
GATTCAGCATCACTAAACCGATAA 2875
                  |  | ||| |      |   |   ||    | |     ||| | |   || ||     |
Db       2133
AACGAAAAGAACAGTAGTTTTTGTAGTTTTATATTGGATACTGAGGCATTAGGGAG---- 2188

Qy       2876
TGCATGAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACAAAATGTCTC 2935
                 ||||||| | ||   ||| |  |  | |||       |     |  ||   ||  || ||
Db       2189 -GCATGAAAGGAAGA-
GGAATGAGGATTGAGACATGTGAAGACATTGTGCATTATATCAA 2246

Qy       2936
AGTTTTCAGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACA 2995
                 ||       || || |||| | ||||||| | |||     || |  | | ||||| | | |
||
Db       2247 TGT-----GC-ATTCCTG-TAGTTCATTAACAA-
GGTACATGCAATAGTCTAAAGAACCA 2298

Qy       2996
CATAAACAATTCATGCCTTTCATAGTTTATTATTATTAAAGTCTAAACAAAATTGCAATT 3055
                    | |||   || |  | ||| |||   ||||     |||| |   ||| |||
||
Db       2299 -------GAGTCACTACTATAGTGGCTTAACATTTAATCTGTCT--CCAATATT----
TT 2345

Qy       3056 TCTTAGGTAAC-CTTATATTTACAATAAATGAAG-
ATTACCCTCAAATGCTAGAAGCTGT 3113
                 | || ||  |    ||| ||   | |  |||| ||| | | ||||||   ||
|
Db       2346 AACCAAGTGACACCGGGGTTT----
TTATCGAAGCATTTCACTTAAATGAACAAA----T 2397

Qy       3114
CTAGGTCCGTCCGGTGTGTCAGATTTCCTCAGATTAGATGTGCCAATAACCAAGTTTATT 3173
                 | ||     |     |||  | ||| || ||   | | |  ||    ||| || || |
Db       2398 CATGG------C----TGTTATATTAACTTGAAATA-
AAATATATTTAAACATGTAAAAA 2446

Qy       3174 CAGTAAA-------
CAACTTGTACTTGTTTCATCTGGTTTATTACTCTCACCCATAAACA 3226
                 |  |||         | || ||| || |      | |||
||
Db       2447 AAAAAAAAAAAAAGGCCACATGTGCTCG----AGCTG----------------------
CA 2480

Qy       3227 GTAATGACTCTCTGACCCTCTGG 3249
                 |         || | | ||  || | |
Db       2481 GG------TCGCGG--CCGCTAG 2495


RESULT 10
US-10-478-914-17
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
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  Query Match   27.2%; Score 5299; DB 1; Length 2198;
  Best Local Similarity   42.3%; Pred. No. 0;
  Matches 1326; Conservative   0; Mismatches 807; Indels 1004;
Gaps 181;

Qy   47
CCTGCTGATCCCAGAACAATCAACCATGACGACCGAATCTGGATCAGACTCGGAATCCAA 106
            ||| ||| | | | || || | ||| || ||| ||
Db   1 CCTACTGGT-CTTGTGTGG------GTGTTTCCAGCAC-GGAAAAG--
TCGAGATAATT 50

Qy   107 GCC---
GGACCAGGAGGCCGAGCCCCAGGAGGCGGCGGGGGCGCAGGGGCGGCGGGGGCC 163
            ||| | | ||| |||| || |
||
Db   51 GCCAATGATCAGGGAAACCGAACCACT--------------------------------
CC 79

Qy   164
GTGCCGGAGCCGCCCAAGGAGGAGCAGCAGCAGGCCCTGGAGCAGTTCGCCGCCGCTGCA 223
               || | |||| | | || | | ||| || |
|||
Db   80 AAGCT-ATGTCGCCTT------------TACGGACACT-
GAACGGTTGATCGGTGATGC- 124

Qy   224
GCGCACAGCACCCCGGTGCGAGGGAGGTCACTGACAAGGAACAGGAGTTTGCTGCCAGGG 283
            |||| || | | | |||| | ||| || ||| |||| ||||
Db   125 -CGCAAAGAATCAAGTTGCAATGAACCCCACCAAC-----ACA-
GTTTTTGATGCC---- 173

Qy   284
CTGCAAAACAGCTCGAATATCAGCAATTAGAAGACGATAAACTTTCTCAGAAATCATCTA 343
            |||| || ||| || | |||| | ||
Db   174 -----AAACGTCT-----------GATTGGA---------------
CGCAGATTTGATGAT 203

Qy   344 GCAGTAAACTCTCTCGGTCT-
CCATTAAAGATTGTCAAAAAGCCTAAAAGCATGCAGTGC 402
            || || | | |||| || ||| |||| | ||| | |
|||

```
Db        204 GCTGTTGTC-----CAGTCTGATATGAAACATTGGC------CCTTTATG------
GTGG 246

Qy        403 AAAGTGATACTTCTCGATGGATCAGAATATACCTGTGATGTAGAGAAACGCTCCAGAGGA 462
                | |||| ||     |  | ||   |    | ||     |  ||| |  ||      ||||
Db        247 TGAATGATGCTG---GCAGGCCCAAGGT---CC----AAGTAGA-
ATACAAGGGAGAGAC 295

Qy        463 CAAGTGCTGTTTGATAAAGTGTGTGAACACTTGAACTTGCTAGAGAA--
AGACTACTTTG 520
                |||   ||||                       ||  | |||| |   | ||| ||
                                                                          ||
Db        296 CAAAAGCT-------------------------
TCTATCCAGAGGAGGTGTCTTCTATG 329

Qy        521 GGCTTACGTATCGAGATGCTGAAAAC--
CAGAAGAATTGGTTGGACCCTGCTAAGGAAAT 578
                |   | |  |   ||||| |  ||||  ||||||        ||| |    ||
                                                                          ||
Db        330 G---TTCTGACAAAGATGAAGGAAATTGCAGAAG------------
CCTACCTTGGGAAG 374

Qy        579 AAAAAAACAGGTTCGAAGTGGT-
GCTTGGCACTTTTCATTTAATGTGAAATTTTATCCAC 637
                |  || | |   ||||| |  | ||  ||  |||||||  | | |   |
Db        375 ACTGTTACCAATGC--TGTGGTCACAGTGCCAGCTTACTTTAATG----
ACTCTCAGCGT 428

Qy        638 CAGACCCTGCCCAACTATCTGAAGATATCACCAGGTACTACCTCTGCTTGCAGTTGCGAG 697
                |||   || || ||    ||| | ||  | ||| | |   ||  | | |||
                                                                          ||
Db        429 CAGG--CTACCAAAGATGCTGGAACTATTG-CTGGT-CTCAATGTACTT---------
AG 475

Qy        698 ATGACATCGTGTCCGGAAGGCTGCCCTGCTCCTTTGTTACCCTGGCCTTGCTGGGCTCCT 757
                |      |  | |  |||  |||||  |||| |   ||| |    | ||  |
                                                                          |
Db        476 AATTATTAATGAGCCAACTGCTG--CTGCT--ATTGCTTAC--GGCTTAG------
ACA 522

Qy        758 ACACTGTC----CAGTCAGA-----
GCTCGGAGACTATGACCCAGATGAATGTGGGAGCG 808
                |  |  ||    ||| ||     ||||     || ||||| |      | ||
                                                                          ||
Db        523 AAAAGGTTGGAGCAGAAAGAAACGTGCTC---ATCTTTGACCTGG------
GAGGTGGCA 573

Qy        809 ATTACATTAGTGAGTTCCGCTTTGCACCAAACCACACTAAAGAACTGGAAGACAAAGTGA 868
                |   || || ||              ||| || ||||| ||    | | |    |
                                                                          |
Db        574 CTT---TTGATGTGT------------
CAATCCTCACTATTGAGGATGGAATCTTTGAGG 618

Qy        869 TCGAGCTGCACAAGAGCCACAGAGGAATGACGCGCCAGCAGAAGCAGAGATGCATTTCTTGG 928
                ||  ||             |  | |||| |  | ||| ||    |      | |||| |  |||
```

```
|
Db        619  TCAAGT----------CTACAGCTGGA-
GACACCCACTTGGGTGGAGAAGATTTT----G 663


Qy        929
AAAATGCCAAAAAATTATCAATGTATGGGGTAGATTTACATCATGCTAAGGACTCAGAAG 988
               | ||   || ||   |  | | ||   | |   ||     | || | | |
|||||
Db        664  ACAA--CCGAATGGTCAACCATTTTATTGCTGAGTTT-----
AAGCGCAAGCATAAGAAG 716


Qy        989  GGGTAGAAATTATGTTAGGAGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCG-
GCTG 1047
               |       |   |  || || |        |||| | |||    ||    ||| |||
|||
Db        717  G------ACATCAGTGAGAA-------CAAGAGAGCTG----
TAAGACGCCTCCGTACTG 759


Qy        1048 CGAATAAAC-
AGATTTGCCTGGCCCAAGGTTCTAAAGATTTCATACAAACGGAACAACTT 1106
               |  | |||| | |  ||  || | ||  | |||    |||     ||| || | | ||
Db        760  CTTGTGAACGTGCTAAGCGT-ACCC-----TCTC-----
TTCCAGCACCCAGGCCA---- 804


Qy        1107 TTACATTAAGATCCGGCCGGGAGAGTTTGAACAATTTGAAAGCACCATTGGGTT-
TAAGC 1165
                   ||| |||||       || | |  | |   | ||||| | |     ||  | || ||
|
Db        805  --GTATTGAGATC---------GATTCT---CTCTATGAAGGAATC---
GACTTCTATAC 847


Qy        1166 TGCCA-
AACCATCGAGCTGCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTT 1224
                   ||| ||| ||   ||||  || ||             || || |    ||
Db        848  CTCCATTACC--CG---TGCC---CGATT------------
TGAAGAACTGAATG----- 882


Qy        1225 TTCAGACTACTGTTACCAGAAGCACC----TCCCA----
AGAAATTCCTAACCTTGGGTT 1276
                   | |||  ||||| | |  ||||| |    |||    ||||| |||    | | |
|
Db        883  --CTGAC--CTGTT--CCGTGGCACCCTGGACCCAGTAGAGAAAGCCCT----
TCGAGAT 932


Qy        1277 -
CCAAGTTTCGTTATAGTGGCAGGACACAAGCGCAAACGAGAAGAGCCAGTGCGTTGATA 1335
                   |||| |             | || |||  ||  | |   || |   || | ||||
|
Db        933  GCCAAACT---------AGACAAGTCACAGATTCAT--GATATTGTCCTG---
GTTGGTG 978


Qy        1336 GATCGCCCAG---
CACCTTACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCGC 1392
                   | || | | |  |   || || |    |||| | || || | | |||
Db        979  GTTCTACTCGTATCCCCAAGATTCAGAAGCTTCTCCA--AGAC-
TTCTTCAATGGAAAAG 1035


Qy        1393
AGCTTGGATGGAGCATCAGTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCT 1452
                   | ||      |||||||         |||| ||          ||||||
```

```
||
Db       1036 AACTGAATAAGAGCATC----------AACCCTG--------ATGAAG----------
CT 1067

Qy       1453
GCTGCAGAGGTTGGTACTGGCCAGTACGCCACAACAAAAGGCATCTCTCAGACCAACTTG 1512
             | ||| | | |||| | | || |           |||||          |||
||||
Db       1068 GTTGCTTA---TGGTGCAG--CTGTCC-----------AGGCA--------
GCCATCTTG 1103

Qy       1513
ATCACCACTGTGACTCCGGAGAAGAAGGCTGAGGAGGAGCGGGACGAGGAAGAGGACAAA 1572
                          || ||||| ||| ||||| | | |          | ||
Db       1104 --------------TCTGGAGAC-AAGTCTGAGAATGTTC------------
AAGATTTG 1136

Qy       1573
CGGAGGAAGGGGGAAGAAGTCACGCCCATCTCGGCCATCCAGCACGAGGGAAAGACTGAC 1632
             | |    |    || ||||| || | || || | |           || |
Db       1137 CTGCTCTTG------GATGTCACTCCTCTTTC--CCTT----------
GGTAT------- 1171

Qy       1633
AGTGAGCGCACGGACACCGCAGCCGACGGGGAGACCACTGCCACTGAGGAGCTAGAAAAA 1692
                       || ||| || | |    | |||| |   || |
Db       1172 -----------TGAAACTGCTG-----GTGGAGTC--
ATGAC----------------- 1195

Qy       1693
ACTCAAGATGACCTGATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAACCTTCTTA 1752
                      || ||| || || | | |||| ||||            ||| |
|
Db       1196 --------TGTCCTCATCAAGCGTAATACCACCATT-----------------
CCTACCAA 1231

Qy       1753 GAAACCTCAACAGACACTG-
CCGTAACGAATGAATGGGAGAAGAGGCTTTCCACCTCCCC 1811
             |      |||||||| | | || | |              || | | |||
||
Db       1232 G---------CAGACACAGACCTTCACTACCTATT-----------
CTGACAACCAGCCT 1271

Qy       1812
CGTGCGACTGGCCGCCAGGCAGGAGGATGCCCCCATGATCGAACCACTTGTCCCTGAAGA 1871
             ||| | |      |||| | | ||     || || |||
Db       1272 GGTGTGCTT---ATTCAGGTTTATGAAGGC------
GAGCGTGCCA-------------T 1309

Qy       1872 GAAAATGGAAACCAAGACGGAGTCCAG--TGGATAGAGACGGAACCCACCGTGC--
ACCA 1927
             || || ||| | |||      || |   ||| ||    |||| ||| | ||
|||
Db       1310 GACAAAGGATAACAA--------CCTGCTTGGCAAGTTT--GAACTCACAG-
GCATACCT 1358

Qy       1928 CCTGCCGCTTAGCACTGAGAAGGTGGTGC------
AGGAGACCGTGTTGGTGGAGGAGCG 1981
             |||||     | | |   |||||| | |     | || | | ||| |
||
```

```
Db      1359 CCTGC------ACCCCG---
AGGTGTTCCTCAGATTGAAGTCACTTTTGACATTGATGC- 1408

Qy      1982
GCGTGTGGTGCACGCGAGTGGGGATGCTTCTTACTCGGCGGGAGACAGCGGGGATGCTGC 2041
             |  |||| || |  |              |  ||| || |  |||| |   |  | |
                                                                   |
Db      1409 -C-AATGGTATACTCAA-------------TGTCTCTGCTGTGGACA---
AGAGTACGGG 1450

Qy      2042
AGCACAGCCCGCATTCACAGGCATTAAAGGGAAAGAGGGCTCTGCTTGACGGAGGGGGCT 2101
             |  | || |  | |      | ||  || ||| |   |  |||| ||| | |||| 
||
Db      1451 AAAAGAGAACAAGATTACTATCACTAATG---ACAAGGG--CCGTTTGA--------
GCA 1497

Qy      2102
AAAGAGGAAGGAGGGGAGGAGGTCGCTAAAGCTGTCCTGGAACAGGAAGAGACAGCCGCT 2161
             |            ||| ||| |  ||| || |  |  |   |  ||||     |
Db      1498 A-------------GGAAGACATTGAACGTATGGTCCAGGAA---
GCTGAGAAGTACAAA 1541

Qy      2162 GCTTCCCGTGAGCGACAAGAGGAGCAGAGTGCAGCCATCCAC-
ATTTCAGAAACTTTGGA 2220
                ||||      ||||    |  | ||||||  || ||   |  ||||||  |  |||     ||||
Db      1542 GCTGAAGATGAGAAGC-AGAGGGACAAGGT---GTCATCCAAGAATTC----
ACTTGAGT 1593

Qy      2221 ACAAAAACCTCATTTTGAGTCCTCAAC-
GGTGAAGACGGAAACCATCAGTTTTGGCAGTG 2279
               |  |  | ||  |      |||| | |||||| |  || | ||        ||||
                                                                             |
Db      1594 CCTATGCCTTCAACATGA--AAGCAACTGTTGAAGATGAGAAACTTCA----AGGCA-
AG 1646

Qy      2280 TTTCACCGGGAGGAGTAAAGCTAGAAATTTCC--
ACAAGAAGTGCCAGTAGTTCACACCG 2337
                || ||   || ||| |   ||||  |||   |||||         ||| |
Db      1647 ATTAAC---GATGAGGACAAACAGAAGATTCTGGACAAG-------
TGTAAT-------G 1689

Qy      2338
AAACCAAAACCATCACATATGAATCATCACAGGTCGATCCAGGCACAGATCTGGAGCCAG 2397
             |                      | | |||              | |||      ||
|||
Db      1690 A-------------------AATTATCA---------ACTGGCT-TGAT-
AAGAATCAG 1718

Qy      2398 GCGGTGCTGATGAGTGCACAGACGATCA-CATCTGAAACCACCAGTACCA-----
CCACCA 2451
             | |||||| ||        |  || || || || | |||   |   |         |
|||
Db      1719 AC-
TGCTGAGAAGGAAGAATTTGAACATCAACAGAAAGAGCTGGAGAAAGTTTGCAACC- 1776

Qy      2452
CTACCCACATCACCAAAACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAA 2511
```

```
                   ||   ||||||| ||  ||||    ||  |  |||     |||  || |     |||
Db      1777 ---CCATCATCACC-AAGCTGTACCAGAGTGCA----GGAGGCATGCCAGGAG----
GAA 1824

Qy      2512
TAGTCATCACGGGGGATGCAGACATTGACCATGACCAGGCGCTGGCTCAGGCAATTAAAG 2571
             |   |  |||||||  ||       ||        || || ||  ||
Db      1825 TG-----CCTGGGGGAT-------TT--------
CCTGGTGGTG--------------- 1848

Qy      2572
AGGCCAAAGAGCAGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAGACAG 2631
                  ||||  |  |||       ||  |       || |||  |  |
Db      1849 --------GAGCTCCTCCC-------TCTG--------GTGGTGCTTCCT-------
CAG 1878

Qy      2632 AGATCACACCAGAAGATGGAGAGGATTGA-
CCAGAGGAATAACTTAGCTTGCACATGAAT 2690
                    |  |  |||||  ||| |  |||| | ||       |||  ||  || |  |||
Db      1879 GG--CCCACCA-TTGAAGAGGTTGATTAAGCC--------AACCAAG--
TGTAGATGTA- 1924

Qy      2691 GCAGTCATGCAAACCGTTAGGAAAACCAGAGCCTATATGGAGTTCC-
CTCTTCTAACCCA 2749
                   ||||  |  || ||  ||   |||||      ||  || ||  ||    |||  | |
Db      1925 GCATTGTTCCACACATTT---AAAAC--------
ATTTGAAGGACCTAAATTCGTAGCAA 1973

Qy      2750
ACTGTACTTGTATCTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCATTAA 2809
             |                 ||  ||||      |||| |||| ||| | |        |
Db      1974 AT--------------TCTGTGG-------CAGTTTTAAAAAGTTAAGCTG---
CTATAG 2009

Qy      2810
TAAAGACACTGGCAGAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTAAAC 2869
             | |||  |||||     |                     |||  |||    || |  |||
Db      2010 T-AAGTTACTGG----------------------GCATTCT-------
CAATACT---- 2034

Qy      2870
CGATAATGCATGAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACAAAA 2929
                        || || | ||| |||        |   | ||| | || |
Db      2035 ------TGAAT-ATGGAAC-----
ATATGCACAGGGGAAG-------------------- 2062

Qy      2930 TGTCTCAGTTTTCAGCTATACC--
TGCTCGTTCATAACCAACAATATAAACCGTGGTCTC 2987
                         |  |||| | |||  ||| | || |||| | ||  |||     ||||
Db      2063 --------------GAAATAACATTGCAC-TTTATAAAC-
ACTGTATTGTAAGTGG---- 2102

Qy      2988 ATGTAACACACATAAACAATTC-
ATGCCTTTCATAGTTTATTATTATTAAAGTCTAAACAAA 3046
                           | |||| | ||| |||  ||                  ||  |||
```

```
  |||
Db      2103 -------------AAAATGCAATGTCTTAAAT---------------
AAAACTATTTAAA 2134

Qy      3047 ATTGCAATTTCTTAGGTAACCTTATATTTACAATAAATGAAGATTAC---
CCTCAAATGC 3103
              |||           |  ||| || |   | || ||| || |  |    || ||
  |||
Db      2135 ATT-----------
GGCACCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGCCACATGTGC 2182

Qy      3104 TAGAAGCTGTCTAGGTC 3120
              | | |||||  |||||
Db      2183 TCG-AGCTG--CAGGTC 2196


RESULT 11
US-10-478-914-57/c
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 2336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-57

  Query Match             27.1%;  Score 5270.5;  DB 1;  Length 2336;
  Best Local Similarity   40.1%;  Pred. No. 0;
  Matches 1338;  Conservative   0;  Mismatches  883;  Indels 1117;
Gaps  181;

Qy        48 CTGCTGATCCCAGAACAATCAACCATGACGACCGAATCTGGATCAG-
ACTCGGAATCCAA 106
              | |||    | || |||     || |           | |   | | | || |    ||
 |
Db      2336 CAGCT----CGAGCACATGTGGCCTTTTTTTTTTTTTTTTTTTGTATTC----
TCAGA 2285

Qy       107 GCCGGACCAGGAG-GC--
CGAGCCCCAGGAGGCGGCGGGGGCGCAGGGGCGGCGGGGGCC 163
              || |  ||||||| ||  ||||||                    | |    |
 |
Db      2284 GCTG--CCAGGAGTGCATCGAGCC-----------------TGTAATTTC--------
CT 2252

Qy       164 GTGC-CGGAGCCGCCCAAGGAGGAGCAGCAGCAGGCCCTGGAGCAGTTCGCC---
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GCCGC 219
              ||  |  ||   |  ||||       |||||  ||  ||  ||   |     |||    | |
     |
Db     2251
GTTCTCTGAATCCCCCATCTTTCTGCAGCTCCAAGCTTTGTGTCCCACAGCCTGTGACTC 2192

Qy         220 TGCAGCGCACAGCAC-------
CCCGGTGCGAGGGAGGTCACTGACAAGGAACAGGAG-T 271
              ||  ||  |||   |          ||  |||   ||| |       ||  |  |||||   ||
Db     2191 TG-TGCTAACAAATCGCTATTGTCCAGTG---GGGCGAATGGTGGC-
TGGAACTAAAGAA 2137

Qy         272 TTGCTGCCAGGGCTGCAAAACAGCTCGA-ATATC-
AGCAATTAGAAGACGATAAACTTTC 329
              ||||||  |  || | ||  |  || | |  || ||  ||  ||        ||
|||||
Db     2136 TTGCTGTCT-GGTTTCTATTCAAATCCAGGTAGCGAGATATATGA-----
ATGGACTTT- 2084

Qy         330 TCAGAAATCATCTAGCAGTAAAC-TCT-
CTCGGTCTCCATTAAAGATTGTCAAAAAGCCT 387
              ||   ||||  |  |  ||| |||||      ||| ||  |      |   |  |||
Db     2083 TC--GAATCGTCATGTGAATAACGTCTGCTCGG----CATGAAGG-----
CTCAGAGC-- 2037

Qy         388 AAAAGCATGCAGTGCAAAGTGATACTTCTCGATGGAT---
CAGAATATACCTGTGATGTA 444
                    |||||   |  |||   ||   ||||  || |    || |      ||| ||
Db     2036 -----CATGCTAGG--AAGGATTA--
ACTCGTAGGCTGACCACTAACATCCTTTGTGGTA 1986

Qy         445 -----
GAGAAACGCTCCAGAGGACAAGTGCTGTTTGATAAAGTGTGTGAACACTTGAACT 499
              |||||||  |  |  |       |||  |      |||        |  |  ||||||  ||
     |
Db     1985 CGAGGGAGAAACATTCC------CAAGTATCATTT---------TATTCACACTT-
AATT 1942

Qy         500 TGCTAGAGAAAGACTAC---TTTGGGCTTACGTATCGAGATGCTGAAAAC------
CAGA 550
              |  |||   |   |   |    |  |||| |   |   |   |  || |     |
     |
Db     1941
TTCTATCCCATACCCCCAAAATAAGGCTAGCTATTTAATTAGTTGGCCGCTTTTCTCTTA 1882

Qy         551
AGAATTGGTTGGACCCTGCTAAGGAAATAAAAAAAACAGGTTCGAAGTGGTGCTTGGCA-C 609
              |   ||  |  | |      ||  |  |  |        |||  |      |||| |  | |
     |
Db     1881 ATTTTTAGT--GTTTCTGTTGATAATGTGTGA------
GTTTGGGAAAATGCTAAGTAGC 1830

Qy         610 TTTTCATTTAATG---
TGAAATTTTATCCACCAGACCCTGCCCAACTATCTGAAGATATC 666
              ||||||  |||  |         ||  |||||  ||     |    |  |  ||    |
|||
Db     1829 TTTTCACTTAGAACACTGTTATTTTCTCTTTAAAGTTTT--
CTACCTTACATTTATTATA 1772
```

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Qy        667 ACCAGGTACTACCTCTGCTTGC--AGTTGCGAGATGACATCGTG-----------
TCCGG 713
                  |   ||  || || |  | ||  || |||   | |  | | |            ||
|
Db       1771 GCATAGT--TATCTTT-
ATAGCATAGATGCAGAAAGTAAGAGAGAGCTTGTTTTTTCAAG 1715


Qy        714 AAGGCTGCCCT----GCTCCTTTGTTACCCTGGCCTTGCTGGG----
CTCCTACACTGTC 765
                  || |  ||||     |||||    ||   || || |||    |||| |  |
|
Db       1714 AAAACAACCCTTTAAAATACTTT-----
CCAACCCATGAAGGGAAAAATCCTCCTTTTTT 1660


Qy        766
CAGTCAGAGCTCGGAGACTATGACCCAGATGAATGTGGGAGCGATTACATTAGTGAGTTC 825
                    |                      |||| |||            ||| ||| |
||
Db       1659 C--------------------CCCCAAGTGCAT---------TCTAC-
TTATTACTTTG 1631


Qy        826 CGCTTTGCACCAAA---
CCACACTAAAGAACTGGAAGACAAAGTGATCGAGCTGCACAAG 882
                  |  ||| | || ||   ||| | | | |
Db       1630
CATTTTTCTCCCAAAGTCCAAATTTATG------------------------------- 1603


Qy        883 AGCCACAGAGGAATGACGCCAG--
CAGAAGCAGAGATGCATTTCTTGGAAAATGCCAAAA 940
                      || ||| |  || | | ||  || | |||   ||||||||
|||||
Db       1602 ---CAAAGAAAATAGAAACAAGTTCAAATGCA---ATGCATT----------
AACCAAAT 1559


Qy        941
AATTATCAATGTATGGGGTAGATTTACATCATGCTAAGGACTCAGAAGGGGTAGAAATTA 1000
                  || | |||         | | ||| |||   || | ||
Db       1558 AA--AACAA------------
GTCTCCTTCAAATTAGGAAC------------------- 1532


Qy        1001
TGTTAGGAGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGAT 1060
                                                        | |||   || |  | | ||
Db       1531 -------------------------------------CAACC-
TAAGCATTTGTAAAGTG 1510


Qy        1061
TTGCCTGGCCCAAGGTTCTAAAGATTTCATACAAACGGAACAACTTTTACATTAAGATCC 1120
                      | ||        || ||   ||| ||| |   |||       ||| |||  ||
||
Db       1509 TAGC--------AGAATC---AGAATTCTTTTAAA---------
AATTAGATTTGGAACC 1470


Qy        1121
GGCCGGGAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCCAAACCATCGAG 1180
                      |||||  || | || || |||        ||         |||
Db       1469 --------------TGAACTATAT-AATTCATAATT---------CT------- 
CATTTTT 1440


Qy        1181 CTGCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTTTTCAGACTACTGT-
```

```
TA 1239
                |||              ||||||              ||   ||| ||   || ||||
||
Db      1439 CTG-----------TGGAAA----------------
ATTATTTTATCTTTCTCCTGTATA 1407


Qy      1240 CCAGAAGCACC-TCCCAAGAAAT------
TCCTAACCTTGGGTTCCAAGTTTCGTTATAG 1292
                || ||||  |  ||| || |      || |    || ||||   |||
Db      1406 CCTGAAAAAATGTCCATAGGCTTAAAGGGTCATGCTTTTACATTCC----
TTC------- 1358


Qy      1293 TGGCAGGACACAAGCGCAA--
ACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCACCT 1350
                   ||  ||||  |  |  |  | ||| |      |   |||
|
Db      1357 ---CATATCACAGGTACTATGAAGTAAGGAGAC-------
TTTTAGG------------T 1320


Qy      1351
TACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCGCAGCTTGGATGGAGCATCA 1410
                | ||||     | | ||      ||| ||   ||  |||||| |    ||||
|
Db      1319 TTCTTT------TTGTC---------TTAAAC----TCAGACAGCTTTGT--
AAGCAGTA 1281


Qy      1411
GTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAGAGGTTGGTACT 1470
                ||||           || |  |||| ||                    ||| |
Db      1280 GTG-----------TGTAGATTACAAGA-----------------------
GTTAG---- 1259


Qy      1471
GGCCAGTACGCCACAACAAAAGGCATCTCTCAGACCAACTTGATCACCACTGTGACTCCG 1530
                          |||||||     ||| |              | ||||
|
Db      1258 ---------------ACAAAAG--------CAGGC-----------------
GCGACTGAG 1238


Qy      1531 GAGAAGAAGGCTGAGGAGGAGC--
GGGACGAGGAAGAGGACAAACGGAGGAAGGGGGAAG 1588
                || ||  ||  | |||| |||   ||| |         ||    |
Db      1237 AAG-AGTTGGTGGGGGAGAAGCTTGGGGC----------
ACTTCC-------------- 1204


Qy      1589 AAGTCACGCCCATCTCGGCCATCCAG--
CACGAGGGAAAGACTGACAGTGAGCGCACGGA 1646
                 |||||     ||    | ||||| ||| |    ||  |          | |||
Db      1203 -TGTCAC-----TCAACACATTCCAGATCACTAAAAAATTTC----------
CACAC--- 1163


Qy      1647
CACCGCAGCCGACGGGGAGACCACTGCCACTGAGGAGCTAGAAAAAACTCAAGATGACCT 1706
                || | ||    |       || ||||           |||| || |
||
Db      1162 --CCTCTGCATTC------CCCCTTGCC----------------CACTCCAGTT--
CCC 1130


Qy      1707
GATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAACCTTCTTAGAAACCTCAACAGA 1766
```

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                    | |         | |   |||     | | |      | |    | | | |||      |||||
  ||
Db      1129 GGTATTTTCTGATTCCATATGTTGTG----
GTATTTACCATACTTCTCTCCCTCACTAGG 1074


Qy      1767 CACTGCCGTAACGAATGAATGGGAGAAGAGGCTTTCC----ACCTCCCCCGTGCG--
ACT 1820
             | ||| |    | || ||  |  ||| || ||  |||||         | | |    |||
  ||
Db      1073 CTCTGGC---
AAGACTGCTTCAGAGGGGATGCATTCCTTTAGATTGCACAAAGCGGAGCT 1017


Qy      1821
GGCCGCCAGGCAGGAGGATGCCCCCATGATCGAACCACTTGTCCCTGAAGAGAAAATGGA 1880
             ||        ||| ||  | | |              |       || ||| |     |        |||
Db      1016 GGGAAAATGGCTGGCAGTTTC-----------
AGAATCTAGTCACGATCGCACGCATGAG 968


Qy      1881
AACCAAGACGGAGTCCAGTGGATAGAGACGGAACCCACCGTGCACCACCTGCCGCTTAGC 1940
                  |||    || | ||||            | |    || ||| | || || |||||
  |
Db       967 CACCTC-ACACA-TCCA--------TGTC----CCTACC---CGCCCCC--
CCGCT---C 930


Qy      1941
ACTGAGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGGCGTGTGGTGCACGCGAGT 2000
                  |              | || ||  | ||| || |  |
Db       929 CC------------------
GCCCCTGCAGCTGGCTGACCTG------------------ 906


Qy      2001
GGGGATGCTTCTTACTCGGCGGGAGACAGCGGGGATGCTGCAGCACAGCCCGCATTCACA 2060
                      ||| ||  || |||     || || ||  || || |  || ||| | |
  |
Db       905 ---------TCTCACCC--------ACTGCTGG---
CCTATCGAACGGCCAGGACTGTCT 866


Qy      2061 GGCATTAAAGGGAAAGAGGGCTC-TGC--TTGACGGAGG-
GGGCTAAAGAGGAAGGAGGG 2116
                      || ||        ||||| ||| ||| |  |    ||||
Db       865 GGTTTT-----------
GGCTCGTGCCTTTGTCCATGTCTGGCTT-------------- 832


Qy      2117
GAGGAGGTCGCTAAAGCTGTCCTGGAACAGGAAGAGACAGCCGCTGCTTCCCGTGAGCGA 2176
                      || || ||   |||||            |   ||| || | |||     ||
Db       831 ----AGTTC-CTCT--CTGTC-----------TATGCTTGCCTCTAC--
CCCCACCGCCC 792


Qy      2177 CAAGAGGAGC-AGAGTGCAGCCATCCACATTTC-------
AGAAACTTTGGAACAAAAAC 2228
                      || | || || ||  |||| |||| |     ||||| |||
  ||||||
Db       791 CAGGCGGCACAAGTGTTTGGCCA--CACAAAACTAGAGATAGAAAAGGTGGT--
AAAAAC 736


Qy      2229
CTCATTTTGAGTCCTCAACGGTGAAGACGGAAACCATCAGTTTTGGCAGTGTTTCACCGG 2288
                      |||           ||   |  | || |      ||| |||||         | ||||
```

```
Db        735 TTCA-------AACTTTTC--TAAATTC----TCCAACAGTT-------
TATTTCT---- 700

Qy       2289
GAGGAGTAAAGCTAGAAATTTCCACAAGAAGTGCCAGTAGTTCACACCGAAACCAAAACC 2348
                       |  ||||||   | ||    | |   | | | |         |
                       |||||
Db        699 ------------TGTGAATTTCTTCC-----
TTCTTTAAATACTCCATTTTAAGAAAACA 657

Qy       2349
ATCACATATGAATCATCACAGGTCGATCCAGGCACAGATCTGGAGCCAGGCGTGCTGATG 2408
               |  | || ||| |||        |  ||||| ||| |||| | || ||
||
Db        656 A--AAAAATTAATTATC---------TAAAGGCAAAGA-ATGGA---AAGCAACCT-
TTG 613

Qy       2409
AGTGCACAGACGATCACATCTGAAACCACCAGTACCACCACCACTACCCACATCACCAAA 2468
                |  | |          | | | |         ||   |  ||  || |   || ||
              |
Db        612 TGTTC-----------CTTATAATA--------ACTGACTTCATAACTC---
TCTCC--A 577

Qy       2469
ACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAATAGTCATCACGGGGGAT 2528
                   ||| |  |||  | |              | | |||| | ||
              |
Db        576 GCTGCGTTATGGGATGTGT------------
ATAAAAAGCTTCTGTTC-----------T 540

Qy       2529
GCAGACATTGACCATGACCAGGCGCTGGCTCAGGCAATTAAAGAGGCCAAAGAGCAGCAC 2588
                |  | |||        ||| |  | ||| ||     || ||| | ||| |  | |
              |
Db        539 GAGAACA-----------AAGGAGCACGTGCAG-----AAATGAGACGAAAAA--
ATC-C 499

Qy       2589
CCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAGACAGAGATCACACCAGAAGAT 2648
                |||||  ||| ||||||        | |||
Db        498 ACTGAC-----------------AGTATTCCATTA------------
CACA--------- 477

Qy       2649
GGAGAGGATTGACCAGAGGAATAACTTAGCTTGCACATGAATGCAGTCATGCAAACCGTT 2708
                                ||| |||| | | |    | | | |  ||||| |  ||
              |
Db        476 --------------------AATTACTT-------AAAAGATTTTAGTCAAGC---
CCCT- 447

Qy       2709 AGGAAAACCAGAGCCTATATGGAGTTCCCTCTTC-TAACCCAACTGTACTTGTAT---
CT 2764
                        | |||| | || | | | || || | ||    ||    | |||| |
              ||
Db        446 -----
CAACAGATTCAATTTTAAAATGGCTTTTAGTTAAAAAAAAAAAAATTGAAAGTGCT 392

Qy       2765 GTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCATTAATAAAGAC-
ACTGGCA 2823
```

```
                    ||   |  |||       ||   |  ||||   |  |||   ||   |||     |||||    |
Db        391 TACCCAGTAAA-----AGAACCGAAG--
TAGTCCTGAACTGTTACGTAAGACTTTTTACA 339

Qy       2824 GAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTAAACCGAT-
AATGCATGA 2882
                    |   ||||||   |  | ||  |||  |  |                        |||    |  |
                    |
Db        338 GTTGGATCTT--TGTCAAAAGGGGATGGGGGT---------------
GATGGGAGAAAGC 296

Qy       2883 AGCAACGATAAAATTACAAAAGAGC-
AGCATTTTTAATTTTCACAAAATGTCTCAGTTTT 2941
                    |||||||   |  ||| |  ||||| |  |||     |  |    |       | ||  |||
                    ||||
Db        295 AGCAACG--
ACAATCAAAAAAGTTCGAGCTGCTGTGGCTAGAGGACAACTTCTGTGTTTC 238

Qy       2942 CAGCT---
ATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACACAT 2998
                    |||  |     ||  | |||| ||  |  |    |||    |    |  ||                  |
                    ||||
Db        237 CAGATAGGATTCTTGCT-GTAGAAATGGAAC--TTCCAGCC------------
AGCACA- 194

Qy       2999 AAACAATTCATGCCTTTCATAGT----
TTATTATTATTAAAGTCTAAACAAAATTGCAAT 3054
                    |||  |||  ||  ||    ||| | |    |||   |||||||||
                    |||
Db        193 -------GCAT-
CCTGTCCCAGTAGAGAAATGAGTTTGTCAGTTAAAACAAAAAAAAAAT 142

Qy       3055 TTCTTAGGTAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCTAGAAGCTGTC 3114
                    ||  |||       || |    |  |||        |  |||||  |
Db        141 ----------------TAGATAC------TGGA----ACCC----
AGGCTAGACGAGGTA 112

Qy       3115 TAGGTCCGTCCGGTGTGTCAGATTTCCTCAGATTAGATGTGCCAATAACCAAGTTTATTC 3174
                    |  |  |||  |    |||||||||||              |||     |  ||  || |
                    ||
Db        111 TTGAACCGCGC-------CAGATTTCCT-----------TGC----
AGCCCTGTCTGCTC 74

Qy       3175 AGTAAACAACTTGTACTTGTT--
TCATCTGGTTTATTACTCTCACCCATAAACAGTAATG 3232
                    ||   ||    |  |   ||     || |        |  |||         |    |||
Db         73 AGCTCGCA-----TTCCAGTAGGCCAACAG------
TGCTCGAGGAATTCCGCAG----- 30

Qy       3233 ACTCTCTGACCCTCTGGAAATATGTAATGCTTCCAATC 3270
                    ||  |  || |        |  | ||||  |||||    |
Db         29 -CTTTTAGAGC--------AGAAGTAACACTTCCGTAC 1


RESULT 12
US-10-478-914-64/c
```

  Query Match   26.6%; Score 5184; DB 1; Length 2120;
  Best Local Similarity   38.0%; Pred. No. 0;
  Matches 1268; Conservative   0; Mismatches 780; Indels 1286;
Gaps 196;

Qy   14 GCCTAGTCCCCACGCCGCGGCGCGCCCGGGCTC------
CCTGCTGATCCCAGAACAATC 67
             | |||| || || | || || || || | ||| | | |
Db   2120 GTCTAGCGGCCGCGAC-CTGC-
AGCTCGAGCACATGTGGCCTTTTTTTTTTTTTTTTA-A 2064

Qy   68
AACCATGACGACCGAATCTGGATCAGACTCGGAATCCAAGCCGGACCAGGAGGCCGAGCC 127
             || |||| | | | ||| | | || || | | || |
||
Db   2063 AAGAATGAGTTACATTTATTGATATGGTTTG---TCATATGCTTTATAAATGGTC--
ACC 2009

Qy   128 CCAGGAGGCG---------GC-----GGGGGCGCAGGGG-CGG---------
CGGGGGCC 163
             | || | | ||||| | |||| | | | ||||
 |
Db   2008
CTTTGAAACATGTATTATTACTATTTGGGGGAGAGGGGGACTGTTCATTTTACAGGGGAC 1949

Qy   164
GTGCCGGAGCCGCCCAAGGAGGAGCAGCAGCAGGCCCTGGAGCAGTTCGCCGCCGCTGCA 223
               || || || |||||||| || | ||||| | |||
Db   1948 AAGCAAGACAGGCTCAAGGAGGGAAAGGA-CAGGCTC----
AAAGT-------------- 1908

Qy   224
GCGCACAGCACCCCGGTGCGAGGGAGGTCACTGACAAGGAACAGGAGTTTGCTGCCAGGG 283
                      || | | ||| | || ||| | | || | ||||
Db   1907 --------CATCACAGTGTGGGG-------CTGGAATG---CA-------
GTTGCC---- 1877

Qy   284

```
CTGCAAAACAGCTCGAATATCAGCAATTAGAAGACGATAAACTTTCTCAGAAATCATCTA 343
                 || |         ||                      ||||||
                 |||||
Db      1876 CTTC-------CT--------------------------
TCTTTCTTTTTGCACATCTT 1851


Qy       344
GCAGTAAACTCTCTCGGTCTCCATTAAAGATTGTCAAAAAGCCTAAAAGCATGCAGTGCA 403
               |         ||||| ||                             |||
Db      1850 CCG------TCTCTAGG-----------------------------------
GTGAG 1835


Qy       404
AAGTGATACTTCTCGATGGATCAGAATATACCTGTGATGTAGAGAAACGCTCCAGAGGAC 463
             || | |        || |||                  || || |
|||
Db      1834 GAGGGGTGC-------AGGCACAG------------------------GCACCC-
AAGAC 1807


Qy       464
AAGTGCTGTTTGATAAAGTGTGTGAACACTTGAACTTGCTAGAGAAAGACTACTTTGGGC 523
             |  ||| ||                         |  |  |  ||        |  || |||
|
Db      1806 AGCTGCGGT-------------------CCAGCCCCGGCC--------
CCACCTGTGGTC 1774


Qy       524
TTACGTATCGAGATGCTGAAAACCAGAAGAATTGGTTGGACCCTGCTAAGGAAATAAAAA 583
             | |     | || |     |||||          || ||| ||
Db      1773 TCA------GTGACGC-----CCCAGA----------GGCCCCATCT-----------
TC 1746


Qy       584
AACAGGTTCGAAGTGGTGCTTGGCACTTTTCATTTAATGTGAAATTTTATCCACCAGACC 643
             ||    | | ||| ||| ||| |  |              ||| | |
||
Db      1745 CCCA----CATAATGAGGCT--GCTCCATCC------------------
TCCTCAAAGCC 1710


Qy       644
CTGCCCAACTATCTGAAGATATCACCAGGTACTACCTCTGCTTGCAGTTGCGAGATGACA 703
             | | || | || |||    | |||| | |||| | |        | ||
|
Db      1709 CAGACCTA-TTTCATAAG----CCCCAGACCCCACCTTCAC---------
CCAGGGCCCC 1664


Qy       704 TCGTGTCCGGAAGGCTG----
CCCTGCTCCTTTGTTACCCTGGCCTTGCTGGGCTCCTAC 759
             | | ||| |||| ||||   |   | ||   ||| ||   |||| ||
|
Db      1663 AAGAGAACAGA--GCTGGAGACACTTCTACT-------CCTAGC---
ACTGGATGCCCTC 1616


Qy       760
ACTGTCCAGTCAGAGCTCGGAGACTATGACCCAGATGAATGTGGGAGCGATTACATTAGT 819
             |  ||        ||||         || || || ||  || |||||| |            |
Db      1615 TC---CC--------CTC-----CTGTGA---AGCTGTAGGTGGGGG--------
GTGGA 1583
```

```
Qy          820
GAGTTCCGCTTTGCACCAAACCACACTAAAGAACTGGAAGACAAAGTGATCGAGCTGCAC 879
            |   || ||||   ||  || ||        ||  ||||  |    ||
|
Db     1582 GGACACCCCTTT-----AAGGCAGGCTC-------
GGGGGGCTATGAACTC--------C 1543

Qy          880 AAGAGCCACAGAGGAATGACGCCAG-
CAGAAGCAGAGATGCATTTCTTGGAAAATGCCAA 938
               ||||  |  |    || ||||| |||||  |  | |     | ||| |
|||
Db     1542 AAGA-CTCCTG------GAAGCCAGTAAGAAGTGGGAAGG------TAGGCACA--
CCA- 1499

Qy          939
AAAATTATCAATGTATGGGGTAGATTTACATCATGCTAAGGACTCAGAAGGGGTAGAAAT 998
                              | |||    ||||| ||  |   |  || |||
Db     1498 -------------TTTGG----
GATTTTTATTTTTCACTGAGCTAAGAG----------- 1467

Qy          999
TATGTTAGGAGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAG 1058
                      ||||| ||              || |||  | |
|||
Db     1466 ------AGGAGATT----------------------------CCAGCTATGGA-
ATCCAG 1442

Qy          1059
ATTTGCCTGGCCCAAGGTTCTAAAGATTTCATACAAACGGAACAACTTTTACATTAAGAT 1118
            |      ||  |     |||||| ||       ||| ||||||    ||
Db     1441 A------GAGC-----GTTCTACAG---------
GAACAGAACAGAAATT---------- 1412

Qy          1119
CCGGCCGGGAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCCAAACCATCG 1178
                    ||| |||               ||  || || |              |||
|
Db     1411 --GGCTGGG-----------------------CCCTGGG--------------
CCCAGAG 1391

Qy          1179
AGCTGCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTTTTCAGACTACTGTT 1238
            |   |||                          |  |||| | ||| | ||||| |
|
Db     1390 -GAGGCC----------------------TGGAGCCGCTTAC--
TGTTCAG--------T 1364

Qy          1239
ACCAGAAGCACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGTTTCGTTATAGTGGCAG 1298
            ||||      || |                | | |||||
Db     1363 GCCAG------CTTC------------
ATCCTTG------------------------ 1348

Qy          1299
GACACAAGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCACCTTACTTTGA 1358
               ||| |       ||| |||        || | |||| |   ||
|
Db     1347 ---------GCACTC------TGCCT------------CTCACACAGCATC--
GCTCCG- 1318
```

```
Qy        1359 ACGCTCATCCAGCAAACGTTATACCATGTCTCGCAGCT--
TGGATGGAGCATCAGTGAAT 1416
                 ||||  ||||    |      ||  || |  || |||    || ||   ||| |||
|
Db        1317 --GCTC--CCAGAGCCC-----ACAGTGGC-
AGCCGCTGGAGGCTGTGGCAGCAGCTGCT 1268


Qy        1417
GAAAACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAGAGGTTGGTACTGGCCAG 1476
                 |    || ||    || | ||     |||| ||         |||| || |
|||
Db        1267 G----CCCTGC-----CCAAGGAGGG----ATGTGGGC--------TTGGCTCT-
GACAG 1230


Qy        1477 TAC--GCCACAA----
CAAAAGGCATCTCTCAGACCAACTTGATCACCACTGTGACTCCG 1530
                 | |  |||| ||  |    ||   ||   ||  |||| |       || ||| | |       |
|
Db        1229 TTCAAGCCAGAAAGAGCCTTAGAAGTCATTCAGGAC------ATTCCCATTTT---
ACAG 1179


Qy        1531 GAGAAG----AAGGCTGAGGAGGAGC-
GGGACGAGGAAGAGGACAAACGGAGGAAGGGGG 1585
                 || |   |||||| || |||| |||    |||| |   | || ||| |
Db        1178 ATGATGAAATAAGGCTCAGAGAGAGCAGGGGCTTTCAAGAACAATAAAGGTGGA---
GAC 1122


Qy        1586
AAGAAGTCACGCCCATCTCGGCCATCCAGCACGAGGGAAAGACTGACAGTGAGCGCACGG 1645
                 ||| ||| ||| |        || | ||| |||||    | ||| |   ||    | | |
Db        1121 TGGAACTCAGGCCT-------CCTGTCTGCT-GAGGG--
TGTCTGCCCATGCTCTCTC-- 1074


Qy        1646 ACACCGCAGCCGACGGGGGAGACCACTGCCACTGAGGAGCTAGAAAAAACTCA----
AGAT 1701
                 ||   |  | || || |    |||      |||| ||| |   | || ||      ||
|
Db        1073 TCAGAGTTTCTGA-GTGGTGGTGTCTG-----GAGGGGCTGG---
ACACGCAAGGGAGCT 1023


Qy        1702
GACCTGATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAACCTTCTTAGAAACCTCA 1761
                 | ||| ||    |     |  |  | | |||        ||| |
|
Db        1022 GGCCTCGTG-----TGTGTCTGTCTGTGCCGGGATGTG--------TCTGTGG-----
CT 981


Qy        1762 ACAGACACTG-
CCGTAACGAATGAATGGGAGAAGAGGCTTTCCACCTCCCCCGTGCGACT 1820
                 | | ||| |||   |       || || |||        ||| |||  |
||
Db         980 TCTGTCTCTGAACGTGCC--------------AGGGGTTTT--
GTGTCCTGTGTGTGTCT 937


Qy        1821
GGCCGCCAGGCAGGAGGGATGCCCCCATGATCGAACCACTTGTCCCTGAAGAGAAAATGGA 1880
                 | |         | || ||| ||  ||                   || || |||
|||
Db         936 ---CTCT------GTGGGTGCTCCTGTG----------------TGCAG-
GAACTTGGG 904
```

```
Qy      1881 AACCAAGACGGAGTCCAGTGGATAGAGACGGAACCCAC---
CGTGCACCACCTGCCGCTT 1937
             |   | | |     || |    | | |     || ||   | ||     ||| || |
Db       903 GCCATGGCCAG-----AGAGGGATGGGCCTATTCCTACAATCTTGGGAGGCCT-
CCAC-- 852

Qy      1938
AGCACTGAGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGGCGTGTGGTGCACGCG 1997
             || ||||| |||| ||  | | |    || || | | ||| |
Db       851 AG-GCTGAGCTGGTGGGG--AGGGTCC-------TGAAGG-
GTAGAGTGAAG-------- 811

Qy      1998
AGTGGGGATGCTTCTTACTCGGCGGGAGACAGCGGGGATGCTGCAGCACAGCCCGCATTC 2057
             |||||| ||| |    |           |||||| || |  | ||
Db       810 -ATGGGGA--CT--TTACTC--------
CCAGCGGAGAGGAAGAAAC------------- 777

Qy      2058
ACAGGCATTAAAGGGAAAGAGGGCTCTGCTTGACGGAGGGGGCTAAAGAGGAAGGAGGGG 2117
                |||            |||| |   |||| |     ||||| | ||
                                                            | | |||
|||
Db       776 -CAG------------AAGATAG----GCTT-------GGGGC--------
ATGGATGGG 749

Qy      2118 AGGAGGTCGCTAAAGCTGTCCTGGAAC-
AGGAAGAGACAGCCGCTGCTTCCCGTGAGCGA 2176
                        |||| ||| |||||| |||| | || | |       |||
Db       748 -----------AAAG--GTCTTGGAACTAGGATGGGGCAAGGGAAAC------
AAAGCCC 708

Qy      2177
CAAGAGGAGCAGAGTGCAGCCATCCACATTTCAGAAACTTTGGAACAAAAACCTCATTTT 2236
             ||| ||||| | |         |   | |  || | || || ||| ||| |
Db       707 CAAATGGAGTATGG-------GTCC------CTGGAA-GTTGACACA-----
CTCTT--- 670

Qy      2237 GAGTCCTCAACGGTGAAGACGGAAACCATCAGTTTTGGCAGT--
GTTTCACCGGGAGGAG 2294
             || ||||||    || |         ||| |      |||| || | ||||| |
||
Db       669 -AGCCCTCA----TGGGGGC-----CCAGCC-------CAGTGGGTAACCCCGGG-
GAAG 628

Qy      2295 T------AAAGCTAGAAATTTCCACAAGAAGTGCCAGTAGTTCACACC--
GAAACCAAAA 2346
             |       |    | |  || | |||       | ||| | || || | |   |   ||
Db       627 TGGTCACATGACGTGACACTTCTCAGCTGATTGCTTG-
AGATCCCCCAGTGTGGCCTGGG 569

Qy      2347 CCATCACATATGAATCATCACAGG-
TCGATCCAGGCACAGATCTGGAGCCAGGCGTGCTG 2405
             ||| |  | | |  ||| | ||| | |||         | | |||        |
|| | |||
||||
Db       568 CCTTGTCCT-TGAGTGAGCCCAGGTTCAAGCCAG----------
GAAGGCTGGCCAGCTG 520

Qy      2406 -
ATGAGTGCACAGACGATCACATCTGAAACCACCAGTACCACCACCACTACCCACATCAC 2464
```

```
                   ||   |  | |   || |  ||     || || |     || || | | |   | |
                 |
Db      519  CCCAAGGACTGAGGCCTTCTCCTC---
CTCCTCCTCTGTGTCCTCCTCGATCATCTTGGC 463


Qy      2465
CAAAACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAATAGTCATCACGGG 2524
              ||   |       ||||||| ||    ||                   ||| |||
Db      462  CAGCTC------CCGGGGCAGCTC-----CA-----------------
CGTCTCCAC--- 434


Qy      2525
GGATGCAGACATTGACCATGACCAGGCGCTGGCTCAGGCAATTAAAGAGGCCAAAGAGCA 2584
                    | | ||||         | || |||||||
Db      433  -----CTGCCAT----------CTGGATCTGGCTCT---------------------
CA 411


Qy      2585  GC--
ACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAGACAGAGATCACACCA 2642
                    |  | |  ||| ||||   || ||  ||| |||  |||       | || | |
Db      410  TCTGTCTCGTTCTTG--GGTAGCC--GGTATTTGTC---------
TCGGAAGTGGCTCC- 365


Qy      2643
GAAGATGGAGAGGATTGACCAGAGGAATAACTTAGCTTGCACATGAATGCAGTCATGCAA 2702
                        | | || || |         || || | |  || || |
Db      364  ---------GCAGTGTGGCCCG--------CTCTGCCTTCCTCTGTGTGAACT-
GTGCAT 323


Qy      2703
ACCGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCTTCTAACCCAACTGTACTTGTAT 2762
                 ||                       | ||| |||| ||| |   | |||
            |
Db      322  CCC--------------------------GCTCCATCTTCTCTTCCACGAG---
TTGCTT 292


Qy      2763
CTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCATTAATAAAGACACTGGC 2822
                 |||           | |  |||       | | ||   ||          | | |
            ||
Db      291  CTG-----------ATAC--TCC-------TCGTACTCCTCC--------
CGGCTCATGC 260


Qy      2823
AGAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTAAACCGATAATGCATGA 2882
                 ||| ||||  | ||  || |   ||    | |  | | |||| |   || | || |
            |
Db      259  CCTGAG--CTTCGGCT------GCCGACTTGTCCC-CATCTC----CC--
TTATCCTCGC 215


Qy      2883
AGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACAAAATGTCTCAGTTTTC 2942
                 || |          | |       ||       || || |  | ||
            |||
Db      214  CGCCTC----------CCA------GGC-----------TCCCAGTGAGGTTC----
TTC 186
```

```
Qy        2943
AGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACACATAAAC 3002
               ||||    ||  || ||          ||           ||| ||||||    | || |||
|||
Db         185 AGCTG-GCC-GC----------CC----------ACCATGGTCT----TCAC-
CATGAAC 153

Qy        3003
AATTCATGCCTTTCATAGTTTATTATTATTAAAGTCTAAACAAAATTGCAATTTCTTAGG 3062
               ||| |                        |||| |        ||     |
||
Db         152 -------GCCAT--------------------GGTCTTCGCCG----
GCCGGGGCACCGG 124

Qy        3063
TAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCTAGAAGCTGTCTAGGTCCG 3122
               |||             | |  | | |  || ||  | |     ||
||
Db         123 GCGCCT--------------------GCTACCACGC----GCCAGGCACCG----
GGCACG 91

Qy        3123
TCCGGTGTGTCAGATTTCCTCAGATTAGATGTGCCAATAACCAAGTTTATTCAGTAAACA 3182
               ||||         |  |  | ||||          || |           |||||
|
Db          90 TCCG-------CGCCTACTTCAG-----------CACTC------------
CAGTAGGCC 61

Qy        3183
ACTTGTACTTGTTTCATCTGGTTTATTACTCTCACCCATAAACAGTAATGACTCTCTGAC 3242
               |   || || |        || |         |     ||| ||    || |
||
Db          60 AACAGTGCTCG-------AGGAATT----------CC----GCAG------
CTTTTAGAG 28

Qy        3243 CCTCTGGAAATATGTAATGCTTCCAATCTTGCTT 3276
               |          | | |||| ||||| | || |
Db          27 C--------AGAAGTAACACTTCCGTACAGGCCT 2


RESULT 13
US-10-478-914-17/c
; Sequence 17, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 2198
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-17

   Query Match              26.4%;  Score 5132.5;  DB 1;  Length 2198;
   Best Local Similarity    42.1%;  Pred. No. 0;
   Matches 1313;  Conservative     0;  Mismatches  776;  Indels 1033;
Gaps  184;

Qy        214
CGCCGCTGCAGCGCACAGCACCCCGGTGCGAGGGAGGTCACTGACAAGGAACAGGAGTTT 273
                || | |||||||| |  |||||          | ||| |  |
                                                                  |||
Db      2197 CGAC-CTGCAGCTCG-AGCACAT---------
GTGGCCTTTTTTTTTTTTTTTTTTTTTTT 2150

Qy        274
GCTGCCAGGGCTGCAAAACAGCTCGAATATCAGCAATTAGAAGACGATAAACTTTCTCAG 333
                 |    | ||                        ||||| ||   | |  | ||
Db      2149 TTTTATGGTGC---------------------
CAATTTTAAATAGTTTTATTT------ 2118

Qy        334
AAATCATCTAGCAGTAAACTCTCTCGGTCTCCATTAAAGATTGTCAAAAAGCCTAAAAGC 393
                || || | ||| |    | ||       | || || || ||| | ||
Db      2117 AAGACA--TTGCATTTTCCACT-------TACAATACAG--
TGTTTATAA--------- 2079

Qy        394 ATGCAGTGCAAAGTGA--
TACTTCTCGATGGATCAGAATATACCTGTGATGTAGAGAAAC 451
                   ||||||| || |  | ||||             |||||           |
                                                                            |
Db      2078 ----AGTGCAATGTTATTTCCTTC----------------CCCTGTGC-------
ATAT 2047

Qy        452
GCTCCAGAGGACAAGTGCTGTTTGATAAAGTGTGTGAACACTTGAACTTGCTAGAGAAAG 511
                | |||| |  |||||   |||| ||    | |   ||||| ||| || |
Db      2046 GTTCCATA-TTCAAGT----ATTGAGAATG--------
CCCAGTAACTTACTATAGCAGC 2000

Qy        512 ACTACTTTGGGCTTACGTATCGAGATGCTGAAAACCAGAAGAATTGG--------
TTGGA 563
                   |||||    |||      |  |||   |||  |||||| |        ||
                                                                            |
Db      1999 TTAACTTT----TTA---------AAACTG----CCA-
CAGAATTTGCTACGAATTTAGG 1958

Qy        564 CCCTGCTAAGGAAATAAAAAAACAGGTTCGAAGTGGTGCTTGGC-ACTT-
TTCATTTAAT 621
                   ||| | || |  |||       ||   |||| |  || || | | || ||
                                                                            |
Db      1957 TCCTTCAAATGTTTTAAAT------GT-----
GTGGAACAATGCTACATCTACACTTGGT 1909

Qy        622 GTGAAATTTTATCCACCAGACCCT------
GCCCAACTATCTGAAGATATCACCAGGTAC 675
                |   || ||| |||       |         |||       |||| || | ||||
Db      1908 TGGC---TTAATCAACCTCTTCAATGGTGGGCC-------CTGAGGA-
AGCACC------ 1866
```

```
Qy        676 TACCTCTGCTTGCAGTTGCGAGATGACATCGTGTCCGGAAGGCTGCCCTGC--
TCCTTTG 733
              |||   |   | ||| |       || |      |   ||||  |  || ||  ||||
Db       1865 -ACCAGAGGGAGGAGCTCC------ACCAC----
CAGGAAATCCCCCAGGCATTCCT--- 1820

Qy        734 TTACCCTGGCCTTGCTGGGCTCCTACACTGTCCAGTCAGAGCTCGGAGACTATGACCCAG 793
              ||||| | |||  | | ||           |  |  | |||| || ||  |||
Db       1819 ----CCTGG-CATGC----CTCCTGCACT---
CTGGTACAGCTTGGTGATGATG------ 1778

Qy        794 ATGAATGTGGGAGCGATTACATTAGTGAGTTCCGCTTTGCACCAAACCACACTAAAGAAC 853
              |||       ||| ||     |||| | |||  |  | |||   |    ||     ||
Db       1777 -------GGG-----TTGCA-----------AACTTT-
CTCCAGCTCTTTCTGTTGATG 1743

Qy        854 TGGAAGACAAAGTGATCGAGCTGCACAAGAGCCACAGAGGAATGACGCCAGCAGAAGCAG 913
              |       |  ||| ||||  || || || |  |      || | |||||  ||
Db       1742 T-----TCAAATTCTTC---
CTTCTCAGCAGTCTGATTCTTATCAAGCCAGTTGAT---- 1695

Qy        914 AGATGCATTTCTTGGAAAATG-
CCAAAAAATTATCAATGTATGGGGTAGATTTACATCAT 972
              |||||  |   |  || ||| ||  ||      ||| ||    |      |  |||
Db       1694 -----AATTTCATTACACTTGTCCAGAATCTT----
CTGTTTGTCCTCATCGTTAATCTT 1644

Qy        973 GCTAAGGA----CTCA---GAAGGGGTAGAAATTATGTTAGGAGTTTGTG---
CAAGTGG 1022
              || | | ||||    |   || |  | ||||| | |      |  |
||||||
Db       1643 GCCTTGAAGTTTCTCATCTTCAACAGTTGCTTTCATGTTGAAGGCATAGGACTCAAGTGA 1584

Qy       1023 TCTGTTGATATATCGC---GAC---
CGGCTGCGAATAAACAGATTTG------------ 1063
              | |||  || | |  |  | ||| |  ||   ||| ||||
Db       1583 ATTCTTGG-
ATGACACCTTGTCCCTCTGCTTCTCCATCTTCAGCTTTGTACTTCTCAGCTT 1525

Qy       1064 CCTGGCCCA-AGGTTCTAAAGATTTCAT---
ACAAACGGAACAACTTTTACATTAAGATC 1119
              |||||| ||| |||| | |   ||| |    ||||||| |    ||  |||||
Db       1524 CCTGGACCATACGTTC-AATGTCTTCCTTGCTCAAACGGCCC----
TTGTCATTA----- 1475

Qy       1120 CGGCCGGGAGAGT----
TTGAACAATTTGAAAGCACCATTGGGTTTAAGCTGCCAAACCA 1175
              | | ||  ||| |   ||| |  |  | |||  | || |||    |   | || |
||
Db       1474 -----GTGATAGTAATCTTGTTCTCTTTTCCCGTACTCTTG----
TCCACAGCAGAGACA 1424

Qy       1176 TCGAG-
CTGCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACATTTTTCAGACTAC 1234
```

```
                   |  |||   |  |||        |||  |   |||        |||  |   |       ||||
|
Db      1423 TTGAGTATACCA-------TTGGCATCAATG---------TCAAAAGT------
GACTTC 1386


Qy      1235
TGTTACCAGAAGCACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGTTTCGTTATAGTG 1294
              |   |  || | ||                    |||| ||| |
Db      1385 AAT---CTGAGGAAC-----------------
ACCTCGGGGT----------------- 1364


Qy      1295
GCAGGACACAAGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCA------- 1347
              ||||              |||   ||| ||| ||| | |  ||| ||||
Db      1363 GCAG--------------GAGGTATGCCTGTGAGTTCA-
AACTTGCCAAGCAGGTTGTT 1320


Qy      1348 --CCTT--ACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCGCA-
GCTTGGATG 1402
                    ||||   |  |  ||||||| || ||     || |||     ||| |  ||
||
Db      1319 ATCCTTTGTCATGGCACGCTCG-CCTTCA-----
TAAACCTGAATAAGCACACCAGGCTG 1266


Qy      1403
GAGCATCAGTGAATGAAAACCATGAAATATACATGAAGGATTCTATGTCTGCTGCAGAGG 1462
              |      |||| |  | ||      ||||||  ||| ||||||||
||
Db      1265 GT-TGTCAGAATAGGTA---------------GTGAAGG--TCTGTGTCTGCT----
TGG 1228


Qy      1463 TTGGTACTG-GCCAGTACGCC--
ACAACAAAAGGCATCTCTCAGACCAACTTGATCACCA 1519
              |  || |  || | ||||||   |   |  || ||| ||| |||| |    |||
|
Db      1227 TAGGAATGGTGGTATTACGCTTGATGAGGACAGTCATGACTCC-
ACCAGCAGTTTCAATA 1169


Qy      1520
CTGTGACTCCGGAGAAGAAGGCTGAGGAGGAGCGGGACGAGGAAGAGGACAAACGGAGGA 1579
              |     |  | ||        | |||||||          |||| |
||
Db      1168 C-------CAAGGGA---------AAGAGGAGT--------------
GACATCC------ 1145


Qy      1580 AGGGGGAAGAAGTCACGCCCA-TCTCGGCC----ATCCAG-CACGAGGGAAAGACT-
GAC 1632
              | |  | |  || || |  || |  |       ||||| | ||  |   | |
|||
Db      1144 AAGAGCAGCAAATCTTGAACATTCTCAGACTTGTCTCCAGACAAGATGG-
CTGCCTGGAC 1086


Qy      1633 AGTGAGCGCACGGACACCGCAGC--
CGACGGGGAGACCACTGCCACTGAGGAGCTAGAAA 1690
              ||  || | |  |    | ||| | |||       || |    |   |  ||
Db      1085 AGC-TGCAC-CATAAGCAACAGCTTCATCAGGGTTGATGCT-CTTATTCAGTTCT--
TTT 1031


Qy      1691
AAACTCAAGATGACCTGATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAACCTTCT 1750
              | | ||||| | || | ||   ||| ||  ||   || | | | ||    ||  ||||||
```

```
                |
                Db      1030  CCATTGAAGAAGTCTTGGAGAAGCTTCTG---
                AATCTTGGGGATACGAGTAGAACCACC- 975


                Qy      1751  TAGAAACCTCAACAGACACTGCCGTAACGAATGAATGGGAGAAGAGGCTTTCCACCTCCC 1810
                                    ||||      |||| |  |        ||||||
                Db       974  ----AACC----AGGACAATATC-------
                ATGAAT----------------------- 954


                Qy      1811  CCGTGCGACTGGCCGCCAGGCAGGAGGATGCCCCCATGATCGAACCACTTGTCCCTGAAG 1870
                                    | || ||||| | |         ||  || |   |||||  ||| || ||
                Db       953  -C-TGTGACTTGTC---------TAGTTTGGCATC----TCGAAGGGCTT-
                TCTCT---- 914


                Qy      1871  AGAAAATGGAAACCAAGACGGAGTCCAGTGGATAGAGACGGAACCCACCGTGCACCACCT 1930
                                               || | |||||| |   |  |||||||   |   |  |
                Db       913  -----------------ACTGGGTCCAGGG---TGCCCACGGAAC------
                AGGTCAGCAT 880


                Qy      1931  GCCGCTTAGCACTGAGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGG-
                CGTGTGG 1989
                                    | | |   ||  |   |    | | ||  || ||| ||   || | ||  |
                Db       879  TCAGTTCTTCAAATCG-----GGCACGG------
                GTAATGGAGGTATAGAAGTCGATTCC 831


                Qy      1990  TGCA-CGCGAGTGGGGATGCTTCTTACTCGGC--
                GGGAGACAGCGGGGATGCTGCAGCAC 2046
                                    | || | ||| |    ||| ||  ||||  ||| ||| | | | |||| | ||
                Db       830  TTCATAGAGAGAATCGAT-CTCAATACT-GGCCTGGGTGCTGGAAGAGAGGGTAC-
                GCTT 774


                Qy      2047  AGCCCGCATTCACAGGCATTAAAGGGAAAGAGGGCTCTGCTTGACGGAGGGGGCTAAAGA 2106
                                    ||| ||  |||||| ||| |                ||||||| | || |
                Db       773  AGCACG--TTCACAAGCAGT------------------------
                ACGGAGGCGTCTTAC-- 741


                Qy      2107  GGAAGGAGGGGAGGAGGTCGCT-------
                AAAGCTGTCCTGGAACAGGAAGAGACAGCCG 2159
                                              || || |         |  | |||||||     |      |
                Db       740  --------------AGCTCTCTTGTTCTCACTGATGTCCTTCTTATG-------
                CTTGCG 702


                Qy      2160  CTGCTTCCCGTGAGCGACAAGAGGAGCAGAGTGCAGCCATCCACATTTCAGAAACTTTGG 2219
                                    ||    | |   ||| ||||| | |     |||| |   | ||| || |||
                Db       701  CTTAAACTC---AGCAATAAAATG-GTTGA------
                CCATTCGGTTGTCAAAATCTT--- 655


                Qy      2220  AACAAAAACCTCATTTTGAGTCCTCAACGGTGAAGACGGAAACCATCAGTTTTGGCAGTG 2279
                                    ||| ||                    ||| |||        |
                Db       654  -----------------------CTCCAC--------------CCA--AGT-------
                GGG 640
```

```
Qy        2280 TTTCACCGG--GAGGAGTAAAGCTAGAAATTTCCACAAGAAGTGC-
CAGTAGTTCACACC 2336
               | || || | || | || | || || ||||| | | || ||||
Db         639 TGTCTCCAGCTGTAGACTTGACCTCAAAGATTCCA-------
TCCTCAATAGT------ 594

Qy        2337 GAAACCAAAACCATCACATATGAATCATCACAGGTCGATCCAG-
GCACAGATCTGGAGCC 2395
               ||    |  |||||  |  |  || ||||| |  |  |||| |||
Db         593 GAGGATTGACACATCAAAAGTGCCACCTCCCAGGTCAAAGATGAGCACGTTTCT------ 540

Qy        2396 AGGCGTGCTGATGAGTGCACAGACGATCACATCTGAAACC---
ACCAGTACCACCACCAC 2452
                      | |    ||| | ||  | ||| || ||   | || || || ||
||
Db         539 -----TTC-------TGCTCCAACCTTTTTGTCT-
AAGCCGTAAGCAATAGCAGCAGCAG 493

Qy        2453 TACCCACATCACCAAAACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAAT 2512
                   |   | ||| |  || | || |    |||| ||||| ||
|||
Db         492 TTGGCTCATTAATAATTCTAAGTA------CATT---GAGACCAGC-----------
AAT 453

Qy        2513 AGTCATCACGGGGGATGCAGACATTGACCATGACCAGGCGCTGGCTCAGGCAATTAAAGA 2572
                      ||| ||         ||| | |||     |  || |||||
|||
Db         452 AGT--TC-------CAGCA-TCTTTG---GTAGCCTGACGCTG--------------
AGA 420

Qy        2573 GGCCAAAGAGCAGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAGACAGA 2632
                   | |   || |  || |  | |||||| |  | |||||||| |||
||||
Db         419 GTCATTA---AAGTAAGCTGGCA---CTGTGACCACAGCATTGGT---------
AACAG- 376

Qy        2633 GATCACACCAGAAGATGGAGAGGATTGACCAGAGGAATAACTTAGCTTGCACATGAATGC 2692
                    ||   ||  ||| |   ||| ||   | |   ||| |   |||  | |
Db         375 --TCTTCCC--AAGGT----AGGCTT---CTGC--AATTTC----
CTTCATCTT------ 339

Qy        2693 AGTCATGCAAACCGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCT--
TCTAACCC-- 2748
                    ||||    |||| |    | ||| | ||| |     || | | ||| |||
Db         338 TGTCA---GAACCATAGAAGACACCT---
CCTCTGGATAGAAGCTTTTGGTCTCTCCCTT 285

Qy        2749 -
AACTGTACTTGTATCTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCATT 2807
                | | ||||||  | || |||      |  ||||| | ||| |||  |||  |||
Db         284 GTATTCTACTTG-----GACCTTGGG------CCTGCCAGCATCATTCACC---
ACC--- 242

Qy        2808
```

```
AATAAAGACACTGGCAGAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTAA 2867
             ||||||      ||| |    || |  || | |  ||          |||||||| |
||
Db      241 -ATAAAG-----GGCCAATGTTTCATATCAGACTGGA-CAA-------
CAGCATCATCAA 196


Qy     2868
ACCGATAATGCATGAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACAA 2927
             | |     ||| |       | ||        || |  |||          |||
||
Db      195 ATC-----TGCGT------CCAAT-------CAGACGTTTGGCA----------
TCAAAA 164


Qy     2928
AATGTCTCAGTTTTCAGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCTC 2987
             | ||| | ||       |  |      |||||| |||| || | ||
||
Db      163 ACTGTGTTGGTG---GG------------GTTCATTG-
CAACTTGATTCTTTGCGGCATC 120


Qy     2988
ATGTAACACATAAACAATTCATGCCTTTCATAGTTTATTATTATTAAAGTCTAAACAAAA 3047
                          ||   |||   || ||||
Db      119 -------------ACCGATCA-
ACCGTTCA----------------------------- 104


Qy     3048
TTGCAATTTCTTAGGTAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCTAGA 3107
                          || || ||          ||| ||     | |||
|
Db      103 --------------GTGTCCGTA--------------AAGGCGAC-----
ATAGCTTGG 78


Qy     3108
AGCTGTCTAGGTCCGTCCGGTGTGTCAGATTTCCTCAGATTAGATGTGCCAATAACCAAG 3167
           || || ||         || |||      ||||| | ||| |    || |||| | |
Db       77 AG-TG---------GTTCGG---------TTTCC-CTGATCA---
TTGGCAATTATC--- 44


Qy     3168
TTTATTCAGTAAACAACTTGTACTTGTTTCATCTGGTTTATTACTCTCACCCATAAACAG 3227
                        | |||| | | ||    |||| | | || ||| || |
|||
Db       43 ------------TCGACTTTTCCGTG------CTGG---
AAAACACCCACACAAGACCAG 5


Qy     3228 TA 3229
               ||
Db        4 TA 3



RESULT 14
US-10-478-914-57
; Sequence 57, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;   APPLICANT: NAKAGAWARA, AKIRA
;   TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;   FILE REFERENCE: 7388-80899
;   CURRENT APPLICATION NUMBER: US/10/478,914
```

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  Query Match          26.3%;  Score 5110.5;  DB 1;  Length 2336;
  Best Local Similarity   40.5%;  Pred. No. 0;
  Matches 1352;  Conservative    0;  Mismatches  916;  Indels 1067;
Gaps  197;

Qy        4 GCGCGCCCGAG-----CCTAGTCCCCACGCGCGGCGCGCC-CGGGCTC------
CCTGC 51
            |  ||  | |       || || | || ||||   || || || |      |||
|
Db        1
GTACGGAAGTGTTACTTCTGCTCTAAAAGCTGCGGAATTCCTCGAGCACTGTTGGCCTAC 60


Qy       52 TGATCCCAGAAC-AATCAACCATGACGACC---
GAATCTGGATCAGACTCGGAATCCAAG 107
             ||       || | | || || | |  |      |||||||  | |  || |  ||
|
Db       61 TGGAATGCGAGCTGAGCAGACAGGGCTGCAAGGAAATCTGGCGCGGT-TC-
AATACCTCG 118


Qy      108 CCGGACCAGGAGGCCGAGCCCCAG----------
GAGGCGGCGGGGGCGCAGGGGCGGCG 157
              |  || ||  ||    | |          |        | |    ||    |
Db      119 TCTAGCCTGGGTTCCAGTATCTAATTTTTTTTTTGTTTTAACTG----
ACAAACTCATT- 173


Qy      158
GGGGCCGTGCCGGAGCCGCCCAAGGAGGAGCAGCAGCAGGCCCTGGAGCAGTTCGCCGCC 217
              |  | | || | |         |  | | ||  || |||||  |||| ||
Db      174 ---TCTCTACTGGGACAG--------GATGCTG-TGCTGG--CTGGA--AGTT--
CCATT 215


Qy      218
GCTGCAGCGCACAGCACCCCGGTGCGAGGGAGGTCACTGACAAGGAACAGGAGTTTGCTG 277
              || ||||   || | ||            |  ||| ||  |||| ||||  |
Db      216 TCTACAGC---AAGAATCC--------------TATCTGGAAA--
CACAGAAGTTGTCCT 256


Qy      278 CCAGGGCTGCAAAACAGCTCGAATATCAGCAATTAGAAGACGAT-
AAACTTTCTCAGAAA 336
              | | ||  || | || | ||||||||  |       ||  | || |    ||||||||
Db      257 CTA--GC--CACAGCAGCTCGAACTT----
TTTTGATTGTCGTTGCTGCTTTCTCC---- 304


Qy      337
TCATCTAGCAGTAAACTCTCTCGGTCTCCATTAAAGATTGTCAAAAAGCCTAAAAGCATG 396
```

```
                 ||||          || | |     || || |       ||| |||| | || |
Db        305 -CATC---------ACCCCC---ATCCCCTT------
TTGACAAAGATCCAA-------- 337


Qy        397
CAGTGCAAAGTGATACTTCTCGATGGATCAGAATATACCTGTGATGTAGAGAAACGCTCC 456
              | ||  ||||| ||| | |    | |||| |                          ||
|
Db        338 CTGTAAAAAGTCTTACGTAAC---AGTTCAGGA----------------------
CTAC 371


Qy        457
AGAGGACAAGTGCTGTTTGATAAAGTGTGTGAACACTTGAACTTGCTAGAGAAAGACTAC 516
                  |     || || ||      | || || | |||||                  |
Db        372 TTCG-----GTTCTTTT------ACTGGGTAAGCACTT-----------------
TCAAT 403


Qy        517
TTTGGGCTTACGTATCGAGATGCTGAAAACCAGAAGAATTGGTTGGACCCTGCTAAGGAA 576
              |||    || |  | |        || ||| ||
Db        404 TTT----TTTTTTTT-----
AACTAAAAGCC---------------------------- 425


Qy        577 ATAAAAAAACAGGTTC-GAAGTGGTGCTTGGCACTTTTCATTTAATGTGAAATTT-
TATC 634
              ||  |||| |  | || | || ||||| |    || |||| |      | ||||| |
|
Db        426 ATTTTAAAATTGAATCTGTTGAGGGGCTTGACTAAAATCTTTTAA---
GTAATTTGTGT- 481


Qy        635
CACCAGACCCTGCCCAACTATCTGAAGATATCACCAGGTACTACCTCTGCTTGCAGTTGC 694
                          || ||| || ||| |         | | |||   || ||
Db        482 --------AATGGAATACTGTCAGTGGAT---------TTTTTCGTCT-----
CATTT-- 517


Qy        695 GAGATGACATCGTGTCCGGAAGGCTGCCC-TGCTCCTTTGTTACCCTGGCC--
TTGCTGG 751
                              |||| | ||||||||||| | | |    |||
Db        518 -----------------------CTGCACGTGCTCCTTTGTT-
CTCAGAACAGAAGCT-- 551


Qy        752
GCTCCTACACTGTCCAGTCAGAGCTCGGAGACTATGACCCAGATGAATGTGGGAGCGATT 811
              |  ||||| ||                || || ||| ||     | ||| |
Db        552 TTTTATACACATCCC------------------ATAACGCAGCTG-----
GAGAGAG--- 585


Qy        812
ACATTAGTGAGTTCCGCTTTGCACCAAACCACACTAAAGAACTGGAAGACAAAGTGATCG 871
              | ||| || | |                  ||| ||||       |||||||
Db        586 ----TTATGAAGTCAGTTAT------------TATAAGGAAC------
ACAAAG------ 617


Qy        872
AGCTGCACAAGAGCCACAGAGGAATGACGCCAGCAGAAGCAGAGATGCATTTCTTGGAAA 931
              | |||      |||         ||| |||       || |||| || |
Db        618 -GTTGCTTT----CCA------TTCTTTGCCTTTAGA-----
TAATTAATTTTTTTG--- 658
```

```
Qy        932 ATGCCAAAAAATTATCAATGTATGG--
GGTAGATTTACATCATGCTAAGGACTCAGAAGG 989
                  |   |  |||||   || ||  | || |||  | || || |   |   ||| |
              ||
Db        659 TTTTCTTAAAATGGAGTATTTAAAGAAGGAAGAAATTCA-CAAGAAATAAACT--
GTTGG 715


Qy        990 GG----
TAGAAATTATGTTAGGAGTTTGTGCAAGTGGTCTGTTGATATATCGCGACCGGC 1045
                  |   |||||   | ||| ||||| ||  |      |   | ||  ||| || |
              |
Db        716 AGAATTTAGAA---AAGTTTGAAGTTTTTACCA-----
CCTTTTCTATCTCTAGTTTTG- 766


Qy        1046
TGCGAATAAACAGATTTGCCTGGCCCAAGGTTCTAAAGATTTCATACAAACGGAACAACT 1105
                  || |   ||||||  | |||| |||   ||    | |        |  || |
              |
Db        767 TGTGGCCAAACACTTGTGCC--GCCTGGGGCGGTGGGGGT--------AGAGGCA-
AGCA 815


Qy        1106 TTTACATTAAGATCC--
GGCCGGGAGAGTTTGAACAATTTGAAAGCACCATTGGGTTTAA 1163
                  | ||| ||  | ||| |   || |||    || |||    | |
              ||
Db        816 TAGACAGAGAGGAACTAAGCCAGAC----ATGGACA-----AAGGCAC----
GAGCCAAA 862


Qy        1164 GCTGCCAAACCATCGAGCT-
GCCAAGCGTTTATGGAAAGTATGTGTTGAGCATCATACAT 1222
                      ||| ||  ||   || ||| || |   ||  || |   | ||||
              |||
Db        863 ---ACCAGACAGTC---CTGGCCGTTCGAT--AGGCCAGCAGTGGGTGAG------
ACA- 907


Qy        1223
TTTTCAGACTACTGTTACCAGAAGCACCTCCCAAGAAATTCCTAACCTTGGGTTCCAAGT 1282
                  |||| |  ||| | |                        ||| |
              |
Db        908 -GGTCAGCCAGCTG----CAGGGGC------------------------
GGGAGCGGGGG 938


Qy        1283
TTCGTTATAGTGGCAGGACACAAGCGCAAACGAGAAGAGCCAGTGCGTTGATAGATCGCC 1342
                  ||     || | ||||||    | |  | || |   |||||      ||
Db        939 GGCG----GGTAG--GGACA----TGGATGTGTGAGGTGCTCATGCGT-------
GCGAT 981


Qy        1343
CAGCACCTTACTTTGAACGCTCATCCAGCAAACGTTATACCATGTCTCGCAGCTTGGATG 1402
                  |   ||   | |||||    | |||||   | || |||       | | |||| |
              ||
Db        982 CGTGACTAGATTCTGAA---ACTGCCAGC---CATTTTCCCA----GCTCCGCTTTG-
TG 1030


Qy        1403 GAGCATCAGTGAATGAAAACC--
ATGAAATATACATGAAGGATTCTATGTCTGCTGCAGA 1460
                  |   |  | |||||| | ||   |||| |  ||   || ||| |     || |
              |||
```

```
Db        1031 CAATCTAAAGGAATGCATCCCCTCTGAAGCAGTCTTGCCAGAGCCTAG---
TGAGGGAGA 1087

Qy        1461
GGTTGGTACTGGCCAGTACGCCACAACAAAAGGCATCTCTCAGACCAACTTGATCACCAC 1520
               |||  ||| ||| | ||  |||||||| | ||   || |||||  |
Db        1088 G--AAGTA-TGGTAAATA--CCACAACATATGGAA----
TCAGAAAAT----------- 1126

Qy        1521
TGTGACTCCGGAGAAGAAGGCTGAGGAGGAGCGGGACGAGGAAGAGGACAAACGGAGGAA 1580
                    ||||   ||| ||  ||||  ||| ||| |  || |  | |||| ||||
Db        1127 ------ACCGG----GAA--CT-----GGAGTGGG-CAAGG----
GGGAATGCAGAGGGT 1164

Qy        1581
GGGGGAAGAAGTCACGCCCATCTCGGCCATCCAGCACGAGGGAAAGACTGACAGTGAGCG 1640
               | || ||               | |  | | ||| | | ||     || ||||||| ||
|
Db        1165 GTGGAAA-----------TTTTTTAGTGATCTGGAATGTG---
TTGAGTGACAGGAAGTG 1210

Qy        1641 CACGGA-
CACCGCAGCCGACGGGGAGACCACTGCCACTGAGGAGCTAGAAAAAACTCAAG 1699
               | |  | |  | |  ||        |||| | ||              ||||
Db        1211 CCCCAAGCTTCTC--CC----------CCACCAACTCT--------------
TCTCA-- 1241

Qy        1700
ATGACCTGATGAAACATCAAACCAACATTAGCGAGCTGAAAAGAACCTTCTTAGAAACCT 1759
                                   ||  | | ||  ||    | ||| |||| ||
|
Db        1242 ---------------GTCGCGCCTGCTTTTGT---CT------AAC--
TCTTGTAA---T 1272

Qy        1760 CAACAGAC-
ACTGCCGTAACGAATGAATGGGAGAAGAGGCTTTCCACCTCCCCCGTGCGA 1818
               | ||| ||||| |  |||              ||| ||              ||
Db        1273 CTACACACTACTGC--TTACAAA---------------GCTGTC-----------
TGAGT 1304

Qy        1819
CTGGCCGCCAGGCAGGAGGATGCCCCCATGATCGAACCACTTGTCCCTGAAGAGAAAATG 1878
               |         || || | || | |  ||   |     | ||  || | || |
Db        1305 TT------AAGACAAAAGAAACCTAAAAG-----TCTCCTT---
ACTTCATAGTA---- 1346

Qy        1879 GAAACCAAGACGGAGTCCAGTGGATAGAGACGGAACCCACCGTGCACCA-
CCTGCCGCTT 1937
                             || | |||| ||  || ||||       || | | ||| || |
|||
Db        1347 ----------------CCTGT-GATATGGAAGGAA-------
TGTAAAAGCATGACCCTT 1382

Qy        1938 --
AGCACTGAGAAGGTGGTGCAGGAGACCGTGTTGGTGGAGGAGCGGCGTGTGGTGCACG 1995
                   ||| ||  |        ||| |||         |  |||
||
Db        1383 TAAGC-CTATG--------------GACATTTTT----------------
```

```
TCAGGTATACA 1412

Qy        1996 CGAGTGGGGATGCTTCTTACTCGGCGGGAGACAGCGG-----
GGATGCTGCAGCACAG-- 2048
                 |||    |      |   |  ||  | | | |  | |       | ||   |   ||  |||
Db        1413 GGAGAAAGATAAAATAATTTTCCACAGAAAAATGAGAATTATGAATTATATAGTTCAGGT 1472

Qy        2049 CCCGCATTCACAGGCATTAAAGGGAAAGAGGGCTCTGCTTGACGGAGGGGGCTAAAGAGG 2108
                 || ||    |       || || |||   |  | | |||||| ||         || | |
Db        1473 TCCAAAT---CTAATTTTTAAAAGAATTCTGATTCTGCTACAC------- 
TTTACAAA-- 1520

Qy        2109 AAGGAGGGGAGGAGGTCGCTAAAGCTG--
TCCTGGAACAGGAAGAGACAGCCGCTGCTTC 2166
                 ||| | || |||| |   | | | ||||         ||
| ||
Db        1521 ----------------TGCTTAGGTTGGTTCCT-AATTTGAAGGAGACT-----
TGTTTT 1558

Qy        2167 CCGTGAGCGACAAGAGGAGCAGAGTGCAGCCATCCACATTTC-
AGAAACTTTGGAACAAA 2225
                 ||  |  ||  |  |  | ||||        |   |||| |      |||||
Db        1559 ATTTG---GTTAA----TGC--
ATTGCATTTGAACTTGTTTCTATTTTCTTTG------- 1602

Qy        2226 
AACCTCATTTTGAGTCCTCAACGGTGAAGACGGAAACCATCAGTTTTGGCAGTGTTTCAC 2285
                 |  | | |||| | | |       ||  ||| |  | ||        ||| |            |
Db        1603 --CATAAATTTG-GACTTTG--GGAGAAAAATGCAA----- 
AGTAATAAGTAGAATGCAC 1652

Qy        2286 CGGGAGGAGTAAAGCTAGAAATTTCC--
ACAAGAAGTGCCAGTAGTTCACACCGAAACCA 2343
                 ||  | ||| |||  |||| |      ||| || |     ||                      ||||
Db        1653 TTGGGGGAAAAAAGGAGGATTTTTCCCTTCATGGGTTG--------------- 
GAAA--- 1694

Qy        2344 
AAACCATCACATATGAATCATCACAGGTCGATCCAGGCACAGATCTGGAGCCAGGCGTGC 2403
                 | || |  | |||  |          |||
Db        1695 --------------GTATTTTAAAGGGTTGTT----------
TTCT-------------- 1716

Qy        2404 
TGATGAGTGCACAGACGATCACATCTGAAACCACCAGTACCACCACCACTACCCACATCA 2463
                 ||  | || |  | |       |   |  || |     | |    ||| |  | ||
|
Db        1717 -------TGAAAAAACAAGCTC-TCTCTTACTTTCTG---
CATCTATGCTATAAAGAT-A 1764

Qy        2464 CCAAAACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAGCGAATAGTCATC-
ACG 2522
                 |  | || | | |   |    |  |   | |   || |||||   || ||| || | |
|
Db        1765 ACTATGCTATAATAAATGTAAGGTAGAAAACTTTAA-
AGAGAAAATAACAGTGTTCTAAG 1823
```

```
Qy       2523
GGGGATGCAGACATTGACCATGACCAGGCGCTGGCTCAGGCAATTAAAGAGGCCAAAGAG 2582
           |  | ||  || | | |  | ||      |   |||| || |         | |
|||
Db       1824 TGAAAAGCT-ACTTAG-CATTTTCC-----CAAACTCACACATTAT------
CAACAGA- 1869

Qy       2583
CAGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAGACAGAGATCACACCA 2642
            || || | | ||| | | |  ||      |    ||| |   | | || |
||
Db       1870 ---AACACTAAAAATTAAGAGA--AAAGCGG----CCAACTAATTAAATAG--
CTAGCCT 1918

Qy       2643
GAAGATGGAGAGGATTGACCAGAGGAATAACTTAGCTTGCACATGAATGCAGTCATGCAA 2702
            |   ||| | | |  ||  |   ||| | ||| |          ||||| | | || |
Db       1919 TATTTTGG-GGGTATGGGATAGAAAATTAAGT----------
GTGAATAAAATGATAC-- 1965

Qy       2703
ACCGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCTTCTAACCCAACTGTACTTGTAT 2762
            || ||||           |||   |||||| || ||||  |
Db       1966 ----TTGGGA--------------ATGTTTCTCCCTCG--
TACCACAAAGG--------- 1996

Qy       2763 CTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGA-
CCTTGACCATTAATAAAGACACTGG 2821
            |||  |||||       |||| ||  | || | ||| |||||  ||    ||   | | ||
Db       1997 ATGTTAGTGG------TCAG-CCT-ACGAGTTAATCCTT--CCTAGCAT---
GGCTCT-- 2041

Qy       2822 CAGAGAGATCTTCCCATAATAAAGCAATC-
TGATTCAGCATCACTAAACCGATAATGCAT 2880
               |||  || | ||     |||| | | |||||
|||
Db       2042 --GAGCCTTCATGCC------GAGCAGACGTTATTCA--------------------
CAT 2073

Qy       2881
GAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACAAAATGTCTCAGTTT 2940
            |     ||||      | | |||      |     | | ||    |    |  | ||
|||
Db       2074 G-----ACGA------TTCGAAAAGTC--CATTCATATATCTCGC----
TACCTGGATTT 2116

Qy       2941
TCAGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCTCATGTAACACATAA 3000
            |   | |||| |              ||| | |         ||| || ||   ||
Db       2117 GAATAGAAACCAG-----------ACAGCAAT-----------TCTTTAGTT--
CCAGCC 2152

Qy       3001
ACAATTCATGCCTTTCATAGTTTATTATTATTAAAGTCTAAACAAAATTGCAATTTCTTA 3060
            || |||| |||   |               || ||  ||   ||| || |||| ||||
|||
Db       2153 ACCATTC--GCC--CCA--------------------CTGGAC--
AATAGCGATTTGTTA 2186

Qy       3061
```

```
GGTAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCTAGAAGCTGTCTAGGTC 3120
           |     |  | | | |||       ||       || |   || ||| |  |||||
                                                                     |
Db       2187 G-----CACAGAGTCACAGGCTGTGGG----ACAC---
AAAGCTTGGAGCTG-------C 2227


Qy        3121
CGTCCGGTGTGTCAGATTTCCTCAGATTAGATGTGCCAATAACCAAGTTTATTCAGTAAA 3180
             |  | ||| |              |||             ||   | || |    |  |||
Db       2228 AGAAAGATGGG------------GGATT--------
CAGAGAACAGGAAATTACAG---G 2264


Qy        3181 CAACTTGTACTTGTTTCATCTGGTTTATTACTCTCA----
CCCATAAACAGTAATGACTC 3236
             |    || |||       ||||       |||| |     | | ||| |  || |
Db       2265 CTCGATGCACT-------CCTGG----
CAGCTCTGAGAATACAAAAAAAAAAAAAAAAA 2313


Qy        3237 TCTGACCCTCTGGAAATATGTAATGCTTCCAATCT 3271
               | ||  ||      |||| | | ||
Db       2314 AAAGGCCACATG-----------TGCT--CGAGCT 2335


RESULT 15
US-10-478-914-3/c
; Sequence 3, Application US/10478914
; Patent No. 7335755
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWARA, AKIRA
;  TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED IN NEUROBLASTOMA
;  FILE REFERENCE: 7388-80899
;  CURRENT APPLICATION NUMBER: US/10/478,914
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/05294
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-162775
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-255226
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 417
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 2083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-478-914-3

   Query Match             24.2%;  Score 4714;  DB 1;  Length 2083;
   Best Local Similarity   39.2%;  Pred. No. 0;
   Matches 1256;  Conservative    0;  Mismatches  770;  Indels 1176;
Gaps  181;

Qy        152 GCGGCGGGGGCCGTGCCGGAGCCGCCCAAGGAGGAGCAGCAGCAGGCC----------
CT 201
              ||||| | | ||       || ||| |      ||||| ||   ||||
                                                                     |
Db       2080 GCGGCCGCGACC-------TGCAGCTC------GAGCA-
CATGTGGCCTTTTTTTTTTTT 2035

Qy        202
```

```
GGAGCAGTTCGCCGCCGCTGCAGCGCACAGCACCCCGGTGCGAGGGAGGTCACTGACAAG 261
          |  || ||| |  ||               |||  ||   || | ||| |  ||
                                                                     |
Db      2034 TTTTTATTTTGCCTTC-TTGCT-----------CTGGT----
GGTTAGTCTCCTACTAT 1992


Qy       262 GAACAGGAGTTTGCTGCCAGGGCTGCAAAACAGC-
TCGAATATCAGCAATTAGAAGACGA 320
              ||||  ||  ||| ||       || |     ||| ||   | |||    ||      ||
Db      1991 AAACATGATTTTCCT------TCTTCCCTTCAGAGTC--CTGTCAATCTTT-----
ACTT 1945


Qy       321 TAAACTTTCTCAGAAATCATCTAGCAG-
TAAACTCTCTCGGTCTCCATTAAAGATTGTCA 379
              |    ||||||| |||    | || || ||  |||     | |   | |||| ||| |
Db      1944 TT---TTTCTCATTAATATAC-AGAAGTTATACT---ACAG-
ATACATTCAAGCT----- 1898


Qy       380
AAAAGCCTAAAAGCATGCAGTGCAAAGTGATACTTCTCGATGGATCAGAATATACCTGTG 439
                              |||| | ||| ||   | ||||| ||       |||    |||
                                                                     |
Db      1897 -------------CATG-ACTGCTAA---AAACTTCCTGA--------AATGAGCCT-
TA 1864


Qy       440
ATGTAGAGAAACGCTCCAGAGGACAAGTGCTGTTTGATAAAGTGTGTGAACACTTGAACT 499
              ||            ||   | | | | | |||| |               |||
                                                                     |
Db      1863 AT------------TCATACGAATCATTTCTATTTGTT--------------
CTTTTTT 1830


Qy       500
TGCTAGAGAAAGACTACTTTGGGCTTACGTATCGAGATGCTGAAAACCAGAAGAATTGGT 559
              |  | |||| ||||||        |||||          ||| |||   |||
                                                                     ||
Db      1829 T--TTGAGACAGACT--------CTTAC----------TCTGTCGCCCA-------
GGC 1798


Qy       560 TGGACCCTGCTAAGGAAATAAAAAAACAGGTTCGAAGTGGTGCTTGGCACTTTTCATTTA 619
              ||||  ||| ||  ||        || | |         || ||| |
Db      1797 TGGA--GTGCACTGG-----------CATGAT----------
CTCGGCTC---------- 1771


Qy       620 ATGTGAAATTTTATCCACCAGACCCTGCCCAACTATCTGAAGATATCACCAGG-
TACTAC 678
                           |  || | |||||| ||  |  | ||  |    | |  | | ||
                                                                     |
Db      1770 --------------ACTGCAACCTCTGCCTCACGAGTT--
AGGTCAAGCAATTCTTCTGC 1727


Qy       679 CTCTGCTTGCAGTTGCGAGATGACATCGTGTCCGGAAGGCTGCC-
CTGCTCCTTTGTTAC 737
              ||| || | | | ||     |  | |    ||||   |||||| |    ||| |||
Db      1726 CTCAGCCTCCCGAGGAGCTAGGATTACAGGTCC------
CTGCCACCATGCCTGAGTAAT 1673


Qy       738 CCTGGCCTT---------GCTGGGCTCCTACACTGT---
```

```
CCAGTCAGAGCTCGGAGACTA 785
  |  |   ||            | | |||| |   ||  ||| |   ||| | | |||| | |
Db     1672
TTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTAGCCAAGCTGGTCTCGAATTC-C 1614

Qy      786 TGACC-CAGATGAATGTGGGAGCGATTACATTAGTGAGTTCCGCTTTGCACC-
AAACCAC 843
            ||||| ||| |||                          ||||| ||||  | ||
                                                                    |
Db     1613 TGACCTCAGGTGA--------------------------TCCGCC---
CACCTCAGCCTC 1583

Qy      844
ACTAAAGAACTGGAAGACAAAGTGATCGAGCTGCACAAGAGCCACAGAGGAATGACGCCA 903
              | |||| ||||        |    || |      |  |||||||| |
|||
Db     1582 CC-AAAGTGCTGG--------GATTACGGG-----CGTGAGCCACGGT--------
GCCT 1545

Qy      904 GCAGAAGCAGAGATGCATTTCTTGGAAAA-----
TGCCAAAAAATTATCAATGTATGGGG 958
            |    ||   ||  || |  || |    ||||  |  |  ||| ||||
Db     1544 G-----GCCTCTATTTTTTATTTTAAATACCTTTTGCCCTGAA---
ATCTATGTCC---T 1496

Qy      959 TAGATTTACATCA-
TGCTAAGGACTCAGAAGGGGTAGAAATTATGTTAGGAGTTTGTGCA 1017
                |||| || || |||| |    |||           || | ||    |||||
Db     1495 CTGATTATCAACACTGCTTA----CCAG------------TTTTATT-----
TTTGT--- 1460

Qy      1018
AGTGGTCTGTTGATATATCGCGACCGGCTGCGAATAAACAGATTTGCCTGGCCCAAGGTT 1077
               |||| | |  ||    |    || ||    |   |  | | ||  |  ||
|
Db     1459 --TGGTATTTATTTCATTCAATCCCAGC------TCTACA-
ACTTACCAG---------T 1418

Qy      1078
CTAAAGATTTCATACAAACGGAACAACTTTTACATTAAGATCCGGCCGGGAGAGTTTGAA 1137
            |||| ||||         ||| ||  |||| |    |||  ||  |
|||||
Db     1417 ATAAAAATTT--------GGATCAG---TTACTT---AATCTTGC------
AGTTTCTT 1379

Qy      1138
CAATTTGAAAGCACCATTGGGTTTAAGCTGCCAAACCATCGAGCTGCCAAGCGTTTATGG 1197
            |  ||| ||     ||  || |     | | | |  | | |     | ||||  |
Db     1378 CCTTTTAAA------AATGGAATAATATTATCTATCATATAAAATGCCCAG-----
TTAA 1330

Qy      1198
AAAGTATGTGTTGAGCATCATACATTTTTCAGACTACTGTTACCAGAAGCACCTCCCAAG 1257
               || |||| | | |   || | |    || |  ||| | |  |      |||    |
||
Db     1329 CAAAATATGAACT-
AACACCTACAATGTGCCAGGCACCATTCTAGGGAATAGAATGTAAAT 1271

Qy      1258 AAATTCCTAACCTTGGGTTCC-----AAGTTT-
CGTTATAGTGGCAGGACACAAGCGCAA 1311
               || |||     |||| ||     ||||||| | || ||||| | |||
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```
Db        1270 AAGTTCAAGTTCTTG---
ACCTGAATAAGTTTACATTTTAGTGAGAAGAC---------- 1224


Qy        1312
ACGAGAAGAGCCAGTGCGTTGATAGATCGCCCAGCACCTTACTTTGAACGCTCATCCAGC 1371
                        || || |  | ||| |   | | |      | | |
                     ||||
Db        1223 --------AGACAATAAATCAATAACATGTCC--------ATTATG---------
CCAG- 1190


Qy        1372 AAACGTTATACCATGTCTCGCAG-CTTGGATGGAGC-
ATCAGTGAATGAAAACCATGAAA 1429
                       |  ||| ||  ||||| |  ||      |  ||||| ||||| |  ||       |||
                 ||
Db        1189 -ATAGTTTTA-AATGTCACAAAGAAAAAGGGGGAGCAATCAGATAGTG------
ATGGAA 1138


Qy        1430
TATACATGAAGGATTCTATGTCTGCTGCAGAGGTTGGTACTGGCCAGTACGCCACAACAA 1489
                      ||||           || ||  |||||        ||| |||
                 ||
Db        1137 GTTACA---------------CT-CTAGAGAGGG------TGGACAG-----------
AA 1111


Qy        1490
AAGGCATCTCTCAGACCAACTTGATCACCACTGTGACTCCGGAGAAGAAGGCTGAGGAGG 1549
                      || |  ||||| ||        ||| ||  ||| |   | ||||         || |
Db        1110 AAAGTTTCTCTTAGG------AGATGACATCTG----AACAGAGAT-----
CTAA----- 1071


Qy        1550
AGCGGGACGAGGAAGAGGACAAACGGAGGAAGGGGGAAGAAGTCACGCCCATCTCGGCCA 1609
                       |||      ||| |||||| |                              ||||
Db        1070 ---ATGAC-----TGAGTACAAAC------------------------
CCCA--------- 1051


Qy        1610 TCCAGCACGAGGGAAAGACTGACAGTGAGCGCACGGACACCGCA--
GCCGACGGGGAGAC 1667
                        || |||| |||  |  | ||    || || |||   |  | | |
                 |||
Db        1050 --------ATGGAAAAG--TGATTG-
GTGTGTTGTGAAACAGCAACACAGCCAGTTTGAC 1002


Qy        1668
CACTGCCACTGAGGAGCTAGAAAAAAACTCAAGATGACCTGATGAAACATCAAACCAACAT 1727
                        |        |||| || |   || ||| | |  |  ||| |   ||||||
Db        1001 TA-----GATGAGTAGATCGAAATGACTGAGGTGGGACTGTGG--
TCATCAA-------- 957


Qy        1728
TAGCGAGCTGAAAAGAACCTTCTTAGAAACCTCAACAGACACTGCCGTAACGAATGAATG 1787
                       || || | | || || |  |                            |||
                 ||
Db         956 -AGAGATCAGAGAGGTA--------------------------GCC-------------
TG 936


Qy        1788
GGAGAAGAGGCTTTCCACCTCCCCCGTGCGACTGGCCGCCAGGCAGGAGGATGCCCCCAT 1847
                        |||    |||   |||| || |                     || ||| ||
Db         935 GGA----AGG----CCACATCAC------------------------
```

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AGAATGTCC---- 912


Qy        1848
GATCGAACCACTTGTCCCTGAAGAGAAAATGGAAACCAAGACGGAGTCCAGTGGATAGAG 1907
               |  |  || | |||     ||||  |  | |||   || ||  ||| | | | | ||
Db        911 -TTTGGGCCTC-TGT-----AAGAGCGTTTTGAA---AAAAC--
AGTTCTGAGCAAAGGT 864


Qy        1908
ACGGAACCCACCGTGCACCACCTGCCGCTTAGCACTGAGAAGGTGGTGCAGGAGACCGTG 1967
              |   |   |  | | |         ||  |  |||      |||||        || |
Db        863 TAGTCATTTAACTTG-----ACTTACTCTTT------AGAAG-----------
GATCACT 826


Qy        1968
TTGGTGGAGGAGCGGCGTGTGGTGCACGCGAGTGGGGATGCTTCTTACTCGGCGGGAGAC 2027
               ||||     ||| |||                               |  |  |
 |||||
Db        825 TTGGCTATTGAGTGGC------------------------------
AAACAACTGGAGA- 797


Qy        2028
AGCGGGGATGCTGCAGCACAGCCCGCATTCACAGGCATTAAAGGGAAAGAGGGCTCTGCT 2087
               || ||    |  |               |  ||   |    || | |||    || |||
Db        796 AGTGG--------------------------------TTAGGGGA------
GCACTGT- 777


Qy        2088
TGACGGAGGGGGCTAAAGAGGAAGGAGGGGAGGAGGTCGCTAAAGCTGTCCTGGAACAGG 2147
                         ||||   |   ||||||||          ||||| |  ||||| |
Db        776 ---------GGGCAGGAATAGAAGGAGG------------AAAAGCAG-
ACTGGAGCC-- 741


Qy        2148
AAGAGACAGCCGCTGCTTCCCGTGAGCGACAAGAGGAGCAGAGTGCAGCCATCCACATTT 2207
                      | ||  |  ||||   ||| ||  ||    |||| |   |||
Db        740 -----TAATCCAGTACTTCAGATGA--GAAATGA----CAGATT--
TGCC---------- 704


Qy        2208
CAGAAACTTTGGAACAAAAACCTCATTTTGAGTCCTCAACGGTGAAGACGGAAACCATCA 2267
                        ||| |||      |||||    ||||              |  || |
 |
Db        703 ---------TGGTACA------TCATT-----TCCT---------------
ATCCCTTTA 679


Qy        2268
GTTTTGGCAGTGTTTCACCGGGAGGAGTAAAGCTAGAAATTTCCACAAGAAGTGCCAGTA 2327
               || | | | ||         || ||        |||| |   ||||| |
Db        678 CTTATAACT-TATT---------GGTGT----------
ATTTTTATTTTAAGTGTAAATT 639


Qy        2328
GTTCACACCGAAACCAAAACCATCACATATGAATCATCACAGGTCGATCCAGGCACAGAT 2387
                      ||                    | | ||||| ||| |   |  |||
 |||
Db        638 TTT---------------------ATAAATGAAGCATAATTTGAAGAT--------
TGAT 608
```

```
Qy      2388
CTGGAGCCAGGCGTGCTGATGAGTGCACAGACGATCACATCTGAAACCACCAGTACCACC 2447
              ||    | | | || |                    |||   | ||    ||   |
|
Db      607 ATGTT--CGGACTTG-TGTT------------------TTCTATTATCA-
TGGTGTCT-C 571

Qy      2448
ACCACTACCCACATCACCAAAACTGTGAAAGGGGGCATTTCAGAGACAAGAATTGAGAAG 2507
              ||||  ||   || |     |             ||| |   | ||||  |
Db      570 TCCACATACCTTTTCCCTTTAG----------------TTCTGCTTCT--
TATTGTGC-- 531

Qy      2508
CGAATAGTCATCACGGGGGATGCAGACATTGACCATGACCAGGCGCTGGCTCAGGCAATT 2567
              || |||  |           |      ||| |  | ||   | ||  ||     |
||
Db      530 -------TCCTCAAG------TCTATTTTTGTTCTTTTCC---CTCT-
ACTTCTACTGTT 488

Qy      2568
AAAGAGGCCAAAGAGCAGCACCCTGACATGTCAGTGACCAAAGTAGTGGTCCATAAAGAG 2627
                               ||| ||| ||       || | | ||
|
Db      487 T---------------------TGAACTGTATATGC------TATT--TCTATTT--
TG 460

Qy      2628
ACAGAGATCACACCAGAAGATGGGAGGATTGACCAGAGGAATAACTTAGCTTGCACATG 2687
              |||  | || ||||            || |   | | | | |     | |
Db      459 CCAGGAGTTACCCC--------------CTT---CA----
ATTTTCGTTGTACTCTCT-- 423

Qy      2688
AATGCAGTCATGCAAACCGTTAGGAAAACCAGAGCCTATATGGAGTTCCCTCTTCTAACC 2747
                  ||||| |||||           || | | |||     | |||||||
|
Db      422 ----CAGTCT--CAAAC-----------ACATACCC---ATG-----
CTCTCTTCTGT-C 389

Qy      2748 CAACTGTACTTGT-
ATCTGTCCGTGGAAAATTTCAGTCCAGAAGAATTGACCTTGACCAT 2806
              |  || | | | | | |  |  |  |   ||| | |
||
Db      388 CTTCTCTTCATATCATC--TTCTAGAATTAGTTCTACCCCG----ATTTTC--
TACCAAT 337

Qy      2807
TAATAAAGACACTGGCAGAGAGATCTTCCCATAATAAAGCAATCTGATTCAGCATCACTA 2866
              | ||             |||| ||| ||      | | ||||||||
|
Db      336 TTATTTTAT----------------TTCCAAT----CAGTACATTGATTCAG-----
ATT 302

Qy      2867
AACCGATAATGCATGAAGCAACGATAAAATTACAAAAGAGCAGCATTTTTAATTTTCACA 2926
              | | ||     ||| | | || ||       ||||||||  |
|
Db      301 TATCAAT-----ATGTTTTACCAATTTTAT-------------
CATTTTTTTTGGAGGCT 260
```

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Qy        2927
AAATGTCTCAGTTTTCAGCTATACCTGCTCGTTCATAACCAACAATATAAACCGTGGTCT 2986
                   | | | || |||| | | ||    || ||| || || |         |
|||
Db        259 TGTTATTTAAG-GTTCA--TTTTTCTTGGAGTACAT--CCTTCAGAA--------
GTTCT 213


Qy        2987
CATGTAACACATAAACAATTCATGCCTTTCATAGTTTATTATTATTAAAGTCTAAACAAA 3046
                  |   || |||           |||| | || ||| | ||  ||||
Db        212 ----TTCAGCAAGAAC------------TCATGG-
TTGTTAATCTTTGAGTC-------C 177


Qy        3047
ATTGCAATTTCTTAGGTAACCTTATATTTACAATAAATGAAGATTACCCTCAAATGCTAG 3106
                 |||    |||||| ||      | | || ||  |        || ||||||
||
Db        176 TTTG---TTTCT--GG------TGTTTTAACTTT---------
TTCCCCTCACTCTTGAG 137


Qy        3107
AAGCTGTCTAGGTCCGTCCGGTGTGTCAGATTTCCTCAGATTAGATGTGCCAATAACCAA 3166
                 |   || |||    | | | |||| | |||||||| |
Db        136 TAATAGTTTAG-------CTGGGCATAAAATT---
TCAGATTGG---------------- 103


Qy        3167
GTTTATTCAGTAAACAACTTGTACTTGTTTCATCTGGTTTATTACTCTCACCCATAAACA 3226
                  ||||     |||| | ||||            | ||
Db        102 -------CAGT----TACTTTTCCTTG----------------GCACT---------
ACG 79


Qy        3227
GTAATGACTCTCTGACCCTCTGGAAATATGTAATGCTTCCAATCTTGCTTTGTGTATCTC 3286
                  ||| | |||| |    |||       || | | ||||| || || | |||
||
Db        78 AAGATGCCGCTCCGT-TATCT---------TATTACAGCCAATATTACTAT-
TGTTCCTT 30


Qy        3287 ATTTAATTTGTTCCGGTTAAGG 3308
                   |   |   ||| || |||
Db         29 TGTAGGTAATCTCCAGT--AGG 10



Search completed: March  9, 2010, 15:53:00
Job time : 14.4648 secs
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